OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
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Run on: August 10, 2005, 05:00:04 ; Search time 3121 Seconds
(without alignments)
3063.017 Million cell updates/sec

Title: US-10-660-763-2
Perfect score: 3879
Sequence: 1 MGFSSELCSPQGHGVLQQMQ.........QRPSFSTIYQELQSIRKRHR 752

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2196066 seqs, 635616942 residues

Total number of hits satisfying chosen parameters: 43932132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Db=Pending_Patents_NA_New -QMT=fastap -SUFFIX=rnpn -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10660763 @CGN_1_1_268 @runat_03082005_182825_28664 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=10 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Pending_Patents_NA_New:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	3783.5	97.5	6609	8	US-10-302-689A-149942	Sequence 149942,
	2	2405	62.0	6055	8	US-10-302-689A-149941	Sequence 149941,
	3	1850	47.7	2947	19	PCT-US05-00517-3524	Sequence 3524, Ap
	4	1654	42.6	1400	19	US-11-060-755-796	Sequence 796, App
	5	1654	42.6	1400	19	US-11-060-756-5068	Sequence 5068, Ap
	6	1206.5	31.1	3369	22	US-11-097-143-18926	Sequence 18926, A
	7	1074.5	27.7	1183	22	US-11-136-527-3335	Sequence 3335, Ap
	8	1074.5	27.7	1183	22	US-11-136-527-7431	Sequence 7431, Ap
	9	1057	27.2	600	19	US-11-060-756-3332	Sequence 3332, Ap
	10	1057	27.2	600	19	US-11-060-756-3333	Sequence 3333, Ap
	11	1057	27.2	600	19	US-11-060-756-7604	Sequence 7604, Ap
	12	1057	27.2	600	19	US-11-060-756-7605	Sequence 7605, Ap
	13	1017	26.2	638	23	US-60-680-544-39317	Sequence 39317, A
	14	1017	26.2	638	23	US-60-680-473-39317	Sequence 39317, A
	15	1013	26.1	3198	22	US-11-097-143-24845	Sequence 24845, A
	16	913.5	23.5	1433	23	US-60-669-241-2794	Sequence 2794, Ap
o	17	833	21.5	699	22	US-11-136-527-1734	Sequence 1734, Ap
	18	792	20.4	657	23	US-60-680-544-17507	Sequence 17507, A
	19	792	20.4	657	23	US-60-680-473-17507	Sequence 17507, A
o	20	753.5	19.4	8277	22	US-11-097-143-24844	Sequence 24844, A
o	21	753.5	19.4	28918	22	US-11-097-143-18925	Sequence 18925, A
o	22	740	19.1	798	23	US-60-680-544-19988	Sequence 19988, A
	23	740	19.1	798	23	US-60-680-473-19988	Sequence 19988, A
	24	666.5	17.2	6021	18	US-11-191-644-13	Sequence 13, Appl
	25	664	17.1	600	22	US-11-136-527-5830	Sequence 5830, Ap
	26	655	16.9	6096	18	US-11-191-644-15	Sequence 15, Appl
	27	625	16.1	4158	18	US-11-191-644-19	Sequence 19, Appl
	28	624.5	16.1	3393	23	US-60-699-675-1	Sequence 1, Appl
	29	624.5	16.1	3840	22	US-11-012-067-9	Sequence 9, Appli
	30	624.5	16.1	5434	13	US-10-940-774A-927	Sequence 927, App
	31	623.5	16.1	5744	22	US-11-012-067-10	Sequence 10, Appl
	32	623	16.1	5881	18	US-11-191-644-8	Sequence 8, Appli
	33	622	16.0	3393	11	US-10-491-603-1	Sequence 1, Appli
	34	622	16.0	5384	18	US-11-191-644-7	Sequence 7, Appli
	35	622	16.0	5763	13	US-10-940-774A-3759	Sequence 3759, Ap
	36	618.5	15.9	4221	18	US-11-191-644-17	Sequence 17, Appl
	37	617.5	15.9	5446	23	US-60-659-397-590	Sequence 590, Appl
	38	617.5	15.9	5763	23	US-60-659-397-589	Sequence 589, Appl
	39	609.5	15.7	1937	22	US-11-015-730-19	Sequence 19, Appl
	40	609.5	15.7	2293	22	US-11-097-143-122	Sequence 122, App
	41	609.5	15.7	2422	22	US-11-097-143-26930	Sequence 26930, A
	42	607.5	15.7	3849	18	US-11-191-644-3	Sequence 3, Appli
	43	605.5	15.6	1933	2	PCT-US04-23309-10	Sequence 10, Appl
	44	605.5	15.6	2104	2	PCT-US04-23309-9	Sequence 9, Appli
	45	605.5	15.6	2183	2	PCT-US04-23309-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-10-302-689A-149442
; Sequence 149442, Application US/10302689A
; GENERAL INFORMATION:
;   APPLICANT: Tang, Y. Tom
;   APPLICANT: Asundi, Vinod
;   APPLICANT: Ballinger, Dennis
;   APPLICANT: Labat, Ivan
;   APPLICANT: Leshkowitz, Dena
;   APPLICANT: Liu, Jin
;   APPLICANT: Loeb, Deborah
;   APPLICANT: Montgomery, Julia, R.
;   APPLICANT: Pace, Ann M.
;   APPLICANT: Sheridan, James P.
;   APPLICANT: Drmanac, Radoje T.
;   TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
;   FILE REFERENCE: 502CIP
;   CURRENT APPLICATION NUMBER: US/10/302,689A
;   CURRENT FILING DATE: 2002-11-22

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PRIOR APPLICATION NUMBER: 10/273,573
PRIOR FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: 10/084,643
PRIOR FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/989,660
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 10/014,487
PRIOR FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: 09/952,981
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: 09/922,279
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 09/905,059
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 09/898,888
PRIOR FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: 09/919,002
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2001-01-26
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 158931
SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 149442
  LENGTH: 6609
  TYPE: DNA
  ORGANISM: Homo sapiens
US-10-302-689A-149442

Alignment Scores:
Pred. No.:              2.81e-220        Length:         6609
Score:                  3783.50          Matches:        751
Percent Similarity:     84.29%           Conservative:   0
Best Local Similarity:  84.29%           Mismatches:     1
Query Match:            97.54%           Indels:         139
DB:                     8                Gaps:           2
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US-10-660-763-2 (1-752) x US-10-302-689A-149442 (1-6609)

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Qy      1 MetGlyPheSerGluLeuCysSerProGlnGlyHisGlyValLeuGlnMetGln 20
Db      1 ATGGGCTTCTCTTCGACGTGTGCAGCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG 60

Qy     21 GluAlaLeuArgLeuLeuGluArgLeuArgLysTrpMetAlaGlnArgValLysSer 40
Db     61 GAGGCCGAGCTTCGTCTACTGGAGCGGCATGAGAAAGTGGATGGCCCAGCGGGTCAAGAGT 120

Qy     41 AspArgGluTyrAlaGlyValLeuHisHisMetSerLeuGlnAspSerGlyGlnSer 60
Db    121 GACAGGGAGTATGCAGGACACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGCCAGAGC 180

Qy     61 ArgAlaIleSerProAspSerProIleSerGlnSerProIleAlaGluLeuThrSerGlnThr 80
Db    181 CGGGCCATCAGCCCTGACAGCCCCATCAGTCAGTCTCCGGGCTGAGATCACCATCCAAACT 240

Qy     81 GluGlyLeuSerArgLeuLeuArgGlnHisAlaGluArgGlnHisAlaLeuAsnSerGlyProLeuSer 100
Db    241 GAGGGCCTGAGCCGCCTGCTGCGCCAGCACGCAGAGGATCTGAACCTCAGGGGCCCCTGAGC 300

Qy    101 LysLeuSerLeuLeuIleArgGluArgGlnIleArgLeuArgLysThrTyrSerGluGlnTrp 120
Db    301 AAGCTGAGCCTGCTCATCCGGGAACGACAGATCCGGCTTCGGAAGACCTACAGCGAGCAGTGG 360

Qy    121 GlnIleLeuGlnIleGluLeuThrLysThrHisSerGlnAspIleGluLeuLysSerLeuLysSer 140
Db    361 CAGCAGATCGAGCTGACCAAGACCCACAGCCAGGACATTGAGCTGAAGAGC 420

Qy    141 GlnTyrArgAlaLeuAlaAlaArgAspSerAlaGlnAlaLysArgLysTyrGlnAlaSer 160
Db    421 CAGTACCGAGCTCTGGCACGGGAGCCAAGCGCCAGGAGCCAGC 480

Qy    161 LysAspLysAspArgAspLysLysAlaLysAspLysTyrValArgSerLeuTrpLysLeuPhe 180
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Db    481 AAAGACAAGGACCGTGACAAGGCCAAGGACAAGTATGTGCGCAGCCTGTGGAAGCTCTTT 540
Qy    181 AlaHisAsnArgTyrValLeuGlyValArgAlaAlaGlnLeuHisGlnHisHis 200
Db    541 GCTCACCACAACCGCTATGTGCTGGGCGTGCGGGCTGCGCAGCTACACCAGCACCAC 600
Qy    201 HisGlnLeuLeuProGlyLeuLeuArgSerLeuArgLeuArgLeuHisGlyMetAla 220
Db    601 CACCAGCTCCTGCCTGGGCTGCTGCGGTCACTGCGACTGCGACTGCACGAGGAGATGGCT 660
Qy    221 CysIleLeuLysGlyGluIleGluGlyTyrLeuGlnValSerLeuValAlaAspGlu 240
Db    661 TGCATCCTGAAGGAGGAGATCGAGGAATACCTGGAGATTAGCAGCGTGGTGCAGGAGATGAG 720
Qy    241 ValValAlaIleHisArgGluMetAlaAlaAlaAlaAlaAlaLeuGlnProGluAlaGlu 260
Db    721 GTGGTGGCCATTCACCGGGAGATGGCTGCAGCTGCTGCCGCCATCCAGCCTGAGGGCTGAG 780
Qy    261 TyrGlnGlyPheLeuArgGlnTyrGlySerAlaProAspValProProCysValThrPhe 280
Db    781 TACCAAGGCTTCCTGCGACAGTATGGGTCCGCACCTGATGTCCCACCCTGTGTCACGTTC 840
Qy    281 AspGluSerLeuLeuGluGluGluGlyProLeuGluProGlyGluLeuGlnLeuAsnGlu 300
Db    841 GATGAGTCACTGCTTGAGGAGGGTGAACCGCTGGAGCCTGGGGAGCTCCAGCTGAACGAG 900
Qy    301 LeuThrValGluSerValGlnHisThrLeuThrHisSerValThrAspGluLeuAlaValAla 320
Db    901 CTGACTGTGGAGAGCGTGCAGCACACGCTGACCCTCAGTGCAGATGAGCTGGCTGTGGCC 960
Qy    321 ThrGluMetValPheArgArgGlnGlnMetValThrGlnLeuGlnGlnLeuLeuArgAsn 340
Db    961 ACCGAGATGGTGTTCAGGCGCGCAGGAGATGGTTACGCAGCTGCAACAGAGCTCCGGAAT 1020
Qy    341 GluGluGluAsnThrHisProArgGluArgGluArgValGlnLysArgGlnGlnLysArg 360
Db   1021 GAAGAGGAGAACACCCACCCCAGGGAGCGGGAGCGCGTGCAGCTGCTGGGCAAGAGGCAAGTGCTG 1080
Qy    361 GlnGluAlaLeuGlnGlyLeuGlnLeuValAlaLeuCysSerGlnAlaLysLeuGlnAlaGln 380
Db   1081 CAAGAGGCACTGCAGGGGCTGCAGCTGGTCGCCCTGTGCAGCCAGGCCAAGCTGCAGGCCCAG 1140
Qy    381 GlnGluLeuGlnThrLysLeuGluHisLeuGluGlyLyroGlyGluProProValLeu 400
Db   1141 CAGGAGTTGCTGCAGACCAAGCTGGAGCACCTGGGCGGCCCGGGGGAGCCCCCTGTGCTG 1200
Qy    401 LeuLeuGlnAsnAspAsnArgHisSerThrSerSerSerGluGlnGluArgGlyLyGlyArg 420
Db   1201 CTCCTGCAGGATGACCCACTCCACGTGCTCCTCGGAGCAGGAGCGAGGGGGGAAGG 1260
Qy    421 ThrProThrLeuGlnIleLeuLysSerHisIleSerGlyIlePheArgProLysPheSer 440
Db   1261 ACACCCACGCTGCAGATCCTTAAGAGCCACATCTCAGGAATCTTCAGACCCAAGTTCTCG 1320
Qy    440 --------------------------------------------------- 440
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Qy    440 --------------------------------------------------- 440
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Qy    440 --------------------------------------------------- 440
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Qy    441 ---------------------------AsnLeuTyrArgLeuGlyGlyPheProSer 452
Db   1501 CCCCGGCACTTCATCATCCAGTCCTTGGAATGGCTCACGCCCCTCAGAATGAGGAGGGCTGCT 1560
Qy    161 LysAspLysAspArgAspLysLysAlaLysAspLysTyrValArgSerLeuTrpLysLeuPhe 180
Db   1561 GACCCCGGTGCCCTGCCCTGAGAACCCTACCGACTGGAAGGGGAAGGCGTTTCCTAGC 1620
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RESULT 2
US-10-302-689A-149441
; Sequence 149441, Application US/10302689A
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Asundi, Vinod
; APPLICANT: Ballinger, Dennis
; APPLICANT: Labat, Ivan
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Liu, Jin
; APPLICANT: Loeb, Deborah
; APPLICANT: Montgomery, Julia, R.
; APPLICANT: Pace, Ann M.
; APPLICANT: Sheridan, James P.
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 502CIP
; CURRENT APPLICATION NUMBER: US/10/302,689A
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: 10/273,573
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 10/084,643
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/989,660
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 10/014,487
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: 09/952,981
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/905,059
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/898,888
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/919,002
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 158931
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 149441
; LENGTH: 6055
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-302-689A-149441

Alignment Scores:
Pred. No.:
Score: 2.53e-136
Percent Similarity: 2405.00
Best Local Similarity: 73.05%
Query Match: 73.05%
DB: 62.00%

Length: 6055
Matches: 488
Conservative: 0
Mismatches: 0
Indels: 180
Gaps: 3

US-10-660-763-2 (1-752) x US-10-302-689A-149441 (1-6055)

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           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 ATTCCCTTGCTCATCGACCACCTACTGAGCACCCAGCCCCTCACCAAGAAGAGTGGT 1680

Qy   473 ValValLeuHisArgAlaValAlaProLysAspLysTrpValLeuAsnHisGluAsnLeuVal 492
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GTTGTCCTGCACAGGGCTGTGGCCCAAGACAAGTGGGTGCTGAACCATGAGAACCTGGTG 1740

Qy   493 LeuGlyGluGlnIleGlyArg------------------------------ 499
           |||||||||||||||
Db   1741 TTGGGGTGAGCAGATTGGACGGGGTTCCCCAGCGAGGGTCAAACTCCCAGAGAGCCTGGGTG 1800

Qy   499 --- 499
Db   1801 AGGGGTCCGAACACGGGGCCCCTCACCCAGGGTAGGAAGCAGAATGGGTAGGAAGCGG 1860

Qy   500 ---GlyAsn 501
                                                     |||||
Db   1861 AGAAGAGAACTGCGGGACTGGGAAGGCCGTGTGAGGAGCCCAGACCGTTCAGGGGAAC 1920

Qy   502 PheGlyGluValPheSerGlyArgLeuArgAlaAspAsnThrLeuValAlaValLysSer 521
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 TTTGGCGAAGTGTTCAGGGAGCGACGCCTGCGAGCCGACAACACCCTGGTGGCGGTGAAGTCT 1980

Qy   522 CysArgGluThrLeuProProAspLeuLysAlaLysPheLeuGlnGluAlaArgIleLeu 541
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 TGTCGAGAGACGCTCCCACCTGACCTCAAGGCCAAGTTTCTACAGGAGGCGAGGATCCTG 2040

Qy   542 LysGlnTyrSerHisProAsnIleValArgLeuIleGlyValCysThrGlnLysGlnPro 561
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 AAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCCAGAAGCAGCCC 2100

Qy   562 IleTyrIleValMetGluLeuValGlnGlyGlyAspPheLeuThrPheLeuArgThrGlu 581
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Db   2101 ATCTACATCGTCATGGAGCTTGTGCAGGGGGGCGACTTCCTGACCTTCCTCCGCACCGAG 2160

Qy   582 GlyAlaArgLeuArgValLysThrLeuLeuGlnMetValGlyAspAlaAlaAlaGlyMet 601
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGATGCAGCTGCTGGCCATG 2220

Qy   602 GluTyrLeuGluSerLysCysCysIleHisArgAspLeuAlaAlaArgAsnCysLeuVal 621
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 GAGTACCTGGAGCAAGTGCTGCATCCACCGGACCTGGCTGCCCGGAACTGCCTCGTG 2280

Qy   622 ThrGluLysAsnValLeuLysIleSerAspPheGlyMetSerArgGluGluAlaAspGly 641
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 ACAGAGAAGAATGTCCTGAAGATCAGTGACTTTGGGATGTCCCGAGAGGAAGCTGATGGG 2340

Qy   642 ValTyrAlaAlaSerGlyGlyLeuArgGlyLeuValProValLysTrpThrAlaProGluAla 661
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Db   2341 GTCTATGCAGCTCAGCGGGGCCTCAGACAAGTCCCCGTGAAGTGGACCGCACCTGAGGCC 2400

Qy   662 LeuAsnTyrArgGlyTyrSerGluSerAspValTrpSerPheGlyIleLeuLeuTrp 681
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 CTTAACTACCGGGCCGTACTCCCTCCGAAAGCGACGTGTGGAGCTTTGCATCTTGCTCTGG 2460

Qy   682 GluThrPheSerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnGlnThrArgGlu 701
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 GAGACCTTCAGCCTGGGGGCCTCGGGGCCCTATGAGCCTGCAATCAGCAGACACGGGAG 2520

Qy   702 PheValGluLysGlyGlyArgLeuProGluLeuProCysProAspAlaValPheArg 721
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 TTTGTGGAGAAGGGGGGCCGTCTGCCCGAGCTGCCCTGCCCTGATGCCGTGTTCAGG 2580

Qy   722 LeuMetGluGlnCysTrpAlaTyrGluProGlnGlnArgProSerPheThrIleTyr 741
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 CTCATGGAGCAGTGCTGGGCCTATGAGCCTCAGCAGCGGCCCAGCTTCAGCACCATCTAC 2640

Qy   742 GlnGluLeuGlnSerIleArgLysArgHisArg 752
           ||||||||||||||||||||||||||||
Db   2641 CAGGAGCTGCAGAGCATCCGAAAGCGGCATCGG 2673

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Qy  304 GluSerValGlnHisThrSerValThrAspGluLeuAlaValAlaAlaAlaThrGluMet 323
             |||||||||||||
Db  242 GAGAGCTGCAGCACACG---------------------------------------- 259

Qy  324 ValPheArgArgGlnGluMetValThrArgLeuGlnLeuGlnLeuGluArgAsnGluGlu 343

Db  259 -------------------------------------------------------- 259

Qy  344 AsnThrHisProArgGluArgValGlnIleLeuLeuGlyLysArgGlnValLeuGlnGluAla 363
                                    |||||||||||||||||||||||||||||
Db  260 -----------GTGCAGCTGCTGGGCAAGAGGCAAGTGCTGCAAGAGCA 298

Qy  364 LeuGlnGlyLeuGlnValAlaLeuCysSerGlnHisAlaLysLeuGlnAlaGlnGlnLeu 383
          |||||||||||||||||||||||||||||||||||||||||||
Db  299 CTGCAGGGGCTGCAGGTAGCGCTGTGCAGCCAGCATGCCAAGCTGCAGGCCCAGCAGGAGTTG 358

Qy  384 LeuGlnThrLysLeuGluHisIleSerLeuGluGluHisLysProGlyGluProProValLeuLeuGlnLeuGln 403
          ||||||||||||||||||||
Db  359 CTGCAGACCAAGCTGGAGCACATCTCCCTGTGCTCCTGCTCCTGCAG 418

Qy  404 AspAspArgHisSerSerThrSerSerGluGlnGlnGluGlyGlyArgGluGlyGlyArgThrProThr 423
          ||||||||||||||||||||||||
Db  419 GATGACCGCCACTCCACGTCGTCCGGAGCAGCAGGAGGGGGGAGGACACCCACG 478

Qy  424 LeuGluIleLeuLysSerHisIleSerGlyIlePheArgProLysPheSer---------- 440
          |||||||||||||||||||||||||||||||||||
Db  479 CTGGAGATCCTTAAGAGCCACATCTCAGGAATCTTCCGCCCCAAGTTCTGCTCCCTCCA 538

Qy  440 ---------------------------------------------------------- 440

Db  539 CCGCTGCAGCTCATTCCGGAGGTGCAGAGCCCCTGCGAGAGCCCCTGTGGTACCATGGG 598

Qy  440 ---------------------------------------------------------- 440

Db  599 GCCATCCCGAGGGGCAGAGGTGGCTGAGCTGGTGCACTCTGGGGACTTCCGTGGTGCGG 658

Qy  440 ---------------------------------------------------------- 440

Db  659 GAGAGCCCAGGGCAAGCAGCAGAGTACGTGCTGTCGTCGTGTGGGATGGTCTGCCCCGCAC 718

Qy  440 ---------------------------------------------------------- 440

Db  719 TTTCATCATCCAGTCCTTGGATGGCTCAGCGCCCCTCAGCAATGAGGCTGCTGACCCGGG 778

Qy  441 -------------AsnLeuTyrArgLeuGluGlyLysGluGlyPheProSerIleProLeu 455
                       ||||||||||
Db  779 TCCCCTGCCCCAGAACCTGTACCGGCTGGAGGGGAAGGGGAGGCCTTTCCTAGCATTCCTTTG 838

Qy  456 LeuIleAspHisLeuSerThrGlnGlnProLeuThrLysLysGlySerGlyValValLeu 475
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  839 CTCATCGACCACCTACTGAGCACCCAGCAGCCCCTCACCAAGAAGAGTGGTGTTGTCCTG 898

Qy  476 HisArgAlaValProLysLysProAspHisLysAsnHisGluAspLeuArgLeuGlyGlu 495
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  899 CACAGGGCTGTCCCAAGGACAAGTGGGTGCTGAACCATGAGGACCTGAGGCTGGGTGGGGAG 958

Qy  496 GlnIleGlyArg--------------------------------------------- 499
          |||||||||||
Db  959 CAGATTGGACGGGTTCCCAGCGAGGGTCAAACTCCCAGAGAGCCTGGGTGAGGGGTCCG 1018

Qy  499 ---------------------------------------------------------- 499

Db 1019 AACACGGGGGCCCCTCACCCAGGGGTAGGAGGCAGAATGGGTAGGAGCGGAGGAGAGAA 1078

Qy  500 -------------------------------------------GlyAsnPheGlyGlu 504
                                                      ||||||||||
Db 1079 CTGCCGGGACTGGGAAGGCCGTGTAGGAGCCCAGGCCCAAGACCGTTTCAGGGGAACTTTGCGAA 1138

Qy  505 ValPheSerGlyArgLeuArgAlaAlaAspAsnThrLeuValAlaValLysSerCysArgGlu 524
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db 1139 GTGTTCAGCGGACGGCACCCTGCGGGCCACAACACCCCTGGTGCGGGTGAAGTCTTGTCGAGAG 1198
```

```
Qy  525 ThrLeuProProAspLeuGlyLysAlaLysPheLeuGlnGluAlaArgIleLeuLysGlnTyr 544
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db 1199 ACGCTTCCCACCTGACCTCAAGGCCAAGTTTCTACAGGAGGCGGGGATCCTGAAGCAGTAC 1258

Qy  545 SerHisProAsnIleValArgLeuIleGlyValCysThrGlnLysGlnProIleTyrIle 564
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1259 AGCCACCCCAACATCGTGCGTCTCATTGGTGTCTCCACCCAGAAGCAGCCCATCTACATC 1318

Qy  565 ValMetGluLeuValGlnGlyGlyAspPheLeuThrPheLeuArgThrGluGlyAlaArg 584
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1319 GTCATGGAGCTTGTGCAGGGGGGCGACTTCCTGACCTTCCTCCGCACGGAGGGGGCCCGC 1378

Qy  585 LeuArgValTyrThrLeuLeuGlnMetValGlyAspAlaAlaAlaGlyMetGluTyrLeu 604
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1379 CTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGATGCAGCTGCTGGCGATGGAGTACCTG 1438

Qy  605 GluSerLysCysIleHisArgAspLeuAlaAlaArgAsnCysLeuValThrGluLysGlu 624
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1439 GAGAGCAAGTGCTGCATCACCGGGACCTGGCTGCTGGTGACAGAGAAG 1498

Qy  625 AsnValLeuLysIleSerAspPheGlyMetSerArgGluGluAlaAspGlyValTyrAla 644
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1499 AATGTCCTGAAGATCAGTGACTTTGGAATGTCCCGAGAGGAAGCTGATGGGGTCTATGCA 1558

Qy  645 AlaSerGlyGlyLeuArgGlnValProValLysTrpThrAlaProGluAlaLeuAsnTyr 664
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1559 GCCTCAGGGGGCCTCAGACAAGTCCCCGTGAAGTGGACCGCACCTGAGGCCCTTAACTAC 1618

Qy  665 GlyArgTyrSerSerGluSerAspValTrpSerPheGlyIleLeuLeuTrpGluThrPhe 684
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1619 GGCCGCTACTCCTCCGAAAGCGACGTGTGGAGCTTTGGCATCTTGCTCTGGGAGACCTTC 1678

Qy  685 SerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnGlnThrArgGluValGlu 704
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1679 AGCCTGGGGGCCTCCCCCTATCCCAACCTCAGCAATCAGCAGACACGGGAGTTTGTGGAG 1738

Qy  705 LysGlyGlyArgLeuProCysProGluLeuCysProAspProGlyValPheLeuMetGlu 724
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1739 AAGGGGGGGCGCCTGCCCTGCCCTGAGCTGTGTCCTGATCCGGTTCAGGGTCATGGAG 1798

Qy  725 GlnCysTrpAlaTyrAlaTyrGluProGlyGlnArgProSerPheSerThrIleTyrGlnGluLeu 744
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1799 CAGTGCTGGGCCTATGCCTATGAGCCTGGGCAGCGGCCCAGCTTCAGCACCATCTACCAGGAGCTG 1858

Qy  745 GlnSerIleArgLysArgHisArg 752
          ||||||||||||||||||||||||
Db 1859 CAGAGCATCCGAAAGCGGCATCGG 1882
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Alignment Scores:

Pred. No.:	7.79e-103	Length:	2947
Score:	1850.00	Matches:	382
Percent Similarity:	63.86%	Conservative:	148
Best Local Similarity:	46.02%	Mismatches:	210

us-10-660-763-2.rnpn

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Query Match:      47.69%       Indels:   90
DB:                             Gaps:     11

US-10-660-763-2 (1-752) x PCT-US05-00517-3524 (1-2947)
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Qy    1 MetGlyPheSerGluLeuCysSerProGlnGlyHisGlyValLeuGlyValLeuGlnMetGln 20
          |||||||||  |||:::|||                     |||    :::::|||
Db  314 ATGGGGTTTGGGAGTGACCTG------AAGAATTCACATGAAGCTGTGCTAAAATTGCAA 367

Qy   21 GluAlaGluLeuArgLeuHisGluGlyMetArgLysTrpMetAlaGlnArgValLysSer 40
          :::   |||||:::|||||  |||     ||| :::::  ||||||
Db  368 GACTCGGGAATTACGGTTACTGAAACAGTGAAGAAATTTATGGCCCTGAGAATAAAAAGT 427

Qy   41 AspArgGluTyrAlaGlyLeuLeuHisHisMetSerLeuArgGlnSer 60
          |||||:::||| ||||||||  ||| :::|||||
Db  428 GATAAAGAATATGCATCTACTTTACAGAACCTTTGTAATCAAGTGATAAGGAAAGTACT 487

Qy   61 ArgAlaIleSerProAspSerProIleSerGlnSerTrpAlaGluIleThrSerGlnThr 80
          :::::     |||  :::::::|||||   |||  :::
Db  488 GTTCAAATGAATTATGTCAGCAATGTATCCAAGTCTTGGCTACTTATGATTCAGCAAACA 547

Qy   81 GluGlyLeuSerArgLeuArgGlnHisAlaGluAsnLeuAsnSerGlyProLeuSer 100
          |||||:::|||||:::|||::||:::|:::|||||  |||    ::::|||
Db  548 GAACAACTTAGCAGAATCATGAAGACACATGAGAGGACCTAAATTCGGACCCTTACAC 607

Qy  101 LysLeuSerLeuLeuIleLeuArgGluArgGlnLeuArgLysThrTyrSerGluGlnTrp 120
          :::::||| :::|||:::|||:::|::||:::||||||||||:::|||||||::|||
Db  608 AGGCTCACCATGATCATCAAAGACAGGCCAGGTGAAGAGAAAGTTTTATAGGTGTTCAT 667

Qy  121 GlnLeuGluGlnGlnGluLeuThrLysHisSerGlnAspIleGluLeuLysLysSer 140
          |||||:::||| |||||:::||||||:::|||  ||||| :::||:::
Db  668 CAGCAGATAGAGGCGGAAATGATCAAGGTTACAAAGCACAGAGTTAAAATCC 727

Qy  141 GlnTyrArgAlaLeuAlaArgAspSerAlaGlnAlaLysArgLysTyrGlnGlnAla--- 159
          |||:::     :::::       |||   ||::::|||||::||
Db  728 AGCTATAGACAGTTAATAAACAGAAAAATATCTGCCAAGAAAATATAAAGAAGCTTTA 787

Qy  160 SerLysAspLysAspArgGlnLysLysLysLysAspLysLysTyrValArgSerLeuTrpLysLeu 179
          :::||| :::|||||  :::|||  :::    |||  :::::: |||
Db  788 GCTAAAGGGAAGAAAACCGAAAGCGAAAGGCCCAAGAACCAGAATAACCAAAGCCACAATGAAACTT 847

Qy  180 PheAlaHisHisAsnArgTyrValLeuGlyValArgAlaAlaAlaAlaAlaLeuGlnLeuHisHisGlnHis 199
          ||||||:::|||       :::::|||:::|||||||     |||||||||
Db  848 CATGTATTGCATAATCAGTATGTATTGGCACGAAAGGGCACAGTCTCATCAGAATCAG 907

Qy  200 HisHisGlnLeuLeuLeuLeuProGlyLeuLeuArgSerLeuArgSerLeuAspAspLeuHisGluHisMet 219
          ||||||     |||  |||||||||||:::|||  :::||||||
Db  908 TATTATGACACACCAATGTTCCTTGCTTCTGGACTCTCTTCAGAAGATGTCAAGAAGAAATG 967

Qy  220 AlaCysIleLeuLeuLysGluLeuGluGlyIleLeuGluLeuIleSerSerLeuValGlnAspLysProGln 239
          |||||:::|||||:::     :::::   :::|||||:::
Db  968 GCTAAAGCAACTAAAAGGTCTATTTTGATGAATACAGCCCAGATAACCAGTCTCGTTACCAGAG 1027

Qy  240 GluValAlaIleAlaHisArgGluMetAlaAlaAlaAlaAlaAlaArgIleArgProGluAla 259
          ||||| :::||| :::::  ||||||
Db 1028 GAAATAGTGAATGAATGCCATAAAGAGATTCAGTTGAACAGATAGACCCTAGCACA 1087

Qy  260 GluTyrGlnPheLeuArgGlnTyrGlySerAlaProAspValProProCysValThr 279
          |||||:::||| |||::||:::     :::   :::
Db 1088 GAATATAATAATTCATTAGATGTTCACAGAACAAGCCGTGCTAAAGACCAAGAGAAAATTGAG 1147

Qy  280 PheAspGluSerLeuLeuGluGlyGluLeuIleLeuSerGlyGlyLeuGluLeuLeuAsn 299
          ||||||   :::||| ||:::|||||
Db 1148 TTTGATACTTCCTTACTAGAAGAAATCTTCAGGCAAATGAAAATTATGTGGAAT 1207

Qy  300 GluLeuThrValGluSerValGlnHisThrLeuThrSerValThrAspGluValAlaVal 319
          ||||||   ::||:::::|||  :::|||::|||||
Db 1208 AATTTAACAGCAGAAAGTTTGACAGATAATGTTAGCAGAACTTATACAG 1267

Qy  320 AlaThrGluMetValPheArgArgGlnGluMetValThrGlnLeuGlnGlnGlnLeuGluLeuArg 339
          :::::||  ||| |||||:::|||::   :::
Db 1268 ACACAGCAGATGCTTGTAAACAGGAGGGGCCGTCCTGGAGCTAGGAGAGAGAATT--- 1324
```

```
Qy  340 AsnGluGluAsnThrHisProArgGluArg------------ValGlnLeuLeuGly 355
          :::::   ||:::::                        ::::
Db 1325 -----GAGGAGTGCTCTCTAAGACCTGTGAAAAGAAGTCTGATATTGTGCTTCTGCTAAGC 1378

Qy  356 LysArgGlnValLeuGlnGluAlaLeuGlnGluLeuGlnLeuValAlaLeuValAlaLeuSerGlnAla 375
          |||||:::|||||:::::|||:::||||||:::|||
Db 1379 CAAAAACAGACACTAGAAGAGCTGAAACAGTCAGTCAGCTGACACTGAGGCA 1438

Qy  376 LysLeuGlnAlaGlnHisGluGlnLeuLeuLeuGlnLnThrLysLeuGluHisLeuGlyProGlyGlu 395
          |||  :::||||||    |||||| :::|||:::
Db 1439 AAGTTTACGACACAGAAAGAATTACTAGACAAAAGTACAAGAAAATGAAGGGAAAGAG 1498

Qy  396 ProProProValLeuLeuLeuGlnArgHisSerThrSerSerGluGlnGlu 415
          |||||:::     ||||||    :::|||:::|||
Db 1499 CCACCTCCAGTAGTAAATTATGGAAGATGCACGATCAGTTACATCTATGGAAGAAAG 1558

Qy  416 ArgGluGlyGlyArgThrProThrLeuGluIleLeuSerHisLysSerHisIleSerGlyIlePhe 435
          :::     ::::||||||||::|||::||||:::|||||
Db 1559 AGGCTATCCAAATTTGAGTCATCCGTCATTCAATTGCTGAATAATT 1609

Qy  436 Arg---ProLys------------------------------------PheSer 440
          |||||                                        |||||
Db 1610 AGGTCTCCAAAGTCTGCACTGGCTCCTTCAACATTCCTCTGATACGATCCCATAGTGAG 1669

Qy  440 440
Db 1670 AAGCCCTTGGCAGAACAGGACTGGTACCACGGTGCAATTCCCAGAATAGAAGCCCAAGAT 1729

Qy  440 440
Db 1730 CTATTAAAACAACAAGGAGACTTCTTGGTGCCAGAGAGTCATGGGAAACCTGGTGAATAT 1789

Qy  441 ----Asn 441
            :::
Db 1790 GTCCTTTCTGTATATTCTGATGCAACAAAGGAGACACACTTTATCATCAATTGTTGATAAT 1849

Qy  442 LeuTyrArgLeuGluGlyGlyPheProSerIleProLeuLeuIleLeuAspHisLeuLeu 461
          |||:::   |||::|||  ||||||||||:::
Db 1850 CTATATCGATTTGAAGGACCACTGGTTTTCAAACATTCCTCAACTTATAGATCATCACTAT 1909

Qy  462 SerThrGlnLeuGlnProLeuThrLysLysSerGlyValValLeuHisHisArgGlyValAlaValProLys 481
          :::::|||||      ||||||:::|||||||||:::|||
Db 1910 ACAACAAAACAGGTCATCACTAAGAAGTCAGGTGTAGTTCTGCTGAATCCTATTCCTAAG 1969

Qy  482 Asp---LysTrpLeuAsnHisGluAsnHisGluGlnIleGlyArgGly 500
            :::||||||:::|||    |||   :::
Db 1970 GATAAGAAATGGTTCCAATCACGAGAGTGCCAATTGGGAATTACTGGGCCAAGGGG 2029

Qy  501 AsnPheGlyGluValPheSerGlyArgLeuArgAlaAspAsnThrLeuValAlaValLys 520
          |||||   |||:::|||||||::::::   :::
Db 2030 AATTTTGTGAAGTATATAAGGGCATATTAAAG---GATAAAACTGCTGTTGCCGTTAAA 2086

Qy  521 SerCysArgGluThrLeuProProAspLeuLysProAspLeuLysProGlyProGluAla 540
          :::||  |||:::|||||||:::|||   :::||
Db 2087 ACATGTAAAGAAGATCTTCCTCCAGACTGAAAATAAAATTTTTACAAGGAACCAAAATT 2146

Qy  541 LeuLysGlnTyrSerHisProAsnIleValArgLeuIleGlyValCysThrGlnLysGln 560
          |||  :::|||||:::||:::||||||
Db 2147 CTCAAGCAATACGATCATCCCAATATTGTCAAACTTATAGGGCGTTGCACACAAGACAG 2206

Qy  561 ProIleTyrIleValMetGluLeuValGlnGlyGlyAspPheLeuThrPheLeuArgThr 580
          |||::|||||:::     :::|||:::
Db 2207 CCTATCTACATCATTATGGAACTGGTTCCAGGAGGTGATTTCCTTCCTTTTCTGAGAAAG 2266

Qy  581 GluGlyAlaArgLeuArgValLysThrLeuLeuGlnMetValGlyAspAlaAlaAlaGlyTyr 600
          |||||:::   |||::|||||   :::||||||
Db 2267 AAGAAGGATGAAATAAAACTCAAACAATTAGTGAAGTTTCATTAGAGTGCTGCTTCTGGT 2326

Qy  601 MetGluTyrLeuGluSerCysCysIleHisArgAspLeuAlaAlaArgAsnCysLeu 620
          :::::||||||:::||||||
Db 2327 ATGTCCTATCTCGAGAGTAAAAACTGTATACACAGGGATCTGCTGCAGAAACTGCCTG 2386

Qy  621 ValThrGluLysAsnValLeuLysIleSerAspPheGlyMetSerArgGlyAlaAsp 640
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Db  241 GATAACCTGTACCGACTGGAAGGGAAGGCTTCCCAGCATTCCTTGCTCATCGACCAC 300
        ||||||||||||||||||||||||||||||||||||||||||||||| |||:||||
Qy  460 LeuLeuSerThrGlnGlnProLeuThrLysLysGlyValValLeuHisArgAlaAla 479

Db  301 CTACTGAGCACCAGCCAGCCCTCACCAAGAGAGTGGTGTTGTTCTGCACAGGGCTGTG 360
        ||||||||||||||||||||||||||||||||||||||||||||||||
Qy  480 ProLysAspLysTrpValLeuAsnHisGluAspLeuValLeuGlyGluGlyIleGlyArg 499

Db  361 CCCAAGGACAAGTGGTGCTGAACCATGAGGACCTGGTTGTGGGTGAGCAGATTGGACGG 420
        ||||||||||||||||||||||||||||||||||||||||||||||||
Qy  500 GlyAsnPheSerGlyValPheSerGlyArgLeuArgLeuValAlaAspAsnThrLeuValAlaVal 519

Db  421 GGGAACTTTGGCGAAGTGTTCAGCGGACGACCGCGACAACACCCTGGTGCGGGTG 480
        ||||||||||||||||||||||||||||||||||||||||||||
Qy  520 LysSerCysArgGluThrLeuProProAspLysLysAlaLysPheGlnGluAlaArg 539

Db  481 AAGTCTTGTCGAGAGACGCTCCCACCTGACCTCAAGGCCAAGTTTCAGGAAGCGAGG 540
        ||||||||||||||||||||||||||||||||||||||||||||||
Qy  540 IleLeuLysGlnTyrSerHisProAsnIleValArgLeuIleGluValCysThrGlnLys 559

Db  541 ATCCTGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCCAGAAG 600
        |||||||||||||||||||||||||||||||||||||| :::
Qy  560 GlnProIleTyrIleValMetGluLeuValGlnGlyGlyAspPheLeuThrPheLeuArg 579

Db  601 CAGCCCATCTACATCGTCATGGAGCTTGTGCAGGGGGGCGACTTCCTGACCTTCCTCCGC 660
        ||||||||||||||||||||||||||||||||||||||||||||||||
Qy  580 ThrGluLeuAlaArgLeuArgValLysThrLeuLeuGlnMetValGlyValCysThrGlnLysCys 619

Db  661 ACGGAGGGGGCCCGCCTGCGGGTGAGACTCTGCGAGATGGTGGGGGATGCAGCTGCT 720
        |||||||||||||||||||||||||||||||||||||||||||||
Qy  600 GlyMetGluTyrLeuGluSerLysCysIleHisArgAspLeuAlaAlaArgAsnCys 639

Db  721 GGCATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACCTGGCTGCTCGGAACTGC 780
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  620 LeuValThrGluLysAsnValLeuValIleSerAspPheGlyMetSerArgGluGluAla 659

Db  781 CTGGTGACAGAGAAGAATGTCCTGAAGATCAGTGACTTTGGGATGTCCCGAGAGGAAGCY 840
        ||||||||||||||||||||||||||||||||||||||||||||
Qy  640 AspGlyValTyrAlaAlaSerGlyValTyrLeuArgGlnValProValLysTrpThrAlaPro 679

Db  841 GATGGGGTCTATGCAGCCTCAGGGGGCTCAGACAAGTCCCGGGAAGTGAAGTGGACCGCACCT 900
        ||||||||||||||||||||||||||||||||||||||||||||||
Qy  660 GluAlaLeuAsnTyrGlyArgTyrSerSerGluSerAspValTrpSerPheGlyIleLeu 699

Db  901 GAGGGCCTTAACTACGGCCGCTACTCCTCCGAAAGCGACGTGTGGAGCTTTGGCATCTTG 960
        |||||||||||||||||||||||||||||||||||||||||||||
Qy  680 LeuTrpGluThrPheSerLeuGlyAlaSerProTyrProAsnLeuSerArgAsnGlnInThr 699

Db  961 CTCTGGGAGACCTTCAGCCTGGGGGCCTCGCCCTACCCCAATCAATCAGCAATCAGCAGACA 1020
        ||||||||||||||||||||||||||||||||||||||||||||||
Qy  700 ArgGluPheValGluLysGlyGlyArgLeuProCysProGluLeuCysProAspAlaVal 719

Db  1021 CGGGAGTTTGTGGAGAAGGGGGGCCGTCTGCCCTGCCCCGAGCTGTGTCCTGATGCCGTG 1080
         |||||||||||||||||||||||||||||||||||||||
Qy  720 PheLeuMetGluGlnCysTrpAlaTyrGlnProGlyTrpArgProSerPheSerThr 739

Db  1081 TTCAGGCTCATGGAGCAGTGCTGGGCCTATGAGCCTGGGCAGCGGCCCAGCTTCAGCACC 1140
         |||||||||||||||||||||||||||||||||
Qy  740 IleTyrGlnGluLeuGlnSerIleLeuArgLysArgHisArg 752

Db  1141 ATCTACCAGGAGCTGCAGAGCATCCGAAAGCGGCATCCG 1179
```

RESULT 5
US-11-060-756-5068

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Db  2387                |||     |||              |||||||||||||
        GTAGGTGAAAATAACGTTCTGAAAATCAGTGACTTTGGAATGTCTCGTCAAGAGGATGGT 2446
Qy  641 GlyValTyrAlaAlaSerGlyValTyrLeuArgGlnValProValLysTrpThrAlaProGlu 660

Db  2447 GGCTTAAAGCAGATTCCCATTAAAATGGACAGCACCAGAA 2503
        ||||::::||| |::::|||
Qy  661 AlaLeuAsnTyrGlyArgTyrSerSerGluSerAspValTrpSerPheGlyIleLeuLeu 680

Db  2504 GCTCTCTAATTATGGGAGATACAGTTCTGAGAGCGACGTGTGGAGCTTTCGGCATCCTCCTC 2563
        ||||::|::|:|||||
Qy  681 TrpGluThrPheSerLeuGlyAlaSerProTyrProAsnLeuSerArgAsnGlnInThrArg 700

Db  2564 TGGGAGACCTTCAGCTTAGGAGTGCCCCTACCCCGGAATGACAAATCAGCAGGCGACG 2623
        |||||::|||        :::||||
Qy  701 GluPheValGluLysGlyGlyArgLeuProCysProGluLeuCysProAspAlaValPhe 720

Db  2624 GAGCAAGTGGAAAGAGGGTACCGAATATCAGCCCCCAGCATTGCCCAGAGGACCATTTTT 2683
        ||||||:||:        :::||
Qy  721 ArgLeuMetGluGlnCysTrpAlaTyrGlnProGlyGlnArgProSerPheSerThrIle 740

Db  2684 AAAATTATGATGAAGTGTTGGGATTATAAACCGCCCCCAAGTTCAGTGAACTT 2743
        ||:::|
Qy  741 TyrGlnGluLeuGlnSerIleArgLysArg 750

Db  2744 CAGAAAGAGCTCACGGTCATCAAGAAGAAA 2773
```

RESULT 4
US-11-060-756-796

Alignment Scores:
Pred. No.:   3.12e-91   Length: 1400
Score: 1654.00   Matches: 323
Percent Similarity: 82.19%   Conservative: 0
Best Local Similarity: 82.19%   Mismatches: 0
Query Match: 42.64%   Indels: 70
DB: 19   Gaps: 1

```
US-10-660-763-2 (1-752) x US-11-060-756-796 (1-1400)

Qy  430 HisIleSerGlyIlePheArgProLysPheSer------------------------- 440
        |||||||||||||||||
Db  1   CACATTCAGGAATCTTCCGCCCCCAAGTTCTCGCCCCCTCCACCGCTCCACGCTCATTCCG 60

Qy  440 -------------------------------------------------- 440

Db  61  GAGGTCGCAGAAGCCCCTGCGCATGCAGCAGCTGTGTACCATGGGGCCATCCCGAGGGCAGAG 120

Qy  440 -------------------------------------------------- 440

Db  121 GTGGCTGAGCTGCTGGTGCACTCTGGGACTTCCTGGTGCGGCGGGAGCCGGAGCAAGCAG 180

Qy  440 -------------------------------------------------- 440

Db  181 GAGTACGTGCGTCTGCGTGCTGGGATGGTCTGCCCCGGCACTTCATCATCCAGTCCTTG 240

Qy  441 ---AsnLeuTyrArgLeuGluGluGlyGlyPheProSerIleProLeuLeuIleAspHis 459
```

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; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5068
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-5068

Alignment Scores:
Pred. No.:              3.12e-91        Length:                 1400
Score:                  1654.00         Matches:                 323
Percent Similarity:     82.19%          Conservative:              0
Best Local Similarity:  82.19%          Mismatches:                0
Query Match:            42.64%          Indels:                   70
DB:                                     Gaps:                      1

US-10-660-763-2 (1-752) x US-11-060-756-5068 (1-1400)

Qy    430  HisIleSerGlyIlePheArgProLysPheSer-----------------------     440
                |||||||||||||||||||||||||||
Db      1  CACATCTCAGGAATCTTCCGCCCAGTTCTCGCTCCCTCCACCGCTGCAGCTCATTCCG      60

Qy    440  ---------------------------------------------------------     440

Db     61  GAGGTGCAGAGCCCCTGCAGCTCGTGGTACCATGGGCCATCCCGAGGGCAGAG        120

Qy    440  ---------------------------------------------------------     440

Db    121  GTGGGCTGAGCTGCTGGTGCACTCTCGGGGACTTCCTGTGCGGGAGAGCCAGGCAAGCAG     180

Qy    440  ---------------------------------------------------------     440

Db    181  GAGTACGCGTGCTGTCGGTCGTGGGATGGTCTGCCCCGGCACTTCATCATCCAGTCCTTG     240

Qy    441  ---AsnLeuTyrArgLeuGluGlyGluGlyPheProSerIleProLeuLeuIleAspHis     459
                  ||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  GATAACCTGTACCGACTGGAGGGCGAAGGCTTTCCTAGCATTCCTTTGCTCATCGACCAC     300

Qy    460  LeuLeuSerThrGlnGlnProLeuThrLysSerGlyValValLeuHisArgAlaVal     479
                |||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  CTACTGAGCACCCAGCAGCCCCTCACCAAGAAGAGTGGTGTTGTCCTGCACAGGGCTGTG     360

Qy    480  ProLysAspLysTrpValLeuAsnHisGluAspLeuValLeuGluGlnIleGlyArg     499
                |||||||||||||||||||||||||||||||||||||||||||||
Db    361  CCCAAGGACAAGTGGGTGCTGAACCATGAGGACCTGGTGTTGGGTGAGCAGATTGGACGG     420

Qy    500  GlyAsnPheGlyGluValPheGlyArgLeuArgLeuAlaAspAsnThrLeuValAlaVal     519
                ||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  GGGAACTTTGGCGAAGTGTTCGGACGCCTGCGCGAGCCGGACAACACCCTGGTGGCCGTG     480

Qy    520  LysSerCysArgGluTyrLeuGlyProProAspLeuLysAlaLysPheLeuGlnAlaArg     539
                ||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  AAGTCTTGTCGTGAGGAGACGCTCCCACCTGACCTCAAGGCCAAGTTTCTACAGGAGCGAGG     540

Qy    540  IleLeuLysGlnTyrSerHisProAsnIleValArgLeuIleGlyValCysThrGlnLys     559
                ||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  ATCCTGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCCAGAAG     600

Qy    560  GlnProIleTyrIleValMetGluLeuValGlnGlyGlyAspPheLeuThrPheLeuArg     579
                ||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  CAGCCCATCTACATCGTCATGGAGCTTGTGCAGGGGGCGACCTTCCTCCCGC        660

Qy    580  ThrGluGlyAlaArgLeuArgValLysThrLeuGlnMetValGlyAspAlaAlaAla     599
                ||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  ACGGAGGGGGCCCGCCTGCGGGTGAAGACTCTGCTCGAGATGGTGGGGGATGCAGCTGCT     720

Qy    600  GlyMetGluTyrLeuGluSerLysCysIleHisArgAspAspLeuAlaAlaArgAsnCys     619
                ||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  GGCATGGAGTACCTGGAGAGCAAGTGCATCCACCGGGACCTGGCTGCCCGGAACTGC        780

Qy    620  LeuValThrGluLysAsnValLeuLysIleSerAspPheGlyMetSerArgGluGluAla     639
                ||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    781  CTGGTGACAGAGAAGAATGTCCTGAAGATCAGTGACTTTGGGATGTCCCGAGAGGAAGCY     840

Qy    640  AspGlyValTyrAlaAlaSerGlyValGlyLeuArgLeuAlaProValLysTrpThrAlaPro     659
                |||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  GATGGGGTCTATGCAGCCTCAGGGGTCCCCAGACAAGTCCCGTGAAGTGGACCGCACCT     900

Qy    660  GluAlaLeuAsnTyrArgGlyTyrSerArgGluSerAspValTrpSerPheGlyIleLeu     679
                ||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  GAGGCCCCTAACTACGGCGCGCTACTCCTCCGAAGCGACGTGTGGAGCTTTGGCATCTTG     960

Qy    680  LeuTrpGluThrPheSerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnGlnThr     699
                |||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  CTCTGGGAGACCTTCAGCCTGGGGGCCTCCCCATCCCAACCTCAGCAATCAGCAGACA     1020

Qy    700  ArgGluPheValGluLysGlyGlyArgLeuProGluCysProLeuGluProAspProAlaVal     719
                ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  CGGGAGTTTGTGGAGAAGGGGGCCGTCTGCCCTGCCCTGGAGCTGTGTCCTGATGCCGTG     1080

Qy    720  PheArgLeuMetGluGlnCysTrpAlaTyrGluProGlyGlnArgProSerPheSerThr     739
                |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  TTCAGGCTCATGGAGCAGTGCTGGGCCTATGAGCCTGGGCAGCGGCCCCAGCTTCAGCACC     1140

Qy    740  IleTyrGlnGluLeuGlnSerIleArgLysArgHisArg     752
                |||||||||||||||||||||||||||||||||
Db   1141  ATCTACCAGGAGCTGCAGAGCATCCGAAAGCGGCATCGG     1179
```

```
RESULT 6
US-11-097-143-18926
; Sequence 18926, Application US/1109714 3
; GENERAL INFORMATION:
;  APPLICANT: Venter, J. Craig
;  APPLICANT:  et al.
;  TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
;  TITLE OF INVENTION:  ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
;  TITLE OF INVENTION:  DROSOPHILA GENES.
;  FILE REFERENCE: CL000728
;  CURRENT APPLICATION NUMBER: US/11/097,143
;  CURRENT FILING DATE: 2005-04-04
;  PRIOR APPLICATION NUMBER: 60/157,832
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: 60/160,191
;  PRIOR FILING DATE: 1999-10-19
;  PRIOR APPLICATION NUMBER: 60/161,932
;  PRIOR FILING DATE: 1999-10-28
;  PRIOR APPLICATION NUMBER: 60/164,769
;  PRIOR FILING DATE: 1999-11-12
;  PRIOR APPLICATION NUMBER: 60/173,383
;  PRIOR FILING DATE: 1999-12-28
;  PRIOR APPLICATION NUMBER: 60/175,693
;  PRIOR FILING DATE: 2000-01-12
;  PRIOR APPLICATION NUMBER: 60/184,831
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: 60/191,637
;  PRIOR FILING DATE: 2000-03-23
;  NUMBER OF SEQ ID NOS: 43008
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 18926
;  LENGTH: 3369
;  TYPE: DNA
;  ORGANISM: DROSOPHILA
US-11-097-143-18926

Alignment Scores:
Pred. No.:              1.46e-63        Length:                 3369
Score:                  1206.50         Matches:                 290
Percent Similarity:     52.52%          Conservative:            138
Best Local Similarity:  35.58%          Mismatches:              300
Query Match:            31.10%          Indels:                   87
DB:                     22              Gaps:                     14

US-10-660-763-2 (1-752) x US-11-097-143-18926 (1-3369)

Qy      1  MetGlyPheSerSerGluLeuCysSerProGlnGlyHisGlyValLeuGlnGlnMetGln     20
```

```
Db                                                            ||||   AATGGCAGCATTATATCCAACGGCAGCAACACATCCAACGCATTCAGTCAACAAGGAT 1404
                                                                        LeuGlnAlaGlnGln------
370         :::::::                                         :::: :::                                          381
Qy  AlaLeuCysSerGlnAlaLys

1405 AGCCTATGCCGCCAGTGAGACAGGACCTAATGCACTGGCGTGCCAGGAGAAGCAGAAACAG 1464
Db   -----GluLeuGlnThrLysLeuGluHisLeuGlyProGlyGluProPro---           397
382                                                                    :::
Qy

1465 AAGCTGGTGACATGACCAAGTGCGCCTGAACAGGTGGATGCGGAGGAGTGCCCTCC 1524
Db   ----------ProValLeuLeuGlnAspAspArgHisSerThrSerSerGlu       413
398            ||||| ::                :::                         
Qy   ------ProValLeuLeuGlnAspAspArgHisSerThrSerSerGlu

1525 GGTTGCGACCGATGACCTCACCCTGGAGCAGCAGAACTTCATCGAGAATGGCTATAACAACGAA 1584
Db                                                                     415
414   GlnGlu-
Qy   CAGCAGAATCGCTCTCCACAAATCGTCCCGTTTACGAGGAGGAAGGAATGGTTCCATGGCGTT 1644
1585                                                                   ArgGlu 417

1645 CTGCCGCCGGAGGAGTGGTTCGATTGCTGCTGAATAACGATGTGACTTCCTGGTCCGCGAA 1704
Db   HisIleSer 432
418  GlyGlyArgThrProThrLeuGluIleGluIleLeuLysSer-
Qy

1705 ACGATTCGAAACGAGGAGGACCAGATTGTGCTCACTTGTCTGTTGGAATGGCCATAAGCAC 1764
Db   GlyIlePheArgProLysPheSerAsnLeuTyrArgLeuGluGlyGlyPheProSer 452
433  TTCATTGTCCAGACCACCGGAGAGGTAATTTCCGGTCGAGGGGACCACCATTGCCAGC
Qy

1765 ATCCAGGAGCTGATCATGCATCAGTATCACTCGGAATTGCCAGTGACCGTGAAATCGGGA 1824
Db   IleProLeuLeuIleAspHisLeuSerThrGlnInProLeuThrLysLysSerGly 472
453  GCCATACTCCGACGACCCGTTGCCGGAGCGCTGGGAGCTGAGCAACGATGATGTGGTA
Qy

1825 GCCATACTCCGACGACCCGTTGCCGGAGCGCTGGGAGCTGAGCAACGATGATGTGGTA 1884
Db   ValValLeuHisArgAlaValAlaProLysAspLysTrpValLeuAsnHisGluAspLeuVal 492
473
Qy

1885 CTTCTCGGAGACGGATTGGTCGGGGAAACTTTGGGAGTGCTACAAGGCCAAACTGAAGTCC 1944
Db   LeuGlyGluGlnIleGlyLysArgGlyAsnPheGlyGluValPheSerGlyArgLeuArgAla 512
493
Qy

1945 ACCAAAACTGGATCGGTGGCTGTCAAAACTGTCAAGCAGCCCGACGAACAGAAGCGT 2004
Db   AspAsnThrLeuValAlaValLysSerCysArgGluThrLeuProAspLeuLysSerAla 532
513
Qy

2005 AAATTCCTACAGGAAGGGCCATCCTCAAGCAATACGATCATCCAAATATCCTAAAATTG 2064
Db   LysPheLeuGlnGluLeuAlaArgIleLeuLysLysGlnTyrSerHisProAsnIleValArgLeu 552
533
Qy

2065 ATTGGGCATTGTGTCGAGAAGCAGCAGCCCATCATGATGATTCATGGAATTGGTGTCGGTGGT 2124
Db   IleGlyValCysThrGlnInProIleTyrIleValMetGluGlnInGlyGly 572
553
Qy

2125 TCGCTTTTTAACTTATTATTACGCAAGAACTCCAATGGCCTTCACCACTGCCAACAAATGGGC 2184
Db   AspPheLeuThrPheArgThrGluArgGlyAlaGlyValTyrAlaLeuSerGlyValValThrLeuGlnGln 592
573
Qy

2185 ATGTGCAGAGATGCGGGGCAGGCATGGCGATATCTGGAGTCCAAAAACTGCATTCATCGC 2244
Db   MetValGlyAspAlaAlaAlaGlyMetGluTyrLeuLysLeuCysIleHisArg 612
593
Qy

2245 GATCTCGGCGGCCGTAATTGTGTCGTGAGAGATCTCCGATTTC 2304
Db   AspLeuAlaAlaArgAsnCysValThrGlyLeuGlnAsnValLeuIleSerAspPhe 632
613
Qy

2305 GGAATGTCTCGCGAGGAGAGAA-----TATATAGTTCCGATGGCATGAAAACAAATA 2364
Db   GlyMetSerArgGluGluArgGluGluGlyMetSerArgGluGluArgGluGlu 652
633
Qy

2365                                                                  2418
Db   GlyMetSerArgGluGluArgGluGlu
Qy

2419 CCTGTGAAGTGGACAGCTCCCGAGGGCCTTGAATTCCGCAAGTACACTTCGTTGTGCGAT 2478
Db   ProValTrpThrAlaProGluAlaLeuAsnTyrGlyTyrSerGluSerAsp 672
653
Qy
```

```
Db  ||||||||||||||   |||  ATGGGCTTCTCATCGACCCTTCCAAAGTCGCGGCCGCCCCAGAGGCGCTGATCGTCCGCCAG 375
316
21  GluAlaGlnLeuLeuArgLeuLeuGlyLysMetLeuGlyTrpMetAlaGlnLysArgValLysSer 40
Qy  ::::|||||||:||  :::    :::   :::
376 GATGCGGAACTTCCGGCTAATGGAGACAATCCATCCAGATGAAGGCCAAGTGC 435

436 GACAAGGAGTACGCC 480
Db  AspArgGluTyrAlaGlyLeuLeuHisHisMetSerLeuGlnAspSerGlyGlyGlnSer 60
41            ------ATCAGCTGACCGCTGTGGCCCAGAGGGT
Qy  :::::::

481 CTCAAGATCGATCGGCTGACGAAGTGCAAGGCAGCCTGACCCGATCTCCAAATCCTGCGATCC 540
Db  ArgAlaIleSer-------ProAspSerProIleSerGlnSerTrpAlaGlu
61            ||||||||||  :::                                75
Qy

541 IleThrSerGlnThrGluGlyLeuLeuSerArgLeuArgLeuArgGlnHisAlaGluAspLeuAsn 95
Db
76  TACATGGATGAACTGACCACCAGGCAAACAGTTCAAGTTCAACGGCAGCAGTGGAG 600
Qy

601 GTC--GTCTCGCGATAAGTTGACCCCACCTCTCGCAGGACAAACGGAAGGCCAGAAAGGCC 657
Db  SerGlyProLeuSerLeuLeuIleArgGluArgGlnLeuArgLeuArgLysThr 115
96
Qy

658 TACCAGGAGGACATGCCAAGATCCGCAGCACGCGCTGAATCATCTCACCGACGAGTGGTG 717
Db  TyrSerGluGlnTrpGlnInLeuGlnInGlnInGlnLeuThrLysThrHisSerGlnAsplle 135
116
Qy

718 CGCAAG---AAATCTGAATACCCAAAAACATTGGAGGGCTACAAGGCGCTGCCGCCACGCGC 774
Db  GluLysLeuLysSerGlnInTyrArgAlaLeuAlaArgAspSerArgLeuGlnAlaLysArgLys 155
136
Qy

775 TTCGGAGAACTACATAAAGGCACCACCGGTCGCGAAGCTGGACGATGTGCGT 834
Db  TyrGlnGlu------AlaSerLysLysAspArgAspLysLysAlaLys 169
156
Qy

835 GACAAGTATCAGAAGGCCTGCGACCTCACAGCGACCGGAGATCTCACACAAGTACGTCGTGTCC 894
Db  AspLysTyrValArgSerLeuArgPheAlaHisHisArgTyrLeuGly 189
170
Qy

895 ATCACCGAAGCCCATCAAGTGCGGAGAGGACTTCGCAACGTCTTGCTGCCGGGACTGCTG 954
Db  ValArgAlaAlaAlaGlnLeuHisHisGlnHisHisGlnInLeuLeuLeuGlyLeuProGlyLeuLeu 209
190
Qy

955 GAGCATCAGCAGTTCCGTTCAGATAGAGACGGCTCATCCAGGAG 1014
Db  ArgSerLeuGlnAspLeuHisGluHisGluMetAlaCysIleLeuLeuLysGluLeuGlnGlu 229
210
Qy

1015 GCGGGCCCAGTATGGCGACCTCACGGCCGACAAGTACAAGGAGATCCAGAAGGCCATTGAC 1074
Db  TyrLeuGluIleSerSerValGlnAspGluValAlaIleHisArgGluMetAla 249
230
Qy

1075 ACTGTGATAGGGACGAGCAATCAATCCGACCGGAGAGTACAGCCGAGTTCACCGAGAAATACAAA 1134
Db  AlaAlaAlaAlaArgIleGlnInProGluAlaGluTyrGlnInPheLeuArgThrGlnInTyrGlyGly 269
250
Qy

1135 ACCTCTCCACAACACCGTGCTCTTCCAGTTCGATGAGACGGCTCATCCAGGAT----- 1188
Db  SerAlaProAspValProProCysValThrProPheGluAspGluThrThrLeuLeuGlyGluGluGlyGlu 289
270
Qy

1189 -----ATTCCCGGCAAATTGACAGTGGACAACCTC------ACG 1236
Db  ProLeuGluProGlyGluLeuGlnLeuLeuAsnGluLeuThrValGluSerValGlnInHisThr 309
290
Qy

1237 GTGGGACTGGCTGCGTAATCGTCTCCAGGAACTGGCAGAGGAGCCGTCAGGGATTGCCAGGAG 1296
Db  LeuThrSerValThrArgValGlnAsplLeuGluAlaValAlaValAlaThrGluMetValPheGluArgGlnInGlyGly 329
310
Qy

1297 AAG------ 1344
Db  ------CAGATGAAGATGATCGAGCATGTGAATGGTGGCTCCCGGTGGCC 349
330 MetValThrGlnLeuLeuGlnInGlyLeuLeuGluLeuArgGluAsnGluGluGluAsnThrHisProArgGlu
Qy

1345                                                    369
Db  ArgValGlnLeuLeuLysLysArgGlnInValLeuLeuGlnInAlaLeuLeuGlnInGlyLeuGlnInVal
350
Qy  :::::::
```

RESULT 7

```
Qy  673  ValTrpSerPheGlyIleLeuLeuTrpProGluThrPheSerLeuGlyAlaSerProTyrPro  692
         |||||| ||||::::::|:|:::||||| |||||||   ||||||  :::||||||
Db 2479  GTGTGGTCCATGGCATACTGATGTGGGAGATCTTCCCAAGGGCGACACACCCTACTCC  2538

Qy  693  AsnLeuSerAsnGlnThrArgGluPheValGluLysGlyGlyArgLeuProCysPro  712
         :::::||| ::: ||||||| :::||| |||:||||||
Db 2539  GGCATGACCAACTCCAGAGCCAGAGACGCCGATCGATACGGACAAGCCAAGCCCG  2598

Qy  713  GluLeuCysProAspAlaValPheArgLeuMetGluGlnCysTrpAlaTyrGluProGly  732
         :::
Db 2599  AAGAGCACGCCCGAGGAGATGTACCGACTAGCTCCAGTGCTGGGCAGCCGACGCCGAA  2658

Qy  733  GlnArgProSerPheSerThrIleTyrGlnLeuGlnSerIle  747
         ||||| :::::
Db 2659  TCCCGACCGCCATTCGATGAGATCTACAATGTGGTGATGCACTG  2703
```

RESULT 7
US-11-136-527-3335
; Sequence 3335, Application US/11136527
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3335
; LENGTH: 1183
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3335

Alignment Scores:

Pred. No.:	
Score:	5.34e-56
Percent Similarity:	79.10%
Best Local Similarity:	65.27%
Query Match:	27.70%
DB:	22
Length:	1183
Matches:	203
Conservative:	43
Mismatches:	62
Indels:	3
Gaps:	3

US-10-660-763-2 (1-752) x US-11-136-527-3335 (1-1183)

```
Qy  441  AsnLeuTyrArgLeuGluGlyGlyPheProSerIleProLeuLeuIleAspHisLeu  460
         |||||||| |||||||  :::||||| :::||||||
Db   37  AATCTATATCGATTTGAGGGCACCGGCTTTTCAAATATCCCTCAACTTATAGATCACCAC  96

Qy  461  LeuSerThrLysSerGlyValValLeuHisArgAlaValPro  480
         ||||| ||||||||  :::||||||
Db   97  TTCAATACAAAGCAAGTCATCACCAAGAAGTGGGGGTGGTTCTGTCGAATCCTATTCCA  156

Qy  481  LysAsp--LysTrpValLeuAsnHisGluAsnGlyLeuValLeuValGluGlyIleGlyArg  499
         |||||   ::: |||||||  :::||:::
Db  157  AAGGATAAGAAATGGGTTCTCAATCATGAAGAGATGTTTCATTGGGAGAATTACTGGGCAAG  216

Qy  500  GlyAsnPheGlyValPheSerGlyValArgLeuArgAlaAspAsnThrLeuValAlaVal  519
         ||||||||:::  |||| ||||::::::  ||||||||
Db  217  GGGAATTTTGGTGAGGTGTACAGGGCACACTGAAG--GATAAAACCCCTGTTGCTGTT  273

Qy  520  LysSerCysArgGluThrProLeuProAspLeuLysAlaLysPheLeuGlnAlaLeuArg  539
         ::: ||||| :::||||::||| ||||||||:::
Db  274  AAAACGTGCAAGGAAGACACCTGCCTCAGGAGACTAAAAATAAGTTTTTACAGGAAGCCAA  333

Qy  540  IleLeuLysGlnTyrSerHisProAsnIleValArgLeuIleGlyValCysThrGlnLys  559
         |||||||:::||||||  ||||| |||||||
Db  334  ATTCTCAAGCAATATGATCACCCAATATTGTCAAACTTATAGGCGTGTGCACACAAAGA  393

Qy  560  GlnProIleTyrIleValMetGluLeuValGlnGlyGlyAspLeuLysAspPheLeuLeuArg  579
         |||||||:::
```

RESULT 8

```
Db  394  CAGCCTGCTCACATCATTATGGAACTGGTCCCAGGAGGTGATTTTCTGTCCTTTCTGAGG  453

Qy  580  ThrGluGlyAlaArgLeuArgValLysThrLeuLeuLeuGlnMetValGlyAspAlaAlaAla  599
         ||||| :::|||||| |||||:::  :::||||||
Db  454  AAGAGGAAGGACGACCTAAAGTTGAAGCAGTTGGTAGCAGTTTTCCTTGGACGGTTGCTGCT  513

Qy  600  GlyMetGluTyrLeuGluSerLysCysIleLeuHisArgAspLeuAlaAlaArgAsnCys  619
         ||||| :::|||||| :::||||||
Db  514  GGCATGGCGTATCTCGAGGGCAAGAACTGCATTCACAGGGACCTGGCTGCACGGAACTGC  573

Qy  620  LeuValThrGluLysAsnValLeuLysIleSerAspPheGlyMetSerArgAspGluAla  639
         ||||| :::||||||:::
Db  574  CTGGTAGGTGAAAATATACTCTGAAAATCAGTGACTTTGGSAYGWSKCGGCAAGAGAGAC  633

Qy  640  AspGlyValTyrAlaAlaSerGlyLeuGlyValGlnValProValLysTrpThrAlaPro  659
         ||||| :::|||||| ||:::
Db  634  GGTGGAGTGTATTCATCTTCT---GGCTTAAAGCAGATTCCCATTAARTGGACAGCACCA  690

Qy  660  GluAlaLeuAsnTyrGlyArgTyrSerSerGluSerAspValTrpSerPheGlyIleLeuLeu  679
         ||||| :::|||||| ::::::
Db  691  GAAGCACTGAATTATGGGAGATACAGCTCTGAAAGTGACGTGTGGAGCTTCGGCATCCTG  750

Qy  680  LeuTrpGluThrPheSerLeuGlyAlaSerProTyrProAsnLeuSerAsnLeuGlnGlnThr  699
         ||||| :::|||||| ||||::::::
Db  751  CTCTGGGAGACTTTCAGCCTGGGAGTCTGCCTGTCCGTACCYTGGWTGACAAACCAGCAAGCA  810

Qy  700  ArgGluPheValGluLysGlyGlyArgLeuProCysProGluLeuCysProAspAlaVal  719
         |||| ||||||  :::||||||
Db  811  CGGGAACAAGTGACGTGAGAGGGTATCGGATGTCAGCCCCACAGAACTGTCCCGRGGAAATT  870

Qy  720  PheArgLeuMetGluGlnCysTrpAlaTyrGluProGlyGlnArgProSerPheSerThr  739
         |||||| :::|||||| ||||::::::
Db  871  TTTACAATCATGATGCTGGATTACAAGCCTGAAAACCGCTGAAAACCGCTCAAGTTCAGTGAC  930

Qy  740  IleTyrGlnLeuGlnSerIleArgLysArg  750
         :::|||||| :::||:::
Db  931  CTTCACAAAGAGCTCMCGGCCCATCAAGAAGAAA  963
```

RESULT 8
US-11-136-527-7431
; Sequence 7431, Application US/11136527
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7431
; LENGTH: 1183
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-7431

Alignment Scores:

Pred. No.:	
Score:	5.34e-56
Percent Similarity:	79.10%
Best Local Similarity:	65.27%
Query Match:	27.70%
DB:	22
Length:	1183
Matches:	203
Conservative:	43
Mismatches:	62
Indels:	3
Gaps:	3

US-10-660-763-2 (1-752) x US-11-136-527-7431 (1-1183)

```
Qy  441  AsnLeuTyrArgLeuGluGlyGlyPheProSerIleProLeuLeuIleAspHisLeu  460
         |||||||| |||||||  :::||||| :::||||||
Db   37  AATCTATATCGATTTGAGGGCACCGGCTTTTCAAATATCCCTCAACTTATAGATCACCAC  96

Qy  461  LeuSerThrLysSerGlyValValLeuHisArgAlaValPro  480
         ||||| ||||||||  :::||||||
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Wed Aug 10 16:17:25 2005   us-10-660-763-2.rnpn

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;        LENGTH: 600
;        TYPE: DNA
;        ORGANISM: Homo sapiens
US-11-060-756-3332

Alignment Scores:
Pred. No.:                              Length:              600
Score:                  3.04e-55       Matches:             199
Percent Similarity:     1057.00        Conservative:          0
Best Local Similarity:  100.00%        Mismatches:            0
Query Match:            100.00%        Indels:                0
DB:                     27.25%         Gaps:                  0
                        19

US-10-660-763-2 (1-752) x US-11-060-756-3332 (1-600)

Qy    554  GlyValCysThrGlnLysGlnProIleTyrIleValMetGluLeuValGlnGlyGlyAsp  573
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  GGTGTCTGCACCCAGAAGCAGCCCATCTACATCGTCATGGAGCTTGTGCAGGGGGGCGAC   60

Qy    574  PheLeuThrPheLeuArgThrGluGlyAlaArgLeuValLysThrLeuLysLeuGlnMet  593
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  TTCCTGACCTTCCTCCGCACGGAGGGGGCCCGCCTGGTGAAGACTCTGCTGCAGATG  120

Qy    594  ValGlyAspAlaAlaAlaGlyMetGluTyrLeuGluSerLysCysIleHisArgAsp  613
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  GTGGGGGATGCAGCTGCTGGCATGGAGTACCTGGAGAGCAAGTGCATCCACCGGGAC  180

Qy    614  LeuAlaLeuArgAsnCysLeuValThrGluLysAsnValLeuLysIleSerAspPheGly  633
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  CTGGCTCTGCGCAACTGCCTGGTGACAGAGAAGAATGTCCTGAAGATCAGTGACTTTGGG  240

Qy    634  MetSerArgGluValAlaAlaAspGlyValTyrAlaAlaSerGlyGlyLeuArgGlnValPro  653
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  ATGTCCCGAGAGGAAGCTGATGGGGTCTATGCAGCCTCAGGGGGCCTCAGACAAGTCCCC  300

Qy    654  ValLysTrpThrAlaProAlaLeuAsnTyrSerGluSerAspVal  673
           |||||||||||||||||||||||||||||||||||||||||||||
Db    301  GTGAAGTGGACAGCCCCTGAGGCCTTAACTACGGCCGCTACTCCTCCGAAAGCGACGTG  360

Qy    674  TrpSerPheGlyIleLeuLeuTrpGluThrPheSerLeuGlyAlaSerProTyrProAsn  693
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  TGGAGCTTTGGCATCTTGCTCTGGGAGACCTTCAGCCTGGGGGCCTCCCCCTATCCCAAC  420

Qy    694  LeuSerAsnGlnGlnThrArgGluPheValGluLysGlyGlyArgLeuProGlu  713
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  CTCAGCAATCAGCAGACACGGGAGTTTGTGGAGAAGGGGGGCCGTCTGCCCCAGAG  480

Qy    714  LeuCysProAspAlaValPheArgLeuMetGluGlnCysTrpAlaTyrGluProGlyGln  733
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  CTGTGTCCTGATGCCGTGTTCAGGCTCATGGAGCAGTGCTGGGCCTGGGAGCCTGGGCAG  540

Qy    734  ArgProSerPheThrIleTyrGlnLeuGlnLeuGlnSerIleArgLysArgHisArg  752
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  CGGCCCAGCTTCAGCACCATCTACCAGCTGCAGAGCATCCGAAAGCGGCATCGG  597
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RESULT 10
US-11-060-756-3333
;   Sequence 3333, Application US/11060756
;   GENERAL INFORMATION:
;   APPLICANT: Wyeth
;   APPLICANT: Mounts, William Martin
;   TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
;   TITLE OF INVENTION: Target Genes
;   FILE REFERENCE: AM101083 (031896-042000)
;   CURRENT APPLICATION NUMBER: US/11/060,756
;   CURRENT FILING DATE: 2005-02-18
;   NUMBER OF SEQ ID NOS: 303284
;   SOFTWARE: PatentIn version 3.2
;   SEQ ID NO 3333
;   LENGTH: 600
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-060-756-3333

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Db     97  TTCAATACAAAGCAAGTCATCACCAAGAGTCGGGGTGGTTCTGCTGAATCCTATTCCA  156
              :::|||::|||        :::|||||||||||||||||||

Qy    481  LysAsp---LysTrpValLeuAsnHisGluValGlyGlnIleGlyArg  499
              |||||   :::|||  |||||||||||||  :::
Db    157  AAGGATAAGAAATGGGTTCTCAATCATGAAGATGTTTCATTGGGAGAATTACTGGGCAAG  216

Qy    500  GlyAsnPheGlyGluValPheSerGlyTyrArgLeuArgAlaAspAsnThrLeuValAlaVal  519
              ||||||||  :::|||::|||  |||::|||  |||:||
Db    217  GGGAATTTTGGTGAGGTGTTACAAGGGCACACTGAAG---GATAAACCCCTGTTGCTGTT  273

Qy    520  LysSerCysArgGluThrGluLeuProProAspLeuLysAlaLysPheLeuGlnGlnAlaArg  539
              :::|||  :::||||||||    ::|||||||  |||:::
Db    274  AAAACGTGCAAGGAGACCGAGCTGCCTCAGGAACTAAAAAATAAAGTTTTACAGGAGCCAAA  333

Qy    540  IleLeuLysGlnTyrSerHisProAsnIleValArgLeuIleGlyValCysThrGlnLys  559
              ::|||:::|||        :::|||||||  ::|||
Db    334  ATTCCTAAGCAATATGATCACCCCATATTGTCAAACTTATAGGCGTGTGCACACAAAGA  393

Qy    560  GlnProIleTyrIleValMetGluLeuValGlnGlyGlyAspPheLeuThrPheLeuArg  579
              |||||||||||||||||||||||||||:::||||||||::|||
Db    394  CAGCCCTGTCTACATCATTATGGAACTGGTCCAGGAGGTGATTTTCGTCCTTTCTGAGG  453

Qy    580  ThrGluGlyAlaArgLeuValLysThrLeuLysLeuGlnMetValGlyAspAlaAlaAlaAla  599
              ||||||  :::||||||||||||||||||||||||
Db    454  AAGAGGAAGGACGAGCTAAGTTGAAGCAGTTGGTGAGGTTTTCCTTGACGGTTGCTGCT  513

Qy    600  GlyMetGluTyrLeuGluSerLysCysIleHisArgAspLeuAlaLeuArgAsnCys  619
              ||||||  :::||||||||||  :::|||
Db    514  GGCATGCTGTATCTCGAGGGCAAGAACTGCATTCACAGGGACCTGGCTGCACGGAACTGC  573

Qy    620  LeuValThrGluLysAsnValLeuLysIleSerAspPheGlyMetSerArgGluValAla  639
              ||||||        :::|||||||||||  :::
Db    574  CTGGTAGGTGAAAATAATACTCTGAAAATCAGTGACTTTGGSAYGWSKCCGCAAGAGAC  633

Qy    640  AspGlyValTyrAlaAlaSerGlyGlyLeuArgGlnValProValLysTrpThrAlaPro  659
              |||:::|||  :::|||    ::|||||||  |||
Db    634  GGTGGAGTGTATTCATCTTCT--GGCTTAAAGCAGATTCCCATTAARTGGACAGCACCA  690

Qy    660  GluAlaLeuAsnTyrGlyArgTyrSerSerGluSerAspValTrpSerPheGlyIleLeuLeu  679
              |||||||||||  :::|||    ::|||||||  |||
Db    691  GAAGCACTGAATTATGGGAGATACAGCTCTGAAAGTGACGTGTGGAGCTTTCGGCATCCTG  750

Qy    680  LeuTrpGluThrPheSerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnGlnThr  699
              ||||||  :::|||        :::|||
Db    751  CTCTGGGAGACTTTCAGCCTGGGAGTCTGTCCGTACCYTGGGWTGACAAACCAGCAAGCA  810

Qy    700  ArgGluPheValGluLysGlyGlyArgLeuProGluCysProAspAlaValPheArgLeuMet  719
              |||||||  :::|||    ::|||||||
Db    811  CGGGAACAAGTGGAGAAGGGGTATCCGGATGCTCAGCCCCACAGAACTGTCCCGRGGAAATT  870

Qy    720  PheArgLeuMetGluGlnCysTrpAlaTyrGluProGlySerPheSerThr  739
              |||  :::||||||
Db    871  TTTACAATCATGAGAAGTGCTGGGATTACAAACCGCCCTAAGTTCAGTGAC  930

Qy    740  IleTyrGlnLeuGluLeuGlnSerIleArgLysArg  750
              |||  :::||||||
Db    931  CTTCACAAAGAGAGCTCMCCGGCCATCAAGAAGAAA  963
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RESULT 9
US-11-060-756-3332
;   Sequence 3332, Application US/11060756
;   GENERAL INFORMATION:
;   APPLICANT: Wyeth
;   APPLICANT: Mounts, William Martin
;   TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
;   TITLE OF INVENTION: Target Genes
;   FILE REFERENCE: AM101083 (031896-042000)
;   CURRENT APPLICATION NUMBER: US/11/060,756
;   CURRENT FILING DATE: 2005-02-18
;   NUMBER OF SEQ ID NOS: 303284
;   SOFTWARE: PatentIn version 3.2
;   SEQ ID NO 3332

Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 27.25%   Indels: 0
DB: 19   Gaps: 0

US-10-660-763-2 (1-752) x US-11-060-756-7604 (1-600)

Qy 554 GlyValCysThrGlnLysGlnProIleTyrIleValMetGluLeuValGlnGlyGlyAsp 573
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GGTGTCTGCACCCAGAAGCAGCCCATCTACATCGTCATGGAGCTTGTGCAGGGGGGCGAC 60

Qy 574 PheLeuThrPheLeuArgThrGluGlyAlaArgLeuAlaArgValLysThrLeuLeuGlnMet 593
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TTCCTGACCTTCCTCCGCACGGAGGGGCCCCGCCTGGCGCGCGTGAAGACTCTGCTGCAGATG 120

Qy 594 ValGlyAspAlaAlaAlaGlyMetGluTyrLeuGluSerLysCysCysIleHisArgAsp 613
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 GTGGGGGATGCAGCTGCTGGCATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGAC 180

Qy 614 LeuAlaAlaArgAsnCysLeuValThrGluLysLysAsnValLeuLysIleSerAspPheGly 633
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 CTGGCTGCTCGGAACTGCCTGGTGACAGAGAAGAATGTCCTGAAGATCAGTGACTTTGGG 240

Qy 634 MetSerArgGluGluAlaAspGlyValTyrAlaAlaSerGlyGlyLeuArgGlnValPro 653
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 ATGTCCCGAGAGGAAGCTGATGGGGTCTATGCGGCCTCAGGGGGCCTCAGACAAGTCCCC 300

Qy 654 ValLysTrpThrAlaProGluAlaLeuAsnTyrGlyArgTyrSerSerGluSerAspVal 673
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 GTGAAGTGGACCGCACCTGAGGCCCTTAACTACGGCCGCTACTCCTCCGAAAGCGACGTG 360

Qy 674 TrpSerPheGlyIleLeuLeuTrpGluThrPheSerLeuGlyAlaSerProTyrProAsn 693
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 TGGAGCTTTGGCATCTTGCTCTGGGAGACCTTCAGCCTGGGGGCCTCCCCCATCCCAAC 420

Qy 694 LeuSerAsnGlnInThrArgGlnHisPheValGluLysGlyLysArgLeuProCysProGlu 713
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 421 CTCAGCAATCAGCAGACACGGGAGTTTGTGGAGAAGGGGCGGCCGTCTCGCCCTGCCCAGAG 480

Qy 714 LeuCysProAspAlaValPheArgLeuMetGluGlnCysTrpAlaTyrGluProGlyGln 733
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 481 CTGTGTCCTGATGCCGTGTTCAGGCTCATGGAGCAGTGCTGGGCCTATGAGCCTGGGCAG 540

Qy 734 ArgProSerPheSerThrIleTyrGlnGluLeuGlnSerIleArgLysArgHisArg 752
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 541 CGGCCCAGCTTCAGCACCATCTACCAGGAGCTGCAGAGCATCCGAAAGCGGCATCGG 597

Alignment Scores:
Pred. No.:
Score: 3.04e-55
                         1057.00
Percent Similarity: 100.00%   Length: 600
Best Local Similarity: 100.00%   Matches: 199
Query Match: 27.25%   Conservative: 0
DB: 19   Mismatches: 0
                                        Indels: 0
                                        Gaps: 0

Alignment Scores:
Pred. No.:
Score: 3.04e-55   Length: 600
                         1057.00   Matches: 199
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 27.25%   Indels: 0
DB: 19   Gaps: 0
                                         LENGTH: 600

US-10-660-763-2 (1-752) x US-11-060-756-3333 (1-600)

Qy 554 GlyValCysThrGlnLysGlnProIleTyrIleValMetGluLeuValGlnGlyGlyAsp 573
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GGTGTCTGCACCCAGAAGCAGCCCATCTACATCGTCATGGAGCTTGTGCAGGGGGGCGAC 60

Qy 574 PheLeuThrPheLeuArgThrGluGlyAlaArgLeuAlaArgValLysThrLeuLeuGlnMet 593
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TTCCTGACCTTCCTCCGCACGGAGGGGCCCCGCCTGGCGCGCGTGAAGACTCTGCTGCAGATG 120

Qy 594 ValGlyAspAlaAlaAlaGlyMetGluTyrLeuGluSerLysCysCysIleHisArgAsp 613
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 GTGGGGGATGCAGCTGCTGGCATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGAC 180

Qy 614 LeuAlaAlaArgAsnCysLeuValThrGluLysLysAsnValLeuLysIleSerAspPheGly 633
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 CTGGCTGCTCGGAACTGCCTGGTGACAGAGAAGAATGTCCTGAAGATCAGTGACTTTGGG 240

Qy 634 MetSerArgGluGluAlaAspGlyValTyrAlaAlaSerGlyGlyLeuArgGlnValPro 653
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 ATGTCCCGAGAGGAAGCTGATGGGGTCTATGCGGCCTCAGGGGGCCTCAGACAAGTCCCC 300

Qy 654 ValLysTrpThrAlaProGluAlaLeuAsnTyrGlyArgTyrSerSerGluSerAspVal 673
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 GTGAAGTGGACCGCACCTGAGGCCCTTAACTACGGCCGCTACTCCTCCGAAAGCGACGTG 360

Qy 674 TrpSerPheGlyIleLeuLeuTrpGluThrPheSerLeuGlyAlaSerProTyrProAsn 693
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 TGGAGCTTTGGCATCTTGCTCTGGGAGACCTTCAGCCTGGGGGCCTCCCCCATCCCAAC 420

Qy 694 LeuSerAsnGlnInThrArgGlnHisPheValGluLysGlyLysArgLeuProCysProGlu 713
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 421 CTCAGCAATCAGCAGACACGGGAGTTTGTGGAGAAGGGGCGGCCGTCTCGCCCTGCCCAGAG 480

Qy 714 LeuCysProAspAlaValPheArgLeuMetGluGlnCysTrpAlaTyrGluProGlyGln 733
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 481 CTGTGTCCTGATGCCGTGTTCAGGCTCATGGAGCAGTGCTGGGCCTATGAGCCTGGGCAG 540

Qy 734 ArgProSerPheSerThrIleTyrGlnGluLeuGlnSerIleArgLysArgHisArg 752
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 541 CGGCCCAGCTTCAGCACCATCTACCAGGAGCTGCAGAGCATCCGAAAGCGGCATCGG 597

Alignment Scores:
Pred. No.:
Score: 3.04e-55   Length: 600
                         1057.00   Matches: 199

Query Match: 26.22%   Indels: 0
DB: 23   Gaps: 0

US-10-660-763-2 (1-752) x US-60-680-544-39317 (1-638)

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Qy    1  MetGlyPheSerSerGluLeuCysSerProGlnGlyHisGlyValLeuGlnMetGln   20
              ||||||  ||||::::|||||||||||||||||||:||||
Db   39  ATGGGCTTCTTCTTGGAGTGTGCACCCCCCAGGGCCACGGGTCCTGCAGATGCAG   98

Qy   21  GluAlaGluLeuArgLeuLeuGlyMetGluGlyTrpMetAlaGlnArgValLysSer   40
              |||||||||||||||||||||||||||||||||||||||||||
Db   99  GAGGCTGAGCTTCGTCTACTGGAGGGCATGGAAGTGGACCAACGGGTCAAGAGT   158

Qy   41  AspArgGlyTyrAlaGlyLyaLeuLeuHisHisMetSerLeuGlnAspSerGlyGlnSer   60
              ||||||||||||||||:::|||||||||||||||||||||||||
Db  159  GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCGTGCAGGACAGTGGGGGCCAGAGC   218

Qy   61  ArgAlaIleSerProAspSerProIleSerGlnSerTrpAlaGluIleThrSerIleThr   80
              ||||||||||||||||||||||||||||||||||||||||||||
Db  219  CGGGGGCATCAGCCCTGACAGCCCCATCAGCCAGTCCTGGGCGGAGATCACCAGCCAAACT   278

Qy   81  GluGlyLeuSerArgLeuLeuArgGlnHisAlaGluAsnSerGlyProLeuSer  100
              ||||||||||||||||||||||||||||||||||||||||||
Db  279  GAGGGCCTGAGCCGGTTGCTGCGGCAGCACGCCGGAGGATCTGAACTCAGGGCCCCTGAGC   338

Qy  101  LysLeuSerLeuLeuIleArgGlnGlnLeuGlnLysThrTyrSerGluGlnTrp  120
              ||||||||||||||||||||||||||||||||||||||||
Db  339  AAGTTGAGCCTGCTCATCCGGCAGCAGCTTCGCAAGACCTACAGCGAGCAGTGG   398

Qy  121  GlnGlnLeuGluGlnLeuThrArgThrHisSerGlnAsnIleGluLysLeuLysSer  140
              |||||||||||||||||||||||||||||||||||||||||||||
Db  399  CAGCAGCTGGAGCAGCTCACCAGACTCACAGCCAGGAACATTGAGAAGCTGAAGAGC   458

Qy  141  GlnTyrArgAlaLeuAlaArgAspSerAlaGlnAlaLysArgLysTyrGlnGluAlaSer  160
              |||||||||||||||||||||||||||||||||||||||||||||
Db  459  CAGTACCGAGCCCTGGCACGGGACAGTGCCCAAGCCAAGCGCAAGTACCAGGAGGCCAGC   518

Qy  161  LysAspLysAspAlaLeuAlaLysAspLysTyrValArgSerLeuTrpLysLeuPhe  180
              ||||||||||||||||||||||||||||||||||||||||||||
Db  519  AAAGACAAGGACCGTGACAAGGCCAAGGACAAGTATGTGCGCAGCCTTGTGAAGCTCTTT   578

Qy  181  AlaHisHisAsnArgTyrValLeuGlyValArgAlaAlaGlnLeuHisGlnHisHis  200
              |||||||||||||||||||||||:::||||||||||||||||
Db  579  GCTCACCACCACAACCGCTATGTGCTGGGCGTGCGGGCTGCACAGCTACCAGCACCAC   638
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RESULT 14
US-60-680-473-39317
; Sequence 39317, Application US/60680473
; GENERAL INFORMATION:
; ; APPLICANT: Cooper, Matthew
; ; APPLICANT: Kinch, Deborah
; ; APPLICANT: Rosenberg, Michael
; ; APPLICANT: Subramaniam, S. Sai
; ; APPLICANT: Szak, Suzanne
; ; APPLICANT: Li, Huo
; ; APPLICANT: Bandaru, Raj
; ; APPLICANT: Derbel, Maher
; ; TITLE OF INVENTION: Nucleotide Array Containing Polynucleotide Probes Complementary to
; ; TITLE OF INVENTION: Fragments of, Cynomolgus Monkey Genes and the Use Thereof
; ; FILE REFERENCE: 21590290000
; ; CURRENT APPLICATION NUMBER: US/60/680,473
; ; CURRENT FILING DATE: 2005-05-13
; ; NUMBER OF SEQ ID NOS: 48714
; ; SOFTWARE: Patent Sequence Analysis Tool Version 1.0
; SEQ ID NO 39317
; ; LENGTH: 638
; ; TYPE: DNA
; ; ORGANISM: Macaca Mulatta
US-60-680-473-39317

Alignment Scores:
Pred. No.:
Score: 8.88e-53   Length: 638
                1017.00   Matches: 196

US-10-660-763-2 (1-752) x US-11-060-756-756-7605 (1-600)

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Qy  554  GlyValCysThrGlnLysGlnProIleTyrIleValMetGluLeuValGlnGlyValGlyAsp  573
              |||||||||||||||||||||||||||||||||||||||||||||
Db    1  GGTGTCTGCACCCAGAAGCAGCCCATCTACATCGTCATGGAGCTTGTGCAGGGGGGGGAC   60

Qy  574  PheLeuThrPheLeuArgThrGluGlyAlaAlaArgLeuArgValLysThrLeuLeuGlnMet  593
              ||||||||||||||||||||||||||||||||||||||||||||
Db   61  TTCCTGACCTTCCTCCGCACGGAGGGGGCCGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATG  120

Qy  594  ValGlyAspAlaAlaAlaGlyMetGluTyrLeuGluSerLysCysCysIleHisArgAsp  613
              ||||||||||||||||||||||||||||||||||||||||||
Db  121  GTGGGGGATGCAGCTGCTGGCAGGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGAC   180

Qy  614  LeuAlaAlaArgAsnCysLeuValThrGluLysAsnValLeuLysIleSerAspPheGly  633
              |||||||||||||||||||||||||||||||||||||||||
Db  181  CTGGCTGCTCGGAACTGCCTGGTGACAGAGAAGAATGTCCTGAAGATCAGTGACTTTGGG   240

Qy  634  MetSerArgGluGluGluAlaAspGlyValTyrAlaAlaSerGlyGlyLeuArgGlnValPro  653
              ||||||||||||||||||||||||||||||||||||||||||||
Db  241  ATGTCCCGAGAGGAAGCTGATGGGGTCTATGCAGCCTCAGGGGGCCTCAGACAAGTCCCC   300

Qy  654  ValLysTrpThrAlaProGluAlaLeuAsnTyrGlyArgTyrSerSerGluSerAspVal  673
              ||||||||||||||||||||||||||||||||||||||||||
Db  301  GTGAAGTGGACCGCACCTGAGGCCTAACTACGGGCGCTACTCCTCCGAAAGCGACGTG   360

Qy  674  TrpSerPheGlyIleLeuLeuTrpGluThrPheSerLeuGlyAlaSerProTyrProAsn  693
              |||||||||||||||||||||||||||||||||||||||||||
Db  361  TGGAGCTTTGGCATCTTGCTCTGGGAGACCTTCAGCCTGGGGGCCTCCCCTATCCCAAC   420

Qy  694  LeuSerAsnGlnThrArgGluPheValGlnLysGlyGlyArgLeuProCysProGlu  713
              ||||||||||||||||||||||||||||||||||||||||||
Db  421  CTCAGCAATCAGCAGAGAGTTTGTGCAGAAGGGGGGGCCGTCCCGTCCCAGAG   480

Qy  714  LeuCysProAspAlaValPheArgLeuMetGlnGlnCysTrpAlaTyrGluProGlyGln  733
              ||||||||||||||||||||||||||||||||||||||||||
Db  481  CTGTGTCCTGATGCCGTGTTCAGGCTCATGCAGCAGTGCTGGGCCTATGAGCCTGGGCAG   540

Qy  734  ArgProSerPheSerThrIleTyrGlnGluLeuGlnSerIleArgLysArgHisArg  752
              ||||||||||||||||||||||||||||||||||||||||||
Db  541  CGGCCCAGTTTCAGCACCATCTACCAGGAGCTGCAGAGCATCCGAAAGCGGCATCGG   597
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RESULT 13
US-60-680-544-39317
; Sequence 39317, Application US/60680544
; GENERAL INFORMATION:
; ; APPLICANT: Cooper, Matthew
; ; APPLICANT: Kinch, Deborah
; ; APPLICANT: Rosenberg, Michael
; ; APPLICANT: Subramaniam, S. Sai
; ; APPLICANT: Szak, Suzanne
; ; APPLICANT: Li, Huo
; ; APPLICANT: Bandaru, Raj
; ; APPLICANT: Derbel, Maher
; ; TITLE OF INVENTION: Nucleotide Array Containing Polynucleotide Probes Complementary
; ; TITLE OF INVENTION: Fragments of, Cynomolgus Monkey Genes and the Use Thereof
; ; FILE REFERENCE: 21590290000
; ; CURRENT APPLICATION NUMBER: US/60/680,544
; ; CURRENT FILING DATE: 2005-05-13
; ; NUMBER OF SEQ ID NOS: 48714
; ; SOFTWARE: Patent Sequence Analysis Tool Version 1.0
; SEQ ID NO 39317
; ; LENGTH: 638
; ; TYPE: DNA
; ; ORGANISM: Macaca Mulatta
US-60-680-544-39317

Alignment Scores:
Pred. No.:
Score: 8.88e-53   Length: 638
                            1017.00   Matches: 196
Percent Similarity: 99.50%   Conservative: 3
Best Local Similarity: 98.00%   Mismatches: 1

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Percent Similarity:      99.50%       Conservative:    3
Best Local Similarity:   98.00%       Mismatches:      1
Query Match:             26.22%       Indels:          0
DB:                                   Gaps:            0

US-10-660-763-2 (1-752) x US-60-680-473-39317 (1-638)

Qy    1 MetGlyPheSerSerGluLeuCysSerProGlnGlyHisGlyValLeuGlnMetGln    20
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   39 ATGGGCTTCTCTTCGGAGCTGTGCACCCCCAGGGCCACGGGGTCCTGCAGCAGATGCAG  98

Qy   21 GluAlaGluLeuArgLeuLeuGluGlyMetArgLysTrpMetAlaGlnArgValLysSer 40
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   99 GAGGCTGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAACGGGTCAAGAGT 158

Qy   41 AspArgGluTyrAlaGlyLeuLeuHisHisMetSerLeuGlnAspSerGlyGlySer    60
          |||||||||||||||||||||||||||||||||||||:::||||||||||||
Db  159 GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGCCAGAGC  218

Qy   61 ArgAlaIleSerProAspSerProIleSerGlnSerTrpAlaGluIleThrSerGlnThr 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  219 CGGGGCCATCAGCCCTGACAGCCCCATCAGCCAGTCCTGGGCGGAGATCACCAGCCAAACT 278

Qy   81 GluGlyLeuSerArgLeuLeuArgGlnHisHisAlaGluAsnSerGlyProLeuSer   100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  279 GAGGGGCCTGAGCCGCGGTTGCTGCGACACGGCAGAGATCTGAACTCAGGGCCCCTGAGC 338

Qy  101 LysLeuSerLeuLeuIleArgGluArgGlnLeuArgLysTyrTyrSerGluGlnTrp   120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  339 AAGTTGAGCCTGCTCATCCGGGAACGGCAGCCTACGCAAGACCTACAGCAGCAGTGG   398

Qy  121 GlnLeuGlnLeuGluGluThrLysThrLysTyrHisSerGlnAspIleGluLysLysSer 140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  399 CAGCAGCTGCAGCAGGAGCTCACCAAGACTCACCAGAACATTGAGAAGCTGAAGAGC    458

Qy  141 GlnTyrArgAlaLeuAlaArgAspSerArgAlaAlaLysArgLysTyrGlnGluAlaSer 160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  459 CAGTACCGAGCCCTGGCCCGGGACTCACGTGCCGCCAAGCTACCAGGAGGCCAGC    518

Qy  161 LysAspLysAspArgAspLysLysAlaLysAspAspTyrValArgSerLeuTrpLysPhe 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  519 AAAGACAAGGACCGTGACAAGAAGGCCAAGGACGACTATGTGCGCAGCCTGTGGAAGTTCTTT 578

Qy  181 AlaHisHisAsnArgTyrValLeuGlyValArgAlaAlaAlaGlnLeuHisLeuHisGlnHisHis 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  579 GCTCACCACAACCGCTATGTGCTGGGCGTGCGGGCTGCACAGCTACACTACCAGCACCAC 638
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; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24845
; LENGTH: 3198
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-24845

Alignment Scores:
Pred. No.:                                Length:        3198
Score:                8.5e-52            Matches:        257
Percent Similarity:   42.44%             Conservative:   108
Best Local Similarity: 29.88%            Mismatches:     245
Query Match:                             Indels:         250
DB:                                      Gaps:            13

US-10-660-763-2 (1-752) x US-11-097-143-24845 (1-3198)

Qy  122 GlnLeuGlnLeuGluThrLysThrLysHisSerGlnAspIleGluLysLysSerGln    141
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Db    1 CAGCTCACCGACGAGGTGGTGCGCCAAGAAATCT---GAATACCAAAAACATTGGAGGGC  57

Qy  142 TyrArgAlaLeuAlaArgAspSerArgAlaAlaLysArgLysTyrGlnGluAlaSerLys 161
            :::  ||||   ||    ||:::|||
Db   58 TACAAGGCGCTG----------CGCACGGCCTTCGAGGAGAACTACATAAAGGCACCCAGT 108

Qy  162 AspLysAspArg------AspLysLysAlaLysAspAspTyrValArgSerLeuTrpLysLeu 179
          |||    |||         |||||  ||||||||||||
Db  109 CGCAGTGGCCGCAAGCTGGACGATGTGCGTGACAAGTATCAGAAGGGCCTGCCGCAAATTG 168

Qy  180 PheAlaHisHisAsnArgTyrValLeuGlyValArgAlaAlaGlnLeuHisLeuHisGlnHisHis 199
          |||      ::|         |||    ||  :::
Db  169 CATCTCACACACAACACAGTACGTGCTGTCCATCACGACGGAAGCCATCGAAGTGGAGAAGGAC 228

Qy  200 HisHisGlnLeuLeuLeuPheGlyLeuLeuArgSerLeuGlnAspSerLeuGlnHisGluGluMet 219
            :::|||||  ||    ||||  |||        ||| :::
Db  229 TTTCGCCACGTCTTGCTGCCGGACTGCTGGAGCTGGAGCTTC 288

Qy  220 AlaCysIleLeuLysGluIleLeuGluGlnLeuGlyTyrLeuGluIleSerSerLeuValGlnAsp 239
          ||    :: |||||    || ||| ||||
Db  289 ATCCTGCTGTGGCGCAACATCCTGCAGGAGGGCGCCCAGTATGGCGACACCTCACGGCCGGAC 348

Qy  240 GluValAlaIleAlaIleHisArgGluMetAlaAlaAlaAlaArgIleGluProGluAla   259
          |||      ||| ||  :::
Db  349 AAGTACAAGGAGATCCAAGAGGCCATTGACACTGTGATAGGGAGCATCAATCCGACCGAG  408

Qy  260 GluThrTyrGlnGlyPheLeuArgGlnTyrGlySerAlaProAspValProProCysValThr 279
          |||||      ||| |||     ::|||        ||||
Db  409 GAGTACGGCGAGTTCACCGAGAATACAAAACCTCTCCCACACACCGTGCTCTTCCAG 468

Qy  280 PheAspGluSerLeuLeuGluGluLeuGluGluLeuGluProGlyLeuGluLeuGlnLeuAsn 299
          |||     |||||  ||   ||      ||    :::||||||
Db  469 TTCGATGAGACGCTCATCCAGGAT----------ATTCCCGGCAAATTGCAGTCGAGC 516

Qy  300 GluLeuThrValGluSerValGlnHisHisThrSerThrSerValThrAspGluLeuAlaAlaVal 319
          |||||||||||::::::::|||            ::: |||
Db  517 ACATTGACAGTGGACAACCTC----ACGGTGGACTGGCTGCGTAATCGTCTCCAGGAA  570

Qy  320 AlaThrGluMetValPheArgArgGlnGluMetValThrGlnLeuGlnGlnGluLeuArg   339
          |||     |||||          ::::::
Db  571 CTGGAGGGAGCCGTCAGGAGTTGCCAGGAGAG---------CAGATGAAGATGATC  618

Qy  340 AsnGluGluAsnThrHisProArgGluArgValGlnLeuLeuGlyLysLysGlnGlnVal 359
          |||||||  |||||    ||||||   ||||::::::
Db  619 GAGCATGTGAATGGTGGCTCGCCGGTGCCAATGCAGCAGCATTATATCCAACGGCAGCAAC 678

Qy  360 LeuGlnGluAlaLeuGlnGlyLeuGlnLeuValAlaLeuCysSerGlnAlaLys-------   376
          :::||    ::: |||   :::::::|||
Db  679 ACATCCAACGGCATTCAGTCCAACAAGGATAGCCTATGCCGCAGTCGAAGGACCTTAAT  738

Qy  377 ---LeuGlnAlaGlnGln------------------------GluLeuLeuGlnThrLysLeu 388
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RESULT 15

US-11-097-143-24845

; Sequence 24845, Application US/11097143

; GENERAL INFORMATION:

; APPLICANT: Venter, J. Craig

; APPLICANT: et al.

; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

; TITLE OF INVENTION: DROSOPHILA GENES.

; FILE REFERENCE: CL000728

; CURRENT APPLICATION NUMBER: US/11/097,143

; CURRENT FILING DATE: 2005-04-04

; PRIOR APPLICATION NUMBER: 60/157,832

; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: 60/160,191

; PRIOR FILING DATE: 1999-10-19

; PRIOR APPLICATION NUMBER: 60/161,932

; PRIOR FILING DATE: 1999-10-28

; PRIOR APPLICATION NUMBER: 60/164,769

; PRIOR FILING DATE: 1999-11-12

; PRIOR APPLICATION NUMBER: 60/173,383

; PRIOR FILING DATE: 1999-12-28

; PRIOR APPLICATION NUMBER: 60/175,693

; PRIOR FILING DATE: 2000-01-12

; PRIOR APPLICATION NUMBER: 60/184,831

; PRIOR FILING DATE: 2000-02-24

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Db  1819  GCCAAACTGAAGTCCACCAAACTGGATGTGGCTGTCGTCAAAACCTGTCGAATGACCCTGCCC  1878
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Qy   528  ProAspLeuLysAlaLysPheLeuGlnGluLysLeuGlnTyrSerHisPro                    547

Db  1879  GACGAACAGAGAGCTAAATTCCTACAGGAAGGGCGTAAATTCCTCAAGCAATACGATCATCCA  1938
           :::          ||||||||||||||||        |||||:::||||         |||
Qy   548  AsnIleValArgLeuIleGlyValCysThrGlnLysGlnProIleTyrIleValMetGlu      567

Db  1939  AATATCGTAAAATTGATTGGCATTTGTGTGCAGAAGCAGCCCATCATGATTGTCATGGAA      1998
           ||||||  |||||||||||||  |||||||||||||||||||||||||||||||||||
Qy   568  LeuValGlnGlyGlyAspPheLeuThrPheLeuArgThrGluGlyGlyAlaArgLeuArgVal   587

Db  1999  TTGGTGCTCGGTGGTTCGCTTTTAACTTATTTACGCAAGAACTCCAATGGCCTCACCACT     2058
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Qy   588  LysThrLeuLeuGlnMetValGlyAspAlaAlaAlaGlyMetGluTyrLeuGluSerLys     607

Db  2059  CGCCAACAAATGGGCATGTCAGAGATGCGGCGAGGCATGCAGATATCTGGAGTCCAAA      2118
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Qy   608  CysCysIleHisArgAspLeuAlaAlaArgAsnCysLeuValThrGluLysAsnValLeu     627

Db  2119  AACTGCATTCATCGGCCATCTGGCGCGCGTAATTGTCTCGTTGACTGGAGCACAGTGTG     2178
           |||||||||||||        :::|||        ::::::
Qy   628  LysIleSerAspPheGlyMetSerArgGluGluAlaAspGlyValTyrAlaAlaSerGly     647

Db  2179  AAGATCTCCGATTTCGGAATGTCTCGCGAGGAAGAGGAA------TATATAGTTTCCGAT     2232
           |||||||||||        :::          |||
Qy   648  GlyLeuArgGlnValProValLysTrpThrAlaProGluAlaLeuAsnTyrGlyArgTyr     667

Db  2233  GGCATGAAAACAAATACCTGTGAAGTGGACAGCCCTTGAATTCGGCAAGTAC            2292
           |||:::::                    |||:::|||
Qy   668  SerSerGluSerAspValTrpSerPheGlyIleLeuLeuTrpGluTrpPheSerLeuGly     687

Db  2293  ACTTCGTTGTGCGATGTGTGGTCCTATGGCATACTGATGTGGGAGATCTTCTCCAAGGGC    2352
           :::||||||        |||        |||||||
Qy   688  AlaSerProTyrProAsnLeuSerAsnGlnGlnThrArgGluValGluLysGlyGlyGly     707

Db  2353  GACACACCCTACTCCGGCATGACCAACTCCAGAGCCAGAGAGCGCATCGATACGGGAGATAT   2412
           |||                              |||
Qy   708  ArgLeuProCysProGluLeuCysProAspAlaValPheArgLeuMetGluGlnCysTrp     727

Db  2413  CGTATGCCAACGCCCGAGAGACGCCCGAGGAGATGTACCGACTGATGCTCCAGTGCTGG     2472
           |||:::          :::::::::||||||        |||
Qy   728  AlaTyrGluProGlyGlnArgProSerPheSerThrIleTyrGlnGluLeuGlnLeuSerIle  747

Db  2473  GCAGCCGACGGCGAATCCCGACCGCATTTCGATGAGATCTACAATGGTGGTGACACTG      2532
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Search completed: August 10, 2005, 13:54:17
Job time : 3166 secs

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Db   739  GCACTGCGCTGCCCAGGAGAGCAGAAACGAAGAGTGGTGGTGACATGATCAAGTGCGCCCTG   798
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Qy   389  GluHisLeuProGlyProGly--------ProValLeuLeuGln                      403

Db   799  AACGAGGTGGGATGCGGAGAGCTGCCCTCCGGTTGCGACGATGCCACCCTGGAGCAG        858
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Qy   404  --------AspAspArgHisSer--------                                   408

Db   859  AACTTCATCGAGAATGGCTATAACAACGAGCAGAGCAATCACAGTGCCTCA              918
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Qy   409  --------Thr                                                      409

Db   919  CAGTCCACGATAATAACGACGACGACCATAACGACTACCACGACTACAACTACCACGACG    978
Qy   410  SerSerSerGluGlnGluArgGlyGluGlyTyrArgProThrLeuGluIleLeuLysSer     429

Db   979  CCGTCCAAGAAAAACTCAAGACTGAAATTCAAGTGCCCAGATCCAGAGAAAATCAAAG     1038
           :::          |||        ::::::
Qy   430  HisIleSerGlyIlePheArgProLysPheSerAsnLeu--------                  442

Db  1039  GCCATCCGCAATACATTCCGCTCCAAGTTGCTCAATTTCCAGTTGAAGCCGCTCCAAGCCG  1098
Qy   442  --------                                                         442

Db  1099  TGCAAACAGTGCACCAAGAGACGTCGCATCCATCCCAGCAAAGTGTCTTTGATTTTGCC    1158
Qy   442  --------                                                         442

Db  1159  AAAGAGTTCGAGGTGGAACACCGGCTGGTTCGGCGGCCGATGAGCAATTCTGCAACTGT    1218
Qy   442  --------                                                         442

Db  1219  CCGCCAGCTCGTGTTAAGCCATCCGTCCAAATATCCGGCCACAAAGATCAC            1278
Qy   442  --------                                                         442

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Qy   442  --------                                                         442

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Qy   442  --------                                                         442

Db  1399  GTGCCCAGCCTGGCGGCCAGTATATCGCTCTCCACAAATCGTCCGCTTTACGAGGAGGAA    1458
Qy   442  --------                                                         442

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Qy   442  --------                                                         442

Db  1519  TTCCTGGTCCCGGAAACGATTCGAAACGAGGAGAGCCAGATTGTGCTCGTCTGTGTTGG     1578
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Qy   443  --------TyrArgLeuGluGly                                           447

Db  1579  AATGGCCATAAGCACTTCATTGTCCAGACCACCGGAGAGGGTAATTTCCCGGTTCCAGGGA   1638
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Qy   448  GluGlyPheProSerIleProLeuLeuIleAspHisLeuLeuSerThrGlnGlnProLeu     467

Db  1639  CCACCATTGCCAGCATCCAGGAGCTGATCATGCATCAGTATCACTCGGAATTGCCAGTG    1698
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Qy   468  ThrLysLysSerGlyValValLeuHisArgAlaValProLysAspLysTrpValLeuAsn    487

Db  1699  ACCGGTGAAATCGGGAGCCATACTCCGACGACCCGTTTGCCGGGAGCGGCTGGGAGCTGAGC  1758
           |||||||||            :::          |||||
Qy   488  HisGluAspLeuValLeuGlnIleIleGlyIleArgGlyArgAsnPheGlyValPheSer    507

Db  1759  AACGATGATGGTACTTCTGGAGAGGATTGGTGCGGGGAAACTTTTGGGGATGTCTACAAAG   1818
           ||||||||||            :::::::
Qy   508  GlyArgLeuArgAlaAspAsnThrLeuValAlaValLysSerCysArgGluThrLeuPro    527
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OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: August 10, 2005, 09:00:04 ; Search time 1599 Seconds
(without alignments)
3048.598 Million cell updates/sec

Title: US-10-660-763-2
Perfect score: 3879
Sequence: 1 MGFSSELCSPQGHGVLQQMQ..........QRPSFSTIYQELQSIRKRHR 752

Scoring table: BLOSUM62
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Ygapop   10.0 , Ygapext   0.5
Fgapop   6.0 , Fgapext   7.0
Delop   6.0 , Delext   7.0

Searched: 7297361 seqs, 324162794 residues

Total number of hits satisfying chosen parameters: 14594722

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool_p/US10660763/runat_03082005_182825_28680/app.query.fasta_1.903
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10660763 @CGN 1_1 723 @runat 03082005 182825_28680
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Published Applications NA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	DB	ID	Description
1	3879	100.0	2674	13	US-10-003-295-1	Sequence 1, Appli
2	3879	100.0	2674	18	US-10-660-763-1	Sequence 1, Appli
3	3821	98.5	2889	16	US-10-240-965-256	Sequence 256, App
4	2137	55.1	15297	13	US-10-003-295-3	Sequence 3, Appli
5	2137	55.1	15297	18	US-10-660-763-3	Sequence 3, Appli
6	1853	47.8	2950	21	US-10-887-553A-240	Sequence 240, App
7	892	23.0	1779	18	US-10-280-576-19	Sequence 19, Appl
8	663	17.1	449	10	US-09-918-995-1503	Sequence 1503, Ap
9	624.5	16.1	3840	16	US-10-204-041-3	Sequence 3, Appli
10	624.5	16.1	3840	19	US-10-717-597-234	Sequence 234, App
11	624.5	16.1	3840	19	US-10-802-432-26	Sequence 26, Appl
12	624.5	16.1	5434	17	US-10-170-385-182	Sequence 182, App
13	624.5	16.1	5744	17	US-10-439-703-5	Sequence 5, Appli
14	623	16.1	3450	17	US-10-457-954-5	Sequence 5, Appli
15	622	16.0	3393	17	US-10-263-480-1	Sequence 1, Appli
16	622	16.0	5527	9	US-09-880-107-3710	Sequence 3710, Ap
17	620.5	16.0	3653	17	US-10-258-666-7	Sequence 7, Appli
18	620.5	16.0	4705	16	US-10-312-918-1	Sequence 1, Appli
19	620.5	16.0	4786	16	US-10-312-918-3	Sequence 3, Appli
20	608	15.7	1518	18	US-10-280-576-24	Sequence 24, Appl
21	607.5	15.7	1713	9	US-09-741-154-1	Sequence 1, Appli
22	607.5	15.7	1713	16	US-10-187-900-1	Sequence 1, Appli
23	605.5	15.6	1933	21	US-10-895-225A-10	Sequence 10, Appl
24	605.5	15.6	2000	9	US-09-977-260-1	Sequence 1, Appli
25	605.5	15.6	2000	10	US-09-977-261-1	Sequence 1, Appli
26	605.5	15.6	2104	21	US-10-895-225A-9	Sequence 9, Appli
27	605.5	15.6	2183	21	US-10-895-225A-11	Sequence 11, Appl
28	603.5	15.6	3645	16	US-10-280-576-10	Sequence 10, Appl
29	598	15.4	1995	16	US-10-378-393-6	Sequence 6, Appli
30	598	15.4	2574	9	US-09-735-103-2	Sequence 2, Appli
31	598	15.4	2574	13	US-10-045-428A-2	Sequence 1, Appli
32	598	15.4	2604	15	US-10-171-581-317	Sequence 317, App
33	598	15.4	2604	17	US-10-353-690-33	Sequence 33, Appl
34	598	15.4	8858	16	US-10-378-393-1	Sequence 1, Appli
35	597	15.4	3650	17	US-10-369-022-59	Sequence 59, Appl
36	597	15.4	3650	17	US-10-366-288-17	Sequence 17, Appl
37	597	15.4	3650	21	US-10-497-692-1	Sequence 1, Appl
38	596.5	15.4	3663	9	US-09-919-172-84	Sequence 84, Appl
39	596.5	15.4	3663	20	US-10-752-986-84	Sequence 84, Appl
40	592.5	15.3	3593	15	US-10-220-801-6	Sequence 6, Appli
41	591	15.2	2449	15	US-10-220-801-11	Sequence 11, Appl
42	591	15.2	2456	13	US-10-186-399-1	Sequence 1, Appli
43	591	15.2	2456	16	US-10-021-660-41	Sequence 41, Appl
44	591	15.2	2456	17	US-10-305-720-1476	Sequence 1476, Ap
45	591	15.2	2456	18	US-10-211-462-128	Sequence 128, App

ALIGNMENTS

RESULT 1
US-10-003-295-1
; Sequence 1, Application US/10003295
; Publication No. US2002016741A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001183DIV
; CURRENT APPLICATION NUMBER: US/10/003,295
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2674

us-10-660-763-2.rnpb

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-003-295-1

Alignment Scores:
Pred. No.:                0          Length:              2674
Score:              3879.00          Matches:              752
Percent Similarity:  100.00%         Conservative:           0
Best Local Similarity: 100.00%       Mismatches:             0
Query Match:         100.00%         Indels:                 0
DB:                      13          Gaps:                   0

US-10-660-763-2 (1-752)  x  US-10-003-295-1 (1-2674)
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Qy     1  MetGlyPheSerGluLeuCysSerProGlnGlyHisGlyValLeuGlnGlnMetGln  20
Db    72  ATGGGCTTCTCTTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG  131

Qy    21  GluAlaGlnLeuArgLeuLeuGluGluGlyMetLeuGlyLysTrpMetAlaArgValLysSer  40
Db   132  GAGGCCGAGCTTCGTCTACTGGAGGAAGGCATGAGAAAGTGGATGGCCCGAGTCAAGAGT  191

Qy    41  AspArgGluTyrArgAlaGlyLeuLeuHisMetSerLeuGlnAspSerGlyGlyGlnSer  60
Db   192  GACAGGGAGTATCGAGCACTGCTTCACCACATGTCCTTGCAGGACAGTGGGGGCCAGAGC  251

Qy    61  ArgAlaAlaSerProAspSerProIleSerGlnGlnSerGlnIleThrSerGlnThr  80
Db   252  CGGGCCATCAGCCCTGACAGCCCCATCAGTCAGTCCTGGCTGAGATCACCAGCCAAACT  311

Qy    81  GluGlyLeuSerArgLeuArgGlnHisAlaGluAlaLysArgSerGlyProLeuSer  100
Db   312  GAGGGCCTGAGCCGTTGCTGCGGCAGACGCGGAAGGCTTCAGGGCCCCTGAGC  371

Qy   101  LysLeuSerLeuLeuIleArgGlnArgGlnLeuArgLysThrTyrSerGluGlnTrp  120
Db   372  AAGCTGAGCCTGCTCATCCGGGAACACGCAGCAGCTTCGCAAGACCTACAGCGAGCAGTGG  431

Qy   121  GlnGlnLeuGlnGlnLeuThrLysThrHisSerGlnAspIleGluLysLeuLysSer  140
Db   432  CAGCAGCTGCAGCAGCTCACCAAGACCCACAGCCAGGACATTGAGAAGCTGAAGAGC  491

Qy   141  GlnIleTyrArgAlaLeuAlaArgAspSerArgAlaGlnLysAlaLysArgLysTyrGlnGluAlaSer  160
Db   492  CAGATCTACCGAGCTCTGGCCAGGGACAGTGCCCAAGGCCAAGCGCAAGTACCAGGAGGCCAGC  551

Qy   161  LysAspLysAspLysAspLysSerTyrValArgSerTyrLeuTrpLysGlyLeuPhe  180
Db   552  AAAGACAAGGACCGTGACAAGGACAAGTAGTGTGCCCAAGTATGTGCCGGAAGCTCTTT  611

Qy   181  AlaHisHisAsnArgTyrArgLeuGlyLysValArgAlaGlnLeuHisLeuHisHis  200
Db   612  GCTCACCACAACCGCTATCGTGCTGGGGCGTGCCGCAGCTCACACGCCAGCAGCCAC  671

Qy   201  HisGlnLeuLeuProGlyLeuLeuArgGlnSerLeuGlnAspLeuHisGluGlnMetAla  220
Db   672  CACCAGCTTCTGCCTGGCGGCGCTGTCGCGGTCACTGCAGGACCTGCACGAGGAGATGGCT  731

Qy   221  CysIleLeuLysGluGlnIleGluGluGluIleSerSerLeuValGlnArgAspGlu  240
Db   732  TGCATCCTGAAGGAGCAGATCCTGCAGGAATACCTGGAGATTAGCAGCCTGGTGCAGAGTGAG  791

Qy   241  ValValAlaIleAlaHisGluArgGlnTyrLeuGluMetAlaLysAlaAlaAlaAlaAlaArgAsnCysLeu  260
Db   792  GTGGTGGCCATTCACCGGGAGATGGCTGCAGCTGCTGCGCCATCCAGCCTGAGGCTGAG  851

Qy   261  TyrGlnPheLeuArgGlnTyrTyrGlySerAlaProAspValProProCysValThrPhe  280
Db   852  TACCAAGGCTTCCTGCGACAGTATGGTCCGGCATATGGGTCCGCACCCTGTGTCACGTTC  911

Qy   281  AspGluSerLeuLeuLeuGluGluProLeuGlyLeuGluLeuGlnLeuGlnLeuAsnGlu  300
Db   912  GATGAGTCACTGCTTGAGGAGGGTGAACCGCTGGGAGCCTCCGGAGCTCCAGCTGAACGAG  971
```

```
Qy   301  LeuThrValGluSerValGlnHisHisThrLeuThrSerValThrArgGluLeuLeuAlaVal... Ala  320
Db   972  CTGACTGTGGAGAGCGTGCAGCACCGCACACGCTGACCCTCAGTGACAGATGAGCTGGCTGGCC  1031

Qy   321  ThrGluMetValPheArgArgGlnGlnMetValThrGlnLeuThrLeuGlnLeuGlnLeuArgAsn  340
Db  1032  ACCGAGATGGTGTTCAGGCGGCAGGAGATGGTTACGCAGCTGACACAGCTGCAACAGAGCTCCGGAAT  1091

Qy   341  GluGluGlnAsnThrHisProArgGluArgValGlnGlnLeuLeuGlyLysArgGlnValLeu  360
Db  1092  GAAGAGGAGAACACCACCCCGGGAGCGGGTGCAGCAGCTGCTGGGCAAGAGGCAAGTGCTG  1151

Qy   361  GlnGluAlaLeuGlnGlyLeuGlnValAlaLeuCysSerGlnAlaLeuGlnLysLeuGlnAlaGln  380
Db  1152  CAAGAAGCACTGCAGGGGCTGCAGGTAGCCTGTGCCAGCCAAGCTGCAGGCCAG  1211

Qy   381  GlnGluLeuGlnThrLysLeuGlyHisLeuGlyProGlyGluProProProValLeu  400
Db  1212  CAGGAGTTGCTGACGAAGCTGGGACACCTGGGCCCCGGCGAGCCCCCGCCTGTGCTG  1271

Qy   401  LeuLeuGlnAsnAspAspArgHisSerThrSerSerGluGlnIleArgGluGlyGlyLyrGlyLyrArg  420
Db  1272  CTCCTGCAGAATGACCGCCACTCCACGTCGTCCTCCGGAGCAGGAGCCGGAGGGGGAAGG  1331

Qy   421  ThrProThrLeuGlnIleLeuLysSerHisIleSerGlyIleIlePheArgGlyPheSer  440
Db  1332  ACACCACCGCTGGAGATCCTTAAGAGCCACATCTCAGGAATCTTCCGGGGCTTCTCG  1391

Qy   441  AsnLeuTyrArgLeuGluGluGlyGlyPheProSerIleLeuProLeuIleGluAspHisLeu  460
Db  1392  AACCTGTACCGACTGGAAGGTGTTCAGGGAGGCTTCCTAGCATTCCTTCCTGCTCATCGACCACCTA  1451

Qy   461  LeuSerThrGlnGlnInProLeuThrGlyLysSerGlyValValHisArgAlaValPro  480
Db  1452  CTGAGCACCCAGCAGCCCCTCACCAAGAGAGTGGGTGTTGTCCTGCAGGGCTGTGCCC  1511

Qy   481  LysAspLysTrpValLeuAsnHisSerGluGlyValLeuGluGlnIleGluGlyTyrArgGly  500
Db  1512  AAGGACAAGTGGGTGCTGAACCATTGAGAAGGCTGGTGGTGGAGCAGATTGGACGGGGG  1571

Qy   501  AsnPheGlyGlnValPheSerGlyArgLeuArgGlnAlaGlnAsnThrLeuValAlaValLys  520
Db  1572  AACTTTGGCCAAGTGTTCAGCGGACGTCTGCAGGGAGGCCGACAACACCCTGGTGCGGTGAAG  1631

Qy   521  SerCysSerArgGluThrLeuProProAspLeuLysAlaLysPheLeuGlnLeuGlnAlaArgIle  540
Db  1632  TCTTGTCGACGAGGACCGCTCCCACCTGACCTCAAGGCCAAGTTCTACAGGAAGCAGGAGATC  1691

Qy   541  LeuLysGlnTyrSerHisSerProAsnIleValArgLeuLeuGlyValCysThrGlnLysGlnGln  560
Db  1692  CTGAAGCAGTACAGCCACAGCCCAACATGTGCGTCATTGTGCGTCTCGCACCCAGAAGCAG  1751

Qy   561  ProIleTyrIleValMetGluLeuValGlnTyrGlyAspPheLeuThrPheArgThr  580
Db  1752  CCCATCTACATCGTCATGGAGCTTGTGCAGGGGGACTTCCTGACCTTCCTCCGCACG  1811

Qy   581  GluGlyValAlaArgLeuArgValLysThrLeuGlnMetValGlyAspAlaAlaAlaGly  600
Db  1812  GAGGGGGTCGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGATGCTGCAGGC  1871

Qy   601  MetGluTyrLeuGluSerLysLysCysIleHisArgAspAspLeuAlaAlaArgAsnCysLeu  620
Db  1872  ATGGAGTACCTGGAGAGCAAGAAGTGCATCCACCGGGACTGCCTGGCTGCTCCGCGAGAACTGCCTG  1931

Qy   621  ValThrGluLysAsnValLeuLysIleSerAspPheGlyMetSerArgGluGluAlaAsp  640
Db  1932  GTGACAGAGAAGAATGTCCTGAAGATCAGTGACTTTGGAATGTCCCGAGAAGAAGCCGAT  1991

Qy   641  GlyValTyrAlaAlaSerGlyGlyLeuArgGlnValProValLysTrpThrAlaProGlu  660
Db  1992  GGGGTTCTATGCAGCCTTCAGGGGGGCCCTGAGAAGTCCCCGTGAAGTGACCCCACCTGAG  2051
```

```
Qy   121 GlnGlnLeuGlnGluLeuThrLysThrSerGlnAspIleGluLysLeuLysSer  140
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   432 CAGCAGCTGCAGCAGGAGCTCACCAAGACCAGCCAGGACATTGAGAAGCTGAAGAGC  491

Qy   141 GlnTyrArgAlaLeuAlaArgAspSerAlaGlnAlaAlaLysArgLysTyrGlnGluAlaSer  160
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   492 CAGTACCGAGCTCTGGCACGGGACAGTGCCCAAGCCAAGCCAAGCGCAAGTACCAGGAGCCAGC  551

Qy   161 LysAspLysAspArgAspLysAlaLysAspLysTyrValArgSerLeuTrpLysLeuPhe  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   552 AAAGACAAGGACCGTGACAAGGCCAAGGACAAGTATGTGCGCAGCCTGTGGAAGCTCTTT  611

Qy   181 AlaHisHisAsnArgTyrValLeuGlyValValArgAlaAlaAlaGlnLeuHisHisGlnHisHis  200
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   612 GCTCACCACAACCCGTACGTGCTGGGCGTGGTGCGCGCAGCTGCGCAGCTACACCACCAGCACCAC  671

Qy   201 HisGlnLeuLeuProGlyLeuLeuArgSerLeuLeuArgLeuAspLeuHisGluGluMetAla  220
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   672 CACCAGCTCCTGCCTGGCCTGCTGCGCTCACTGCAGCACCTGCACCTCCAGGAGGAGATGGCT  731

Qy   221 CysIleLeuLysGluIleLeuGlnLeuTyrLeuGluIleSerSerLeuValGlnAspGlu  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   732 TGCATCCTGAAGGAGATCCTGCAGGAATACCTGGAGATTAGCAGCCTGGTGCAGGATGAG  791

Qy   241 ValValAlaIleHisArgGluMetAlaAlaAlaAlaAlaAlaArgIleGlnProGluAlaGlu  260
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   792 GTGGTGGCCATTCACCGGGAGATGGCTGCAGCTGCTGCCGCCATCCAGCCTGAGGCTGAG  851

Qy   261 TyrGlnGlyPheLeuArgGlnTyrGlySerAlaProAspValProProCysValThrPhe  280
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   852 TACCAAGGCTTCCTGCGACAGTATGGGTCCGCACCTGACGTCCCACCCTGTGTCACGTTC  911

Qy   281 AspGluSerLeuGluGluValGluLeuGluProGlyLeuGlnLeuGlnLeuAsnGlu  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   912 GATGAGTCACTGCTTGAGGAGGTGAACCGCTGGGAGCCTGGGAGCTCCAGTGAACAG  971

Qy   301 LeuThrValGluSerValGlnHisThrLeuThrSerValThrAspGluLeuLeuAlaValAlaAla  320
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   972 CTGACTGTGGAGAGCGTGCAGCACACGCTGACCTCAGTGACAGATGAGCTGCTGTGTGCC  1031

Qy   321 ThrGluMetValPheArgArgGlnMetValThrGlnLeuGlnGluLeuArgAsn  340
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1032 ACCGAGATGGTGTTCAGGCGGCAGGAGATGGTTACGCAGCTGCAACAGGAGCTCCGGAAT  1091

Qy   341 GluGluGlnAsnThrHisProArgGluArgValGlnLeuLeuGlyLysLeuGlyLysGlnGlnValLeu  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1092 GAAGAGGAGAACACCCCCCGGGAGCGGGTGCAGCTGCTGGGCAAGAGGCCAAGTGCTG  1151

Qy   361 GlnGluAlaLeuGlnGlyLeuGlnValAlaAlaLeuCysSerGlnAlaLysLeuGlnAlaGln  380
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1152 CAAGAAGCACTGCAGGGGCTGCAGGTAGCGGTGCAGCCCAAGCTGCAGGCCCAG  1211

Qy   381 GlnGluLeuGlnThrLysLeuGluHisLeuGlyProGlyProProValLeu  400
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1212 CAGGAGTTGCTGCAGACCAAGCTGGAGCACCTGGGCCCCGGCCCCCGCTGTGTCTG  1271

Qy   401 LeuLeuGlnAspAspArgHisSerThrSerSerGluGlnLeuArgGluGluGlyGlyArg  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1272 CTCCTGCAGGATGACCGCCACTCCACGTCGTCCTGGAGCAGCTGCGCGAGGAGGGGGGAGG  1331

Qy   421 ThrProThrLeuGluIleLeuLysSerHisIleSerGlyIleLeuSerGlyPheSer  440
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1332 ACACCCACGCTGGAGATCCTTAAGAGCCACATCTCAGGAATCTTCCCCCAGTTCTCG  1391

Qy   441 AsnLeuTyrArgLeuGluGlyIleGlyPheProSerIleLeuProLeuIleLeuAspHisLeu  460
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1392 AACCTGTACCGACTGGAAGGGAAGGCTTCCTAGCATTCCTTTGCTCATCGACCACCTA  1451

Qy   461 LeuSerThrGlnGlnProLeuThrLysLysSerGlyValValLeuHisArgAlaValPro  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1452 CTGAGCACCCAGCAGCCCCTCACCAAGAAGAGTGGTGTTGTCCTGCACAGGGCTGTGCCC  1511
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Qy   661 AlaLeuAsnTyrArgTyrSerGlyArgTyrSerGluSerValTrpSerPheGlyIleLeuLeu  680
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2052 GCCCTTAACTACGGGCCCTACTCCTCCGAAAGCGACGTGTGGAGCTTTGGCATCTTGCTC  2111

Qy   681 TrpGluThrPheSerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnGlnThrArg  700
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2112 TGGGAGACCTTCAGCCTGGGGGCCTCCCCCATCCCAACCTCAGCAATCAGCAGACACGG  2171

Qy   701 GluPheValGluLysGlyGlyArgLeuProGluProGlyCysProGluAspAlaValPhe  720
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2172 GAGTTTGTGGAGAAGGGGCCGTTGCCCGAGCCTGGCTGTCCTGATGCCGTGTTC  2231

Qy   721 ArgLeuMetGluGlnCysTrpAlaTyrGluProGlyGlnArgProSerPheSerThrIle  740
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2232 AGGCTCATGGAGCAGTGCTGGGCCTATGAGCCTGGGCAGCGCCCCAGCTTCAGCACCATC  2291

Qy   741 TyrGlnGluLeuGlnSerIleArgLysArgHisArg  752
             ||||||||||||||||||||||||||||||||||||
Db  2292 TACCAGGAGCTGCAGAGCATCCGAAAGCGGCATCCG  2327
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RESULT 2

US-10-660-763-1

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; Sequence 1, Application US/10660763
; Publication No. US20040063110A1
; GENERAL INFORMATION:
;  APPLICANT: GAN, Weiniu et al.
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION: THEREOF
;  FILE REFERENCE: CL001183DIVI
;  CURRENT APPLICATION NUMBER: US/10/660,763
;  CURRENT FILING DATE:  2003-09-12
;  NUMBER OF SEQ ID NOS:  4
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 1
;  LENGTH: 2674
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-660-763-1
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Alignment Scores:

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Pred. No.:            0                Length:          2674
Score:            3879.00              Matches:          752
Percent Similarity: 100.00%            Conservative:       0
Best Local Similarity: 100.00%         Mismatches:         0
Query Match:       100.00%             Indels:             0
DB:                   18               Gaps:               0
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US-10-660-763-2 (1-752) x US-10-660-763-1 (1-2674)

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Qy     1 MetGlyPheSerGluSerGluLeuCysSerProGlyHisGlyValLeuGlnValGlnMetGln  20
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    72 ATGGGGCTTCTCTTTCTGAGCTGTGCAGCCGTGCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG  131

Qy    21 GluAlaGlyLeuLeuArgLeuGluLeuGluGlyMetArgLysTrpMetAlaGlnLysArgValLysSer  40
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   132 GAGGCCGAGCTTCGTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGAAGAGAGT  191

Qy    41 AspArgGluTyrAlaGlyLeuLeuHisHisMetSerLeuGlnAspGlnSerGlyGlnSer  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   192 GACAAGGGAGGATGCAAGGACTGCTTCACCACATGTCCCTGCAGGACACGTGGGGGCCCGAGC  251

Qy    61 ArgAlaIleSerProAspSerProIleLeuSerGlnTrpAlaGlyIleGluThrGlnThr  80
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   252 CGGGCCATCAGCCCTGACAGCCCCATCAGTCAGTGGGCTGAGATCACCAGCCAAACT  311

Qy    81 GluGlyLeuSerArgLeuArgGlnHisAlaAspLeuAsnSerGlyProLeuSer  100
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   312 GAGGGGCTGAGCCGCTTGCTGCGGCAGCACGCAGGATCTGAACTCAGGGCCCCTGAGC  371

Qy   101 LysLeuSerLeuLeuIleLeuArgGluArgGlnLeuLeuArgLysThrTyrSerGluGlnTrp  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   372 AAGCTGAGCCTGCTCATCCTGCGAGAACGGCAGCAGCTTCGCAAGACCTACAGCGAGCAGTGG  431
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; PRIOR APPLICATION NUMBER: 60/195,106
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: PERL Program
;
; SEQ ID NO 256
; LENGTH: 2889
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030165924A1 997347.6
US-10-240-965-256

Alignment Scores:
Pred. No.:              0                Length:         2889
Score:               3821.00             Matches:         752
Percent Similarity:    91.37%            Conservative:      0
Best Local Similarity: 91.37%            Mismatches:        0
Query Match:           98.50%            Indels:           71
DB:                                      Gaps:              1

US-10-240-965-256   x US-10-240-965-256   (1-2889)
US-10-660-763-2 (1-752)
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Qy      1  MetGlyPheSerSerGluLeuCysSerProGlnGlyHisGlyValLeuGlnMetGln  20
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    188  ATGGGCTTCTCTTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG 247

Qy     21  GluAlaGluLeuArgLeuLeuGlyMetArgTrpMetAlaGlnArgValLysArgValLysSer  40
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    248  GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGCGGGTCAAGAGT 307

Qy     41  AspArgGluTyrAlaGlyTyrLeuLeuHisHisMetSerLeuGlnAspSerGlyGlyGlnSer  60
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    308  GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGCCAGAGC 367

Qy     61  ArgAlaIleSerProProLeuSerGlnSerProAlaGlyIleThrSerGlnThr  80
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    368  CGGGCCATCAGCCCTCCACTCAGTCAGTCTCCGGCTGGAATCAGATCACCAGCCAAACT 427

Qy     81  Glu-GlyLeuSerArgLeuArgGlnHisAlaGluAspLeuAsnSerGlyProLeuSe  100
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    428  GAGGGCGCCTGAGCCGCTTGCTGCGGCAGCACGCGCAGGAGGATCTGAACTCAGGGCCCCTGAG 487

Qy    100  rLysLeuSerLeuLeuIleArgGluArgGlnGlnLeuArgGlyLysThrTyrSerGluGlnTr  120
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    488  CAAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCTTCGCAAGACCTACAGCGAGCAGTG 547

Qy    120  pGlnGlnLeuGlnGlnLeuThrLysThrHisSerGlnAspArgAlaGlnAlaLysArgGlnLysLysSe  140
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    548  GCAGCAGCTGCAGCAGCTCACCAAGACCCACAGCCAGGACATTGAGAGCTGAAGAG 607

Qy    140  rGlnTyrArgAlaLeuAlaLeuArgAspSerAlaGlnAlaLysAspLysTyrArgGlnGluAlaSe  160
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    608  CCAGTACCGAGCTCTGGCACGGGACAGTGCCCAAGCCAAGGCACAGTACCAGGAGGCCAG 667

Qy    160  rLysAspLysAspArgArgAspLysTyrArgSerLeuTrpLysLeuPh  180
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    668  CAAAGACAAGGACCGTGACAAGGCCAAGGACCAAGTACGACCCTGTGGAAGCTCTT 727

Qy    180  eAlaHisHisAsnArgTyrValLeuGlyValArgAlaAlaGlnLeuHisHisGlnHisHi  200
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    728  TGCTCACCACAACCGCTATGTGCTGGGCGTGCGGGCTGCCCAGCTACCACCAGCACCA 787

Qy    200  sHisGlnLeuLeuProGlyLeuLeuArgSerLeuGlnAspLeuHisGluGlnMetAl  220
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    788  CCACCAGCTCCTGCCTGCGCCCGGCCTGCTGCGGTCACTGCAGGACCTGCACGAGGAGATGGC 847

Qy    220  aCysIleLeuLysGlnGluIleLeuGlnGluTyrLeuGluIleSerSerLeuValGlnAspGl  240
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    848  TTGCATCCTGAAGAGGAGATCCTGCAGGAATACCTGGAGATTAGCAGCCTGGTGCAGGATGA 907

Qy    240  uValValAlaIleHisArgGluMetAlaAlaAlaAlaAlaArgIleGlnProGluAlaGl  260
              |||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Qy    481  LysAspLysTrpValLeuAsnHisGluAspLeuAspLeuValLeuGlyGluGlnIleGlyArgGly  500
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1512  AAGGACAAGTGGGTGCTGAACCATGAGGACCTGGTGTTGGGTGAGCAGATTGGACGGGGG 1571

Qy    501  AsnPheGlyGluValPheSerGlyArgLeuArgAlaAspAsnThrLeuValAlaValLys  520
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1572  AACTTTGGCGAAGTGTTCAGCGGACGCCTCCGAGCGACAACACCCTGGTGGCCGTGAAG 1631

Qy    521  SerCysArgGluThrLeuProProAspLeuLysAlaLysPheLeuGlnGluAlaAlaArgIle  540
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1632  TCTTGTCGAGAGACGCTCCCACCTGACCTTAAGGCCAAGTTTCTACAGGAGGCGGAGATC 1691

Qy    541  LeuLysGlnTyrSerHisProAsnIleValArgLeuIleGlyValCysThrGlnLysGln  560
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1692  CTGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCCAGAAGCAG 1751

Qy    561  ProIleTyrIleValMetGluValGlnGlyGlyAspPheLeuThrPheLeuArgThr  580
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1752  CCCATCTACATCGTCATGGAGGTGCAGGGGGGCGACTTCCTGACCTTCCTCCGCACG 1811

Qy    581  GluLeuGlyAlaAlaArgLeuArgLysThrLeuLeuGlnMetValGlyAspAlaAlaGly  600
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1812  GAGGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGATGCAGCTGCTGGC 1871

Qy    601  MetGluTyrLeuGluSerCysCysIleHisArgAspLeuAlaAlaArgAsnCysLeu  620
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1872  ATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACCTGGCTGCTCGGAACTGCCTG 1931

Qy    621  ValThrGluLysAsnValLeuLysIleSerAspPheGlyMetSerArgGluGluAlaAsp  640
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1932  GTGACAGAGAAGAATGTCCTGAAGATCAGTGACTTTGGGATGTCCCGAGAGGAAGCCGAT 1991

Qy    641  GlyValValTyrAlaAlaSerGlyGlyLeuArgGlyValArgGlnValProValLysProThrAlaProGlu  660
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1992  GGGGTCGTCTATGCAGCCTCAGGGGGCCCTCAGACAAGTCCCCGTGAAGTGGACCGCACCTGAG 2051

Qy    661  AlaLeuAsnTyrGlyTyrSerSerGluSerAspValTrpSerPheGlyIleLeuLeuLeu  680
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2052  GCCCTTAACTACGGCTACTCCTCCGAAAGCGACGTGGGAGCTTTGGCATCTTGCTC 2111

Qy    681  TrpGluThrPheSerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnGlnThrArg  700
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2112  TGGGAGACCTTCAGCCTGGGGGCCTCCCCTATCCCAACCTGAGCAATCAGCAGACACG 2171

Qy    701  GluPheValGlnLeuLysGlyGlyTyrArgLeuProGluProCysProGluLeuCysProAspAlaValPhe  720
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2172  GAGTTTGTGGAGAAGGGGGGCCGTCTGCCCGAGCCCTGTCCTGATGCCGTGTTC 2231

Qy    721  ArgLeuMetGluGlnCysTrpAlaTyrGluProGlyGlnArgProSerPheSerThrIle  740
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2232  AGGCTCATGGAGCAGTGCTGGGCCTATGAGCCGGGGCAGCGGCCCAGCTTCAGCACCATC 2291

Qy    741  TyrGlnLeuGlnSerIleArgLysArgHisArg  752
              |||||||||||||||||||||||||||||||||||
Db   2292  TACCAGGAGCTGCAGAGCATCCGAAAGCGGCATCGG 2327
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RESULT 3
US-10-240-965-256
; Sequence 256, Application US/10240965
; Publication No. US20030165924A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: SHIFFMAN, Dov
; APPLICANT: SOMOGYI, Roland
; APPLICANT: LAWN, Richard M.
; APPLICANT: SEILHAMER, Jeffrey J.
; APPLICANT: PORTER, Gordon J.
; APPLICANT: MIKITA, Thomas
; APPLICANT: TAI, Julie
; TITLE OF INVENTION: GENES EXPRESSED IN FOAM CELL DIFFERENTIATION
; FILE REFERENCE: PA-0025 PCT
; CURRENT APPLICATION NUMBER: US/10/240,965
; CURRENT FILING DATE: 2002-10-04
```

RESULT 4
US-10-003-295-3
; Sequence 3, Application US/10003295
; Publication No. US20020016741A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001183DIV
; CURRENT APPLICATION NUMBER: US/10/003,295
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 3
; LENGTH: 15297
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-003-295-3

Alignment Scores:
Pred. No.:
Score: 2137.00
Percent Similarity: 21.28%
Best Local Similarity: 21.28%
Query Match: 55.09%
DB:

Length: 15297
Matches: 747
Conservative: 0
Mismatches: 5
Indels: 2764
Gaps: 16

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US-10-660-763-2 (1-752) x US-10-003-295-3 (1-15297)

Qy      1 MetGlyPheSerSerGluLeuCysSerProGlnGlyHisGlyValLeuGlnMetGln 20
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2563 ATGGGCTTCTTCTTCTTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCACAATGCAG 2622

Qy     21 GluAlaGluLeuArgLeuLeuGluGlyMetAlaGlnLysTrpMetAlaGlnArgValLys 40
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2623 GAGGCCGAGCTCGTCACTGAGGGCATAGAGAAAGTGGATGGCCCCAGGGCTCAAGAGT 2682

Qy     41 AspArgGluThrAlaGlyTyrAlaGlyLeuLeuHisHisMetSerLeuGlnAspGlyGlnGlnSer 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2683 GACACGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGCCAGAGC 2742

Qy     61 ArgAlaIleSerProAspSerProIleSerSerGlnSer------ 72
          |||||||||||||||||||||||||
Db   2743 CGGGCCATCAGCCCCTGACAGCCCCATCAGTCAGGT-GGGTCTCTATGGGACTCTGGTGGG 2801

Qy     72 ------ 72
Db   2802 TGCTCGGCGTATCTGCCTTCGCTTCCTTCCTCTCTCTGGGGGCCCTCTGGGGCAGTGGCTGGAGA 2861

Qy     72 ------ 72
Db   2862 TCTGGCAGGCCAATGCTTGGGAGCCATTGTGCCCCCTCCCCTGCCTCCCCCATCTGTGCT 2921

Qy     73 ------TrpAlaGluIleThrArgSerGlnTyrLeuGluGlyLeuArgLeuLeuArgGln 89
                ||||||||||||||||||||||||||||||||||||||||||||||||
Db   2922 GTATAGTCCTGGGCTGAGATCGACAACTGAGGGGCTTGAGCCGTTGCTGCGGCAG 2981

Qy     90 HisAlaGluAsnAspLeuAsnSerGlyProLeuSerLysSerLeuLeuIleLeuArgGluArg 109
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2982 CACGCCAGAGAATCTGAACTCAGGGGCCCCTGAGCCTGTTGAGCCTGAGCAAGCTGAGCCTCATCCGGGGAACGG 3041

Qy    110 GlnGlnLeuArgLysThrThrTyrSerGluGlnInTrpGlnInLeuGlnInGluLeuThrLeuLys 129
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3042 CAGCAGCTTCGCAAGACCACAGCCTACAGCGAGCAGCAGTGGCAGCAGCCTGCAGCAGGAGCTCACCCAG 3101

Qy    129 ------ 129
Db   3102 GTGAGCGGGGCAGCACTGGGCGTTCTCGGTGTCATTTCTGTCTAAATTTGAGCCTGAAGGGGT 3161

Qy    129 ------ 129
Db   3162 TGTTTTGCACAAGAGGCCCTGGATTCACTGGGAAGTGTAAGTCCCTGACCGCAGGCCTG 3221

Qy    129 ------ 129
Db   3222 GCTTGCTCTAAACCTTGATGTAGCTTCCTCTCTCTCCCTACGTTGAGCTGGCTTGCA 3281

Qy    129 ------ 129
Db   3282 GCAAGGCCCTCTCTGTCTTTTCTGTGCCTGGGCAAAGTGCTGGGAGTGTAAGGATGAGT 3341

Qy    129 ------ 129
Db   3342 GACCGGTCACGTGCTGGGAGAAGCTCAGAATCGTGCCTTCCACACTGTGCCATCT 3401

Qy    129 ------ 129
Db   3402 GGCTCTGGGGTTCTGAGAGTCAGGAGGAATGAGGGGTCAGTCTGTTTGCCTTCGACCTA 3461

Qy    129 ------ 129
Db   3462 TGCAGCCTCCTCTCAGGGCCCCAGGGCATGGGCAGCAGCAGGCCCCCGAAGGTCGAGG 3521

Qy    129 ------ 129
Db   3522 ACTCCGGCCCGTGAAGTCAGCCTGCCTAGGTTGAATCCCACCCAGCTCCTCAGTTCTAGAG 3581

Qy    129 ------ 129
Db   3582 GCTGTGTGGATTTGGAACTATTTATCTGGGAGCCATTCAGTGTGCTGGTCA 3641


Qy    129 ------ 129
Db   3642 CCCTCCCTGCACCACACCCTTCCTCAGTGCAGGAGCCCGAGAGGCCTTGCCATGGACCACCACAG 3701

Qy    129 ------ 129
Db   3702 CGGCCCCTGGTGGCCACCTGGCCCCCCATTCCTCGCCCCAAAAGATCATCGTGATTCAAGGG 3761

Qy    129 ------ 129
Db   3762 TGGGGCCATTTTTATAAAGTTTGCTGGAACACAGCTATGCCCCTTTGTTTTCTATATTGT 3821

Qy    129 ------ 129
Db   3822 CTGTGACTACAATGACAGAGTTGAGTAATTGTGACAGAGAGCTCTATGGCTACAGAGCCTA 3881

Qy    129 ------ 129
Db   3882 AAATATTTATTTACTATCTGCCCTTTAAGAAAAGACTGATCTAGTCGAGGAATCTAGC 3941

Qy    129 ------ 129
Db   3942 TCAGTTACAGATGGGAAACTGAGGTTGGGGGCTTGCCCAACATATCCCAGCACATAAAC 4001

Qy    129 ------ 129
Db   4002 AGGAGAACTGGGACGAGAACACTGATCTCGGCGTGTCATCTATTCCTACTGCCAAGAACA 4061

Qy    129 ------ 129
Db   4062 TAATTTGCAGGACCCAGTGCAAAGTGAAATTGTGGGGGTCTTTGTTAAAGATTGCTAGG 4121

Qy    129 ------ 129
Db   4122 AATTTCCAGGTGGCAATAATGGAGAATGAAACCAAGCACAGGGCCCTTCTACATGTGGAG 4181

Qy    129 ------ 129
Db   4182 CCCCGTGTGACTGCACAGGCCGTGCACACCTGCAACTGGCCCTGCCACCCAGGCTAC 4241

Qy    129 ------ 129
Db   4242 CACTGTCAGTCCAAGGAGGGACCGGTTGTAGCCTGTGTAGTCCTCTTGCCTCTCCCCAAGG 4301

Qy    129 ------ 129
Db   4302 GGTCTGTCTTCAACAGGCTCTCTGATCTTTGACTCTCACGTCAGCAGCCAGCTTTCCCAG 4361

Qy    129 ------ 129
Db   4362 AAGTCTCCAGGTGCTCCTTGCCTGACGACGAGACCTTTCAGGGGCTTCACCCCAGGCAAG 4421

Qy    130 ----ThrHi 131
              |||||
Db   4422 AATCTTCCACAACTGGGAACTGCTGCCCCACACTGGCCTCCTCCTCCTCCCTAGACCCA 4481

Qy    131 sSerGlnAspIleGluLysSerGlnTyrArgAlaLeuAlaArgAspSerAlaGl 151
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4482 CAGCCAGGACATTGAAGAGCTGAAGAGCCAGTACCGAGCTCTGGCCAGTGCCCA 4541

Qy    151 nAlaLysArgLysTyrGlnGluAlaSerLys------- 161
          |||||||||||||||||||||||||||||
Db   4542 AGCCAAGCGCAAGTACCAGGAGGCCAGCAAAGGTTCGTGGTGCTTCCCTTGCTGCGGGGAG 4601

Qy    161 ------ 161
Db   4602 GGAATCCGAAGCCAGTGCTGTCCTGTGGTACCCAGAGTGGGGGTGCCTGGGC 4661

Qy    162 AspLysAspArgAspLysAlaI 168
          |||||||||||||||||||
Db   4662 CTCCATGCTGTCATCTATACCCCTTGCCCCCCTTCTGCGGACAACGAGACCGTGACAAGGC 4721
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Qy   168 aLysAspLysTyrValArgSerLeuTrpLysPheAlaHisHisAsnArgTyrValIle 188
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4722 CAAGGACAAGAGTATGTGCGCAGCCTGTGGAAGCTCTTTGCTCACCACAACCGCTATGTGCT 4781

Qy   188 uGlyValArgAlaAlaGlnLeuHisHisHisHisGlnHisHisGlnLeuLeuGlnProGlyLe 208
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4782 GGGCGTGCGGGCTGCGGCAGCTACACCACCACCAGCACCACCAGCTCCTGCTGCCCGCCT 4841

Qy   208 uLeuArgSerLeuGlnAspLeuHisGluGluMetAlaCysIleLeu- 223
          ||||||||||||||||||||||||||||||||||||||||||||
Db   4842 GCTGCGGTCACTGCAGGACCTGCACGAGGAGATGGCTTGCATCCTGTAAGCCCGCACCCC 4901

Db   4902 CGTCCCCTGGCCCCCCACCCTTGAGCAGCCCATGAGCAGCCCAGAGGCAGGA 4961
Qy   223 --- 223

Db   4962 CCCAGAAAATCCATTGCTGGGAAGGTGCTGGCCATGTAACCACATGAGAACGGGACCTGG 5021
Qy   223 --- 223

Db   5022 GCCAAGGATTGGAAACAGGCAACTTACCTTCTGAATTACACTATTCCAGGGTCTCATTATT 5081
Qy   223 --- 223

Db   5082 CCAGGGTTTTATTACATTCATTGAGCACTGTTCTGGGCTCTGGATTATACCAGAGAACGA 5141
Qy   223 --- 223

Db   5142 TGGTAGACAAAAACATCTGTCCTCAGGGATCTTTCGTGTTAGTGAGTGAGAATGTGAGG 5201
Qy   223 --- 223

Db   5202 AGCACTAAGAGCCATGGAGAAAAATAAAGCAAGAGAAGTCGGGATCGGGACCACG 5261
Qy   223 --- 223

Db   5262 GAGGCAAGGAGGAGGTGACAGTTGTCCATAGAGTCCTTGGGAAAGCCTCTTGAGAGGT 5321
Qy   223 --- 223

Db   5322 GACATTCAAAGAGAGGCCCCTGAGAGGGTACGGGAGTGAATCATGGGGCTATTTGGAGAAA 5381
Qy   223 --- 223

Db   5382 GACCATTCCAGAAGGAGGCAGCAATTACACAGGCCTTGAGGTAGGAGAGTACCAGGGGA 5441
Qy   223 --- 223

Db   5442 CTAATAGCCAGGAACCAGTGGTGCCTCGAGAGTGAGGGAGGGGGAGAGTCATACACGAG 5501
Qy   223 --- 223

Db   5502 GCTGGAGGAGGGCAGGGGTCAGGGCGTCACTGGGTGATAGAAGGTCTAGCAGGGCCATGGTG 5561
Qy   223 --- 223

Db   5562 AGGGACTTTGGCTCTGGGTGAACAAGAATGGCATGATCTGTTTTTTGTTTGTTTCAT 5621
Qy   223 --- 223

Db   5622 TTTGTTTTAACTTTTTTGAGTCAGAGTCTCGCTCTGTCGCCCAGGCTAGAGTGCAGTGG 5681
Qy   223 --- 223

Db   5682 CATGATCTCGGCTTACTGCAACCTCCGCCTCCCAGGTTCAAGTGATTCCCCTGCCTCAGC 5741
Qy   223 --- 223

Db   5742 CTCCCGAGTAGCTGAAACTACGGGCGCCACCACCACCCAGTCAATTTTTGTATTTTTTTT 5801
Qy   223 --- 223

Db   5802 AGTAGAGACGGGGTTTCACCATGTTGCCCAGGCTAGTCTCTAATTCCTGGGCTCAAACGCG 5861
Qy   223 --- 223

Db   5862 ATTTGCCTCCTGCCTCGCCAAAGTGCGGGGATTACAGGCACATGAGCCACCATGCCCAGC 5921
Qy   223 --- 223

Db   5922 CCTGACCTCTGTTTTAATAAGGCCACTCTGGCTGCTGCTGTGCGAAATAGACTTCAGGGAG 5981
Qy   223 --- 223

Db   5982 CAAGGACAGAAGCTGGGAGGCCAGAGAGCAGGCTGCTGCCATAATCCAGATCCAAGCTT 6041
Qy   223 --- 223

Db   6042 TTGGCCAGTACAGGGGAGGTAGCAATGGGAGGTGAGGCGCGTCAGTCCTGGGGCAG 6101
Qy   223 --- 223

Db   6102 GTCCTGGAAGGTGAAGCCAGTGGATTCCCTATGGATTGGAAGTGGGGCGTGAAATAGA 6161
Qy   223 --- 223

Db   6162 GGAGTCAGGGGTCACTCTGGGGATTTGGCCTGGGGAGCAGCTGGAAGATGGAGTGCTGCTGTA 6221
Qy   223 --- 223

Db   6222 ACTTATGTAGGGAAGGCTGTGGGAAGAAGAGGTTTAGGAGACAAGGATAGCAGTTCATTT 6281
Qy   223 --- 223

Db   6282 ATTTATTTATTTATTTATTTATTTATTTAGATGTAGTCTCATTCTTTCGC 6341
Qy   223 --- 223

Db   6342 CAGGCTGGAGTGCAGTGGCGCATGGGCCGAGTCTCACTGCAACCTCCACCTCCCAGGCTCAAG 6401
Qy   223 --- 223

Db   6402 CGATTCTCTTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCATGTGCCAC 6461
Qy   223 --- 223

Db   6462 CATGCCTGGCTAATTTTTGTATTTTTTCAGTAGAGATGGGGTTTCACCACGTTAGC 6521
Qy   223 --- 223

Db   6522 CAGGCTGGTCTCGAACTGACCTCAGGCAATCCACCCGCCTCGACCTCCCAGTGTTGGTAT 6581
Qy   223 --- 223

Db   6582 TATAGGGCGTGAGCCACTGCGCCCGGCGATCCTTATTACAACTGCCAGTGTCCCT 6641
Qy   223 --- 223

Db   6642 CTTATATATATCAGGAAATAGAAGATTAGGAGAGGTTAAATAATTTGCCTAGAGTGGCA 6701
Qy   223 --- 223

Db   6702 TGGCTAGCTCGAAGTGAGCGAGGGGTCAACCCAGCCTGACTCCAAACCCAGGGTCCTA 6761
Qy   223 --- 223

Db   6762 GGGCTGAACTGCCCAGCCTTGCCCGAGGCTCCCGACTGGGCCCGTCTCGG 6821
Qy   224 ------LysGluIleGlnTyrLeuGluTyrLeuGluIleSerSerLeuGluIleSerGluVal 241

Db   6822 GGGCAGGAAGAGATCCTGCAGGAATACCTGGAGATTAGCAGCCTGGTGCAGGATGAGGT 6881
Qy   241 IValAlaIleHisArgGluMetAlaAlaAlaAlaAlaAlaArgIleGlnProGluGluTyr 261
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Db  6882  GGTGGCCATTCACCGGGAGATGGCTGCAGCTGCTGCCCGCCATCCAGCCTGCTGAGCCTGCGAGTA  6941

Qy   261  rGlnGlyPheLeuArgGlnTyr-Gly                                              269
               ||||||||||||| |||
Db  6942  CCAAGGCTTCCTGCGACAGTATGGGTAAGCCCGTCCTTGCTCCTGGCCCAGGGGCT               7001

Qy   270  ------------                                                            270
Db  7002  ---------------SerAlaProAspValProProC                                  277
               |||||||||||||||
Db  7002  GCTGGCCGTGTCCACTGACGGGGCGCGTGTCCCCACAGGTCCCACCTGACGTGTCCCCACCCCT       7061

Qy   277  YsValThrPheAspGluSerLeuLeuGluGluGlyProLeuGlyPheGlyProLeuGlyLeuG        297
               ||||||||||||||||||||||||||
Db  7062  GTGTCACGTTCGATGAGTCACTGCTTGAGGAGGGTGAACCCGGCCTGGGGAGCTCC               7121

Qy   297  lnLeuAsnGluLeuThrValGlnSerValGlnHisThrLeu------                        310
               ||||||
Db  7122  AGCTGAACGAGCTGACTGTGGAGACGGTGCAGCACACGTG-GGTGGTGCTTTGCACCTG            7180

Qy   310  ------------                                                            310
Db  7181  GGCTGCGGCGGGGCCTCCAGCAGACCACCAGAGTGTTTATGTAGGCAGGGCTAGGTTGTGGA         7240

Qy   310  ------------                                                            310
Db  7241  GACTGTCCACACAGAGCTGTCACCAGGTGGCCGGGCTTGCTTGGCTCTACAGGGATGCAC           7300

Qy   310  ------------                                                            310
Db  7301  TGGACCTGGGTGAGGGGCGAGGAGGGCTCCGGTTCTAATGCTGTCCCTTCTCTTGGGTGCA          7360

Qy   311  ----ThrSerValThrAspGluAlaValAlaAlaThrMetValPheGluArgGlnG               329
               |||||||||||||||||||||||
Db  7361  GGCTGACCTCAGTGACAGATGACAGATGAGCTGTGGGCCACCGAGATGGTGTTCAGGCGGCAG        7420

Qy   329  luMetValThrIleGlnLeuGlnGluLeuArgAsnGluGluGlnLeuAsnThrHisProArgG       349
               |||||||||||||||||||||||||||||
Db  7421  AGATGGTTACGCAGCTGCAACAGAGACTCCGGAATGAAGAGGAACACCCCACCCCCGGG            7480

Qy   349  lu---                                                                   349
               ||
Db  7481  AGCGGGTGAGGTGGGGCCCCCTGCCTCAGCAGGCCTCCTGGGCCTTCCTGGCTCCTACCCC          7540

Qy   349  ------------                                                            349
Db  7541  TAACTGCTGCTGGCTAGCCGCCGCAGACCAGACCCTTATTCTTCATCCACCCTCCACCCC           7600

Qy   350  ------ArgValGlnLeuLeuGlyLyGlyArgGlnValLeuGlnGluLeuLeuGln               365
               |||||||||||||||||
Db  7601  GCCCCTGCCTGCAGCTGCAGCTGCTGGGCAAGAGGCAAGTGCTGCAAGAACACTGCAG             7660

Qy   366  GlyLeuGlnValAlaLeuCysSerGlnAlaLysLeuGlnAlaGlnGlnLeuLeuGluGlnLeuGln    385
               ||||||||||||||||||||||||||
Db  7661  GGGGCTGCAGGTAGCGCGTGTGCCAAGCTGCCAAGCTGCAGGAGTTGCTGCAG                  7720

Qy   386  ThrLysLeuGlyHisLeuGlyProGlyGluProProValLeuLeuGlnLeuGlnAspAsp          405
               ||||||||||||||||||||
Db  7721  ACCAAGCTGGACCACCTGGGCCCCGGCGAGCCCCGTGCTGCTCCTGCAGGAGATGAC              7780

Qy   406  ArgHisSerThrSerSer------------                                          412
               |||||||||||
Db  7781  CGCCACTCCACGTCGTCCTC-GGTGAGCTGCCCATCCGGCGGCCGGCCGCACCCGGC              7839

Qy   412  ------------                                                            412
Db  7840  CTGCCCACCTGGGGCGCTTCCCATTTTCGCCCTCCCCTCCCTAAGCCTGGCCACCC               7899

Qy   413  ------GluGlnGluArgGluGlyArgThrProThrLeu                                424
               |||||||||
Db  7900  GCTGACGTCTGTCCCCTGGCCTGGGGCCTCCAGGGATGGGAGGAGGGGGAAGGACACCCCACGCTG     7959

Qy   425  GluIleLeuLysSerHisIleSerGlyIlePheArgProLysSer------------              440
               |||||||||||||||||
Db  7960  GAGAATCCTTAAGAGACCACCATCTCAGGAATCTTCCGCCCAAGTTCTCGGTGAGTGGCGCC         8019


Qy        440
Db  8020  CAGCCTGGGCCCCCTACTGTGTGTTCGAGTTTAATCACTGGGATGTCCTAGAGAGGA              8079

Qy        440
Db  8080  GGCTCTGCCCAGGCTGCTTGATTGGGAAGTTCCTCTCTTCCCTGGGATTCCAGGCTGCA            8139

Qy        440
Db  8140  GATGTCCCCAGACCCTGCCCCCGTGACCCCCTTCCATCGCCCCAGTGTGCTAAAGG               8199

Qy        440
Db  8200  GACCAGCAACCTGACTATTCCATGCTCTCCCGCTTCAGGAGCGGTTGGGGGCCTGTG              8259

Qy        440
Db  8260  GCCTGGAGGAGGAGCACCAGCTTGGTTGGGGTCTTCCTGCCTGGGCTTCCCTTCCCAG             8319

Qy        440
Db  8320  CTCTGCCCAGGGGTGAGCCTGGGCCCACTGTGCCCACTCCAGGGGCCTGTGGATGGCTC            8379

Qy        440
Db  8380  TGCATGCCACTCCATGGTTGTGAAGGCTGAGGGCTTCCCTTCTCTTGGGTGCA                  8439

Qy        440
Db  8440  GCTGCCCCCACGGCCCTTCCCAACAGGTGGTTAAGTGACTCCTCCTGATCCTCCCTTGC            8499

Qy        440
Db  8500  CCAGCTCCCTGCCCACCGCTGCAGCTGCCTCATTCCCGGAGGTGCAGAAGCCCCTGCATGAGCAGCT   8559

Qy        440
Db  8560  GTGGTACCACGGGGCCCATCCCGAGGGCAGAGGTGCTGAGCGTGCTGGTGCACTCTGGGGA         8619

Qy        440
Db  8620  CTTCCTGGTGCGGGAGAGCCCAGGGAGCCAGCAGGAGTACGTGTCGTGTGCGGTGGATGG          8679

Qy        440
Db  8680  TCTGCCCCGGACACTTCATCATCCAGTCCTTGGATGTGAGTGGGGACCCGAGCCTT              8739

Qy        440
Db  8740  CCAGGCCTACTCTTCTCCCCTCCCTTCCCCCAAGGGAAATGGCCTTTCAGGGTAGGG             8799

Qy        440
Db  8800  GGTAGCTGCCAGGTCTTGGATGCCTCCCTAGCAGGCTGCTGGAAGGGGCCACAGAGAC            8859

Qy        440
Db  8860  CACCCTGCCCTGCAACAAAATAGAGGCTTAAGTGTGAGTCTCCCTGGTGGGCAGCA              8919

Qy        440
Db  8920  GGATGTCATGTGCCATCAGATGGCATCTTTTCTGGAGGTCTTCTCTGCCCCTGGTCTCTGGG        8979

Qy        440
Db  8980  CAGGGCCCTTTCTCCCCGCTGCTCCTCCGTCTCCTCCCCCAGGGGCTCAGCCCCCCCCAGA         9039

Qy   441  AsnLeuTyrArgLeuGlyGlu                                                   448
Db  9040  ATGGAGGCTGCTGACCCCGGTCCCCGTCCCCTGCAGAACCTGTACCGACTGGAAGGGGAA          9099
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Qy    449 GlyPheProSerIleProLeuIleAspHisLeuLeuSerThrGlnProLeuThr 468
Db   9100 GGCTTTCCTAGATTCCTTTGCTCATCGACCACCTACTGAGACCCCAGCAGCCAACTTT 9159
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy        AGAGAACTGCGGACTGGGAAGGCCGTGGTAGGAGCCAAGACCGTTTCAGGGGAACTTT 10238

Qy    469 LysLysSerGlyValValLeuValHisArgAlaValProLys---------------- 481
Db   9160 AAGAAGAGTGGTGTGTCCTGCACAGGGCTGTGCCCCAAGGTGAGCCTGCACCCAGCCTGG 9219
          |||||||||||||||||||||||||||||
Qy    503 GlyGluValPheSerGlyArgLeuArgAlaAspAsnThrLeuAlaValLysSerCys 522
Db  10239 GGCGAAGTGTTCAGCGGACGGCTGCGAGCCGACAACACCCTGGCCGTGAAGTCTTGT 10298

Qy    481 -------------------------------------------------------- 481
Db   9220 CCCATGCCACCTGTGGCAGGGCTTGGGAGTGTGGGTCAGGCCCACCCAGCGTCTGAGCA 9279
Qy    523 ArgGluThrLeuProProAspLeuLysAlaLysPheLeuGlnGluAla--------- 538
Db  10299 CGAGAGACGCTCCCACCTGACCTCAAGGCCAAGTTTCTACAGGAAGCGAGGTGGGTGATA 10358

Qy    481 -------------------------------------------------------- 481
Db   9280 GAAAAGGGCTTTCCAGGGCCTCGTCTACATACAAGATGCAGAGTGACCCTCAGGGC 9339
Qy    538 -------------------------------------------------------- 538
Db  10359 AACTAATGATCACCACGGGTCCCGATACACAGAGGTTACACTGCACATGGCACAGTGTGAA 10418

Qy    481 -------------------------------------------------------- 481
Db   9340 CAGCCTTGCTCTAGGTTTGGAATGTCAGGGCCACTCCTATGGCCATGGCTGTACACACCA 9399
Qy    538 -------------------------------------------------------- 538
Db  10419 GTGCTTGACCACCTGTGGTGTTTAGTCCTGAGGCCCCATTGCGGGTAGTACCCCC 10478

Qy    481 -------------------------------------------------------- 481
Db   9400 GGTTGGTGCTTACCTGTCAGGGCACCTGCCTGACCCCGTAGTCATCCAGTGTGCTCC 9459
Qy    538 -------------------------------------------------------- 538
Db  10479 TTATAGTGCCGAAGGGTAGAGGCTGCCCAGTGCACACGTCCGGGTCTGCTGCCTTGA 10538

Qy    481 -------------------------------------------------------- 481
Db   9460 CCACGTGGTCCCACCCCCTGGTCACATATGGAGGGCGCCAAAAAATGGAGGACACAGCCCTT 9519
Qy    538 -------------------------------------------------------- 538
Db  10539 GGCCAAGCTCTTCTCCATCATCCTCGGGGGCGCCTGCCTGGCGGGGGGCCTGGCCACGTAG 10598

Qy    481 -------------------------------------------------------- 481
Db   9520 CTAAGGCCCAGCACCCCTTTCTTCAGACTTCTGATCCCCGTGTCTCCTCTTCCCCAG 9579
Qy    539 ----------------ArgIleLeuLysGlnTyrSerHisProAsnIleValAr 551
Db  10599 ATCCTGAGCAGCAGTGCCCTCCAGGATCCTGAGCAGTACAGCCACCCCAACATCGTGCG 10658

Qy    482 AspLysTrpValLeuAsnHisGluAspLeuAspLeuValLeuGlyIleGlyArg--- 499
Db   9580 GACAAGTGGGTGCTGAACCATGAGGACCTGGTGTTGGGTGAGCCAGATTGGACG-GGTGAG 9638
          ||||||||||||||||||||||||||||||||
Qy    551 gLeuIleGlyValCysThrGlnLysGlnProIleTyrIleValMetGluValGln- 570
Db  10659 TCTCATTGGTGTCTGACCCCAGAAGCAGCCCATCTACACCGTGTGCAGCTGC 10718

Qy    499 -------------------------------------------------------- 499
Db   9639 TGCGCCCTGCTGGCCTTCTGTGGCGACTTCCTGAGTCGGCCTGGGCCCCCT 9698
Qy    570 -------------------------------------------------------- 570
Db  10719 TGAGCGGGGGGCTGAGCTCCAGGTAGGGCCGCAGCCTGTCAGGTGGCAGCCTACC 10778

Qy    499 -------------------------------------------------------- 499
Db   9699 GCCCTACCACCCAGAAACTCCCTGCCCCATCTGAATCCCCACTGTACCCGACTCCCT 9758
Qy    571 ------------GlyGlyAspPheLeuThrPheLeuAr 579
Db  10779 TCAGGAGGCTCAGCAGGGGTCCTCCCACCTGCAGGGGCCGCTTCCTGACCTTCCTCG 10838

Qy    499 -------------------------------------------------------- 499
Db   9759 GCCCAGCGCCCCACCACACACCATCCTCCAGGAAACGGGACTACCTGCTGAAAACTC 9818
Qy    579 gThrGluGlyAlaArgLeuArgValValThrLeuGlnMetValGlyAspAlaAlaAl 599
Db  10839 CACGGAGGGGGCCCGCCTGCGGGTGGAAGACTTCTGCAGATGGTGGGGGATGCAGCTGC 10898

Qy    499 -------------------------------------------------------- 499
Db   9819 CCAGCAGACAGCTCTGCCGCAGCACCCTGACCTCATCACCCCCCAGGCCGCCCCATCG 9878
Qy    599 aGlyMetGluTyrLeuGluSerLysCysCysIleHisArg--------- 612
Db  10899 TGGCATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCG-GTGAGTGGGGCGGTGGCCACG 10957

Qy    499 -------------------------------------------------------- 499
Db   9939 AGCTCTTGTGTGCACGGAGGAGACACCCGTGTTACTGTAAGCCATAAGATACCTGTTTAG 9998
Qy    612 -------------------------------------------------------- 612
Db  11018 GGACCATCAGGGCATCAGCTCCAGAGGGGAGTTGGCCTCTCGTGGTAGACAGGGGTGCCCA 11077

Qy    499 -------------------------------------------------------- 499
Db   9999 GGATTTCCATGTCCACTTCTCTCAGGAGGGGTGGCACATGTCACTTTTCCCTGCCTG 10058
Qy    612 -----------------AspLeuAlaAlaArgAsnCy 619
Db  11138 GACTGTTGGCCAAATGAGCCCTGTCTCACCCAGGACCTGGCTGCTCGGGAACTG 11197

Qy    499 -------------------------------------------------------- 499
Db  10059 CCCCATGTGCTCCTCTAGGTTCCCCAGCGAGGGTCAAACTCCCAGAGAGCCTGGGGTGGAGG 10118
Qy    619 aLeuValThrGluLysAsnValLeuLysIleSerAspPheMetSerArgArgGluGluAl 639
Db  11198 CCTGGTGACAGAGAAGAAATGTCCTGAAGATCAGTAGCTTTGGGATGTCCCGAGAGGAAGC 11257

Qy    499 ---------------GlyAsnPhe 502
Db  10178 GGTCCGAACACGGGGCCCCTCACCCAGGGGTAGGAAGCAGAATGGGTAGGAAGCGGAGA 10178
Qy    639 aAspGlyValTyrAlaAlaSerGlyIleGlyLeuArgGlnValProValLysTrpThrAlaPr 659
Db  11258 ---------...
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Db   11258  CGATGGGTCTATGCAGCCTCAGGGGGCCTCAGACAAGTCCCGTGAAGTGGACCGCACC  11317
Qy     659  oGluAlaLeuAsnTyr                                              664
                    |||||||||
Db   11318  TGAGGCCCTTAACTACGGTACCTAGTCCCTGTCTACCCTGGACTTCCATGGCCAGAGGCCA  11377
Qy     664  ---                                                          664

Db   11378  GGCCTGGGTCCTGCCCGGTCGCCTCGCCCTGCCCCAGGAGGGTGCACTCACGCTGCCTC  11437
Qy     665  ----------GlyArgTyrSerGluSerAspValTrpSerPheGlyI              678
                      ||||||||||||||||||||||||||
Db   11438  ACCTCCTGCCTCCTCTGCAGGCCGTACTCCTCCCGAAAGCGACGTGTGGAGCTTTGGCA  11497
Qy     678  leLeuLeuTrpGluThrPheSerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnG  698
                  |||||||||||||||||||||||||||||
Db   11498  TCTTGCTCTGGGAGACCTTCAGCCTTGGGGGCCTCCCCATCCCAACCTTCAGCAATCAGC  11557
Qy     698  lnThrArgGluPheValGluLys                                      705
                  |||||||||
Db   11558  AGACACGGGAGTTTGTGGAGAAGGGTAAGCACCCTGTGATGACAGCAGCCTCAGGCTGCA  11617
Qy     705  ---                                                          705

Db   11618  CCCTCTTCCAGATGCTTCCAGCCGGACTCTTCTAACTCCCTTAATGCCAACCTTCCCACCA  11677
Qy     705  ---                                                          705

Db   11678  GGCAGAATAAGAATAACCTGGCCAGTTGCTCACGCCTGTCATCCCAGCACACTTTGGGAGGC  11737
Qy     705  ---                                                          705

Db   11738  TGAGCTGGGTGGGATCACTTGAGCCCAGGAGTTCAAGATCAGCAGTTGGACAACACAGTGAAA  11797
Qy     705  ---                                                          705

Db   11798  CTCCATCTGTACAAAAAATACAAAAAATAGACTGGGCACGGTGGCTCACACCTGTAATCCC  11857
Qy     705  ---                                                          705

Db   11858  AGCACTTTGGGAGGCCGAGGCGAGGCGGATCACCTGGTCACCTGTCAGGAGTTTGAGACCAGCCAG  11917
Qy     705  ---                                                          705

Db   11918  ACCAACATGGTGAAACCCCATCTCTACTAAAAATACAAAAAATTAGGCACGGCATGGTGGCA  11977
Qy     705  ---                                                          705

Db   11978  CGTGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGTGGGAGAATTGCTTGAACCCAGGAG  12037
Qy     705  ---                                                          705

Db   12038  GCGGAGGCTGCAGTGAGCCGAGATTGTGCCACTGCACTCCAGCCTGGGCGACAAGAGTGA  12097
Qy     705  ---                                                          705

Db   12098  AACTCCATCTCAAAAAAACCAAAAAACAAAAAATACAAAAAATTAGCTGGGTGTGGTGAC  12157
Qy     705  ---                                                          705

Db   12158  ATGCGCCTGTAGTCCCTGCTACTCGGGAGGCTGAGGTGGGAGGATCACTGGAGCCCGGGA  12217
Qy     705  ---                                                          705

Db   12218  GGTGGAGGTTGCAGTGAGCTGAGTCATGCCACTGCACCCCAACCTGGGTGACAGAGAGA  12277
Qy     705  ---                                                          705

Db   12278  GAGAGAGACCTTGACTCGAAAAGAAAAAACCTGGCGCGCAGTGGCTCACGCCTGTAATT  12337
Qy     705  ---                                                          705

Db   12338  TCAACATTTTGGGAGGCTGAGGCTGGATCACTTGAGGTCTAGGAGTTTGACACTAGCC  12397
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Qy    705  ---                                                          705
Db  12398  TGGCCAACATGGCAAAACCTGTCTCTACTAAAAATACAAAAAATTAGCGAGGTGTAGTGG  12457
Qy    705  ---                                                          705
Db  12458  TGCAAGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAACCTGGG  12517
Qy    705  ---                                                          705
Db  12518  AGGTGGAGGTTGCAGTGAGCTGAGATCACCACCACTGCATTCCAGCCTGGGTGACAGAGCA  12577
Qy    705  ---                                                          705
Db  12578  AGACTCCATCTCAGAAAAGAAAAAAAATGAATATCCCGTGAGCTACTACTACTGAGTG  12637
Qy    705  ---                                                          705
Db  12638  AGCACCTGGTCTGTGCTAGTCACATGTTATTTCATTTGCTCATCACTACATGTGTGGTA  12697
Qy    705  ---                                                          705
Db  12698  GGGATTAATATGTCCCTTTCTCAGATGGGAAAAACAGGCTGGCAGAGGGGACACAGCTAGC  12757
Qy    705  ---                                                          705
Db  12758  ACGTGGTAGGATTAGGATCAGAAGCCAGGCCTCTTTGTCCTTTGGTGTGGAGAA  12817
Qy    705  ---                                                          705
Db  12818  CAGTGCATCCTTCAGAACAGTGCATCTTAAGCAGTCTCATGGCTCATGGTATCCCCCAG  12877
Qy    705  ---                                                          705
Db  12878  AGTCTGCGAGGACCCTCAAACTCCCTCCTCATGCCTGGTGTGCTGCCTCTCCTCACA  12937
Qy    706  GlyGlyArgLeuProCysProGluGluCysProAspAlaValPheArgLeuMetGluGln  725
                   |||||||||||||||||||||||||||||
Db  12938  GGGGGCCGTCTGCCCTGCCCAGAGCTGTGTCCTGATGCCGTGTTCAGGCTCATGGAGCAG  12997
Qy    726  CysTrpAlaTyrGluProGlyGlnArgProSerPheThrIleTyrArgGlnGluLeuGln  745
                   |||||||||||||||||||||||||||||
Db  12998  TGCTGGGCCTATGAGCCTGGGCAGCGGCCCCAGCTTCAGCACCATCTACCAGGAGCTGCAG  13057
Qy    746  SerIleArgLysArgHisArg  752
                   |||||||||||||||
Db  13058  AGCATCCGAAAGCGGCATCGG  13078
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RESULT 5
US-10-660-763-3
; Sequence 3, Application US/10660763
; Publication No. US20040063130A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001183DIVII
; CURRENT APPLICATION NUMBER: US/10/660,763
; CURRENT FILING DATE: 2003-09-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 15297
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-660-763-3

Alignment Scores:
Pred. No.:   Length: 15297
Score: 1.01e-191   Matches: 747
Percent Similarity: 21.28%   Conservative: 0

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Best Local Similarity:   21.28%        Mismatches:   5
Query Match:             55.09%        Indels:       2764
DB:                      18            Gaps:         16

US-10-660-763-2 (1-752) x US-10-660-763-3 (1-15297)

Qy      1 MetGlyPheSerGluLeuCysSerProGlnGlyHisGlyValLeuGlnMetGln 20
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   2563 ATGGGCTTCTCTTCTGAGCTGTGCAGCCCCCAGGGCCACGGGTCCTGCAGCAAATGCAG 2622

Qy     21 GluAlaGluGluArgLeuLeuGluGlyMetArgLysTrpMetAlaArgValLysSer 40
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   2623 GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCAGCGGGTCAAGAGT 2682

Qy     41 AspArgGluTyrAlaGlyLeuLeuHisHisMetSerLeuGlnAspSerGlyGlyGlnSer 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2683 GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGCAGTGGGGGCCAGAGC 2742

Qy     61 ArgAlaIleSerProAspSerProIleSerGlnSer---------------- 72
          |||||||||||||||||||||||||||||||||
Db   2743 CGGGGCCATCAGCCCGACAGCCCCATCAGTCAGGT-GGGTCTCTATGGGACTCTGGTGGG 2801

Qy     72 ------------------------------------------------------- 72
Db   2802 TGCTGGCGTATCTGCCTTCTCCTTCTCCTCTCCTGGGGGCCCTCCTGGGGCAGTGGCTGGAGA 2861

Qy     72 ------------------------------------------------------- 72
Db   2862 TCTGGCAGGCCAATGCTTGGGAGCCATTGTGCCCCCCTCCCCCATCTGTGCT 2921

Qy     73 -------TrpAlaGluIleThrSerGlnThrGluGlyLeuSerArgLeuLeuArgGlnIle 89
                  |||||||||||||||||||||||||||||||||||||||
Db   2922 GTATAGTCCTGGGCTGAGATCACCAGCCAAACTGAGGGCCTTGAGCCGCTTGCTGCGCGCAG 2981

Qy     90 HisAlaGluAsnSerGlyProLeuSerLysLeuLeuSerLeuLeuIleLeuArgGluArg 109
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2982 CACGCAGAGAATCTGAACTCAGGGCCCTGAGCAAGCTGAGCCTGCTCATCCGGAACGG 3041

Qy    110 GlnGlnLeuArgLysThrTyrSerGluGlnTrpGlnLnTrpGlnLeuGluThrLys 129
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   3042 CAGCAGCTTCGCAAGACCTACAGCGAGCAGTGGCAGCAGGAGCTCACCAAG 3101

Qy    129 ------------------------------------------------------- 129
Db   3102 GTGAGCGGGGCAGCACTGGGGCTTCGGTCATTTCGTCTAAATTTTGAGCCTCGAAGGGGT 3161

Qy    129 ------------------------------------------------------- 129
Db   3162 TGTTTTGCACAGAGAGGCCCTGGATTCACTGGGAGTGTAAGTCCCTGACCGCGAGGCCTG 3221

Qy    129 ------------------------------------------------------- 129
Db   3222 GCTTGCTCTAACCTTGATGTAGCTTCCTCTCTTCCTCCCCTACGTTGAGCTGGCTTGCA 3281

Qy    129 ------------------------------------------------------- 129
Db   3282 GCAAGGCCTCTCTGTGCTTTTTCTGTGCCTCTGGCAAAGTGCTGGGAGTGTAAGGATGAGT 3341

Qy    129 ------------------------------------------------------- 129
Db   3342 GACCGGTCACGTGCCTGGGAGAAGCTCAGAATGGTCACTCGCCTCCACACTGTGCCATCT 3401

Qy    129 ------------------------------------------------------- 129
Db   3402 GGCTCTGGGTTCTGAGAGTCAGGGAGGAGGAATGAGGGTCAGTCTGTTTGCCTTCGACCTA 3461

Qy    129 ------------------------------------------------------- 129
Db   3462 TGCAGCCTCCTCTCAGGGCCCCAGACTGGCCAGCAGCATGGCCCCCGAAGGTCGAGG 3521

Qy    129 ------------------------------------------------------- 129
Db   3522 ACTCGGGCGTGAAGTCAGCCTGCCTAGGTTTGAATCCCACCCAGCTCCTCAGTCTAGAG 3581
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Qy    129 ------------------------------------------------------- 129
Db   3582 GCTGTGTGATTGGAACTATTTATCTGGGAGCCTAGTGCCCCATTCAGTGTGCTGTGTCA 3641

Qy    129 ------------------------------------------------------- 129
Db   3642 CCCTCCTGCCACCACCACCCTTCCTCCAGTGCAGAGAGCCCAGCCTTGCCATGGACCCACAG 3701

Qy    129 ------------------------------------------------------- 129
Db   3702 CGGCCCCTGGTGTGGCCACCTGCCCATTCCTCGCCCCAAAAGATCATCTGATTCAAGGG 3761

Qy    129 ------------------------------------------------------- 129
Db   3762 TGGGCCCATTTTTATAAAGTTTGCTGGAACACAGTCATGCCCCTTTGTTTTTCATATTGT 3821

Qy    129 ------------------------------------------------------- 129
Db   3822 CTGTGACTACAATGCAGAGTTGAGTAATTGTGACAGAGGCTCTATGGCCTACAAGCCTA 3881

Qy    129 ------------------------------------------------------- 129
Db   3882 AAATATTATTACTATCTGGCCCTTTAAGAAAAGACTGATCTAGTCGAGGAATCTAGC 3941

Qy    129 ------------------------------------------------------- 129
Db   3942 TCAGTTACAGATGGGGAAACTGAGGTTGGGCGCTTGCCCAACATATCCAGCACATAAAC 4001

Qy    129 ------------------------------------------------------- 129
Db   4002 AGGAGAACTGGGACGAGAGAACACTGATCTCGGGCTGTCATCTATTCCTACTGCCAAGAACA 4061

Qy    129 ------------------------------------------------------- 129
Db   4062 TAATTTGCAGGACCCAGTGCAAAGTGAAATTGTGGGGGTCTTGTTAAAAGATTGCTAGG 4121

Qy    129 ------------------------------------------------------- 129
Db   4122 AATTTCCAGGTGGCAATAATGGAGAATGAAACCAAGCACAGGCGCCCTTCTACATGTGAG 4181

Qy    129 ------------------------------------------------------- 129
Db   4182 CCCCGTGTGACTGACACAGGCCGTGCACACCTGCCAACTGGCCCTGCCACCCAGGCTAC 4241

Qy    129 ------------------------------------------------------- 129
Db   4242 CACTGTGTCAGTCCAAGGAGGGGACCCGTTGTAGCCTGTGTGTACCTCTTTGCCTCCCCAAGG 4301

Qy    129 ------------------------------------------------------- 129
Db   4302 GGTCTGTCTTCAACAGGCTCTCGATCTTTGACTCTCACGTCAGCAGCCAGCTTTCCCAG 4361

Qy    129 ------------------------------------------------------- 129
Db   4362 AAGTCTTCCAGGTGCTCCTTGCCTGGACGACAGCAGCCTTTCACCCCAGGCCAAG 4421

Qy    130 ------------------------------------------ThrHi 131
                                                      ||||
Db   4422 AATCTTCCACAACTGGGAACCTGCTGCCCCACACTGGCCTCTCCTCCTCCTAGACCCA 4481

Qy    131 sSerGlnAspIleGluLysLeuLysSerGlnTyrArgAlaLeuAlaLeuArgAspSerAlaGl 151
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   4482 CAGCCAGGACATTGAAGAGCTGAAGAGCCAGTACCGAGCTCTGGCACGGGACAGTGCCCA 4541

Qy    151 nAlaLysArgLysTyrGlnGluAlaSerLys------------------------- 161
          ||||||||||||||||||||||||
Db   4542 AGCCAAGCGCAAGTACCAGGAGGCCAGCAAAGGTTCGTGGCGTTCCCTGGCTGGCAGGGAG 4601

Qy    161 ------------------------------------------------------- 161
Db   4602 GGAATCCGAAGCCAGCCAGTGCTGCTGACCTGTCTCCTTGGGTACCCAGAGAGTGGGGCTGCCTCGGGC 4661
```

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Qy   162  ----------------------------------------AspLysAspArgAspLysßAl  168
                                                  ||||||||||||
Db  4662  CTCCATGCTGTCATCTATACCCTTGCCCCCTTCTGCCAGACAAGGACCGTGACAAGGC  4721

Qy   168  aLysAspLysTyrValArgSerLeuTrpLysPheAlaHisHisAsnArgTyrValLe  188
          |||||||||||||
Db  4722  CAAGGACAAGTATGTGCGCAGCCTGTGGAAGCCTTTGCTCACCACAACCGCTATGTGCT  4781

Qy   188  uGlyValValArgAlaAlaGlnLeuHisHisGlnHisHisGlnLeuLeuProGlyLe  208
          |||||||||||
Db  4782  GGGCGTGCCGGGCTGCGCAGCTACACCACCACCAGCACCACCACCAGCTCCTGCTGCCGGCCT  4841

Qy   208  uLeuArgSerLeuGlnAspLeuHisGluGluHisGlyMetAlaCysIleLeu------  223
          |||||||||
Db  4842  GCTGCGGTCACTGCAGGACCTGCACGAGGAGATGGCTTGCATCCTGTAAGCCCCCCAGCCC  4901

Qy   223  ----------------------------------------------------------  223
Db  4902  CGTCCCCTGGCCCCACCCTTGAGCAGCCCTAAGCCCAGCCATCAGGCCCCAGAGGCAGGA  4961

Qy   223  ----------------------------------------------------------  223
Db  4962  CCCAGAAAATCCATTGCTGGGAAGTGCTGGCCATGTAACCACCATGAGAACGGGACCTGG  5021

Qy   223  ----------------------------------------------------------  223
Db  5022  GCCAAGGACGGATTGGAAACAGGCAACTTACCTCTGAATTACACTATTCCAGGGTCTCATTATT  5081

Qy   223  ----------------------------------------------------------  223
Db  5082  CCAGGGTTTTATTACATTCATTGAGCACTGTTCTGGGGCTCTGGATTATACCAGAGAACGA  5141

Qy   223  ----------------------------------------------------------  223
Db  5142  TGGTAGACAAAAACATCTGTCCTCAGGGATCTTTCGTGTTGTTAGTGGAGTGAGAATGTGAGG  5201

Qy   223  ----------------------------------------------------------  223
Db  5202  AGCACTAAGAGCCCATGGAGAAAAATAAAGCAAGAGAAGTGGATCGGAGACCTGGGAGCACG  5261

Qy   223  ----------------------------------------------------------  223
Db  5262  GAGGCAAGGAGGAGGTGACAGTTGTCCATAGAGTGATCTGGAAAGCCTCTTGAGAGGT  5321

Qy   223  ----------------------------------------------------------  223
Db  5322  GACATTCAAAGAGGCCCTGAGAGGGTCAGGGTGAATCATGGGGCTATTTGGAGAAA  5381

Qy   223  ----------------------------------------------------------  223
Db  5382  GACCATTCCAGAAAGAGGACAGCAATTACACAGGGCCTTGAGGTAGGAGAGTACCAGGGA  5441

Qy   223  ----------------------------------------------------------  223
Db  5442  CTAATAGCCAGGAACCAGTGTGCCTCTGAGAGTGAGGAGGGGGAGAGTCATCACGAG  5501

Qy   223  ----------------------------------------------------------  223
Db  5502  GCTGGAGGAGGCAGGCGGTCAAGGCGTACTGGGTGATAGAGAAGGTCTACGCAGGGGCCATGGTG  5561

Qy   223  ----------------------------------------------------------  223
Db  5562  AGGACTTTGGGCTCTGGGTGAACAAGAATGGCATGAGATCTGACCTCTGTTTTTTGTTTCAT  5621

Qy   223  ----------------------------------------------------------  223
Db  5622  TTTGTTTTAACTTTTTTTTGAGTCAGATGTCTCGCTCTGCCCGCCCAGGCTAGAGTGCAGTGG  5681

Qy   223  ----------------------------------------------------------  223
Db  5682  CATGATCTCGGCTTACTGCAACCTCCGCCTCCCCAGTTCAAGTGATTCCCTGCCTCAGC  5741

Qy   223  ----------------------------------------------------------  223
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Db  5742  CTCCCGAGTAGCTGAAAATACGGGCATGCGCACCACACCAGCTAATTTTTGTATTTT  5801
Qy   223  ----------------------------------------------------------  223

Db  5802  AGTAGAGACGGGGTTTCACCATGTTGCCCAGGCTAGTCTCTAATTCCTGGCTCAAAGCG  5861
Qy   223  ----------------------------------------------------------  223

Db  5862  ATTTGCCTGCCTCTGCCTCCCAAAGTGCCGGGATTACAGGCATGAGCCACCATGCCCAGC  5921
Qy   223  ----------------------------------------------------------  223

Db  5922  CCTGACCCTCTGTTTTAATAAGGCCACTCTGGCTGTCTGCAATAGACTTCAGGGAG  5981
Qy   223  ----------------------------------------------------------  223

Db  5982  CAAGGACAGAAGCTGGGAGGCCAGAGAGAGCAGGCTGCTTGCCATATCCAGATCCAAGCTT  6041
Qy   223  ----------------------------------------------------------  223

Db  6042  TTGGCCAGTAGGACGGGGAGGTAGCAATGGAGGTGAGCGCGGTCAGGTTCCTGGGCAG  6101
Qy   223  ----------------------------------------------------------  223

Db  6102  GTCCTGGAAGTGAAGCCAGTGGGATTTCCCTATCGGATTGGAAGTGGGCGGCGTGAAATAGA  6161
Qy   223  ----------------------------------------------------------  223

Db  6162  GGAGTCAGGGGTCACTCTGGGGATTTGGCCTGGAGCAGCTGGAAGATGGAGTGGCTGTTA  6221
Qy   223  ----------------------------------------------------------  223

Db  6222  ACTTATGTAGGGAAGGCTGTGGGAAGAAGAGGTTTAGGAGACAAGGATAGCAGTGTCATTT  6281
Qy   223  ----------------------------------------------------------  223

Db  6282  ATTTATTATTATTATTATTATTATTAGAGATGTAGTGTCTCATTCTTCGC  6341
Qy   223  ----------------------------------------------------------  223

Db  6342  CAGGCTGGAGTGCAGTGGCGCGATCTTGGCTCACTGCAACCTCCACCTCCCAGGCTCAAG  6401
Qy   223  ----------------------------------------------------------  223

Db  6402  CGATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCGATGTGCCAC  6461
Qy   223  ----------------------------------------------------------  223

Db  6462  CATGCCTGGCTAATTTTTGTATTTTTTCAGTAGAGATGGGGTTTCACCACGTTTAGC  6521
Qy   223  ----------------------------------------------------------  223

Db  6522  CAGGCTGGTCTCGAACTGACCTCAGGCAATCCACCCGCCTCGACCTCCCAGTGTTGGTAT  6581
Qy   223  ----------------------------------------------------------  223

Db  6582  TATAGGCGTGAGCCACTGTGCCTGCCCACTGTCCTTATTACAACTGCCAGTGTCCCT  6641
Qy   223  ----------------------------------------------------------  223

Db  6642  CTTATATATCAGGAAATAGAAGATTAGGGAGAGGTTAAATAATTGCCTAGAGTGGCA  6701
Qy   223  ----------------------------------------------------------  223

Db  6702  TGGCTAGCTCGAAGTGAGGCAGGGGTCAACCCAGCCCTGACTCCAAACCCAGGGTCCTA  6761
Qy   223  ----------------------------------------------------------  223

Db  6762  GGCCTGAACTGCCCAGCCTCCCTGACTGGGGATCCCGTCTCGG  6821
Qy   224  ------LysGluIleLeuGlnGluTyrLeuGluIleSerSerLeuValGlnAspGluVa  241
                ||||||||||||||||||||||||||||||||
```

```
Db  6822  GGGCAGGAAGGAGAGATCCTGCGAGAATACCTGGAGATTAGCAGCCTTGGTGCAGGATGAGGT  6881

Qy   241  lValAlaIleHisArgGluMetAlaAlaAlaAlaAlaArgIleGlnProGluAlaGluTy
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6882  GGTGGCCATTCACCCGGAGATGGCTGCAGCTGCTGCCCGCATCCAGCCTGAGGCTGAGTA  6941

Qy   261  rGlnGlyPheLeuArgGlnTyr-Gly
          |||||||||||||||||| |||
Db  6942  CCAAGGCTTCCTGCGACAGTATGGGTAAGCCCGTCTTCTGCTGGGCCCAGGGCT  7001

Qy   270  --------SerAlaProAspValProProC
                  ||||||||||||||||||
Db  7002  GCTGGCCGTGTCCACTGACGGGCGCTGTCCCCACAGGTCCGCACCTGACGTCCCACCCT  7061

Qy   277  ysValThrPheAspGluSerLeuLeuGluGluGlyProGluLeuGlyLeuProGlyGluLeuG
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7062  GTGTCACGTTCGATGAGTCACTGGTGAACCCGTGGAGGGGTCCTGGAGCCTCGGGGAGCTCC  7121

Qy   297  lnLeuAsnGluLeuThrValGlnSerValGlnHisThrLeu--------
          ||||||||||||||||||||||||||||||||||||||||
Db  7122  AGCTGAACGAGCTGACTGTGGAAGAGGCTGCGCACACGTG-GGTGGTGGCTTTGCACCTG  7180

Qy   310  ----
Db  7181  GGCTGCGGGGGGTCTCCAGCAGACCACGAGTGTTTATGGCAGGGCTAGGTCGTGGA  7240

Qy   310  ----
Db  7241  GACTGTCCACACAGAGCTGTCACCAGGTGGCCGGGCTTGCTGGCTCTACAGGGATGCAC  7300

Qy   310  ----
Db  7301  TGGACCTGGGTTGAGGGGCCAGGAGGGCTCCGTTCTCAATGCTCCTTCTCTTGGGTGCA  7360

Qy   311  ----ThrSerValThrAspGluLeuAlaValAlaAlaThrGluMetValPheArgArgGlnG
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7361  GGCTGACCTCAGTGACAGAGTGAGCTGGCTGTGGCCACCGAGATGGTTCAGGCGGCCAGG  7420

Qy   329  luMetValThrGlnLeuGlnLeuGluArgAsnGluGluGlnAsnThrHisProArgG
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7421  AGATGGTTACGGCAGCTGCAACAGGAGACTCCGGAATGAAGAGGAGAACACCCACCCCGGG  7480

Qy   349  lu--------
          ||
Db  7481  AGCGGGTGAGTGGCCCCTGCCTGCTCCTGGGCCTTCCTGGCCTCCTCCTCCTACCC  7540

Qy   349  ----
Db  7541  TAACTGCTGCTGGCTAGCCGCCGCAGAGACCGAGCCCTTATTCTTCATCCACCCTCCCACCC  7600

Qy   350  ------ArgValGlnLeuLeuGlyLysArgGlnValLeuGluLeuGlnValAlaLeuGluGln
                ||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db  7601  GCCCCCTGCCTAGCGGTCCTC-GGTGAGCTGCAGCTGCTGGGCAAGAGGCAAGTGCTGCAG  7660

Qy   365  -
Db  7661  GGGCTGCAGGTAGCGGTGTGCGTGCAACAGGCCCAAGCTGCCAGCAGGAGTTGCTGCAG  7720

Qy   366  GlyLeuGlnValAlaLeuCysSerGlnAlaLysLeuGlnAlaGlnGluLeuLeuGln
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7721  GGGCTGCAGGTAGCGGTGTGCGTGCAACAGGCCCAAGCTGCCAGCAGGAGTTGCTGCAG  7780

Qy   386  ThrLysGluHisHisLeuGlyProGlyGlyProValLeuLeuLeuGlnLeuGlnAspAsp
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7781  ACCAAGGTGGAGCACCTGGGCCCCGGCGGCCCCGTGCTGCTGCTCCTGCAGGATGAC  7839

Qy   406  ArgHisSerThrSerSer----------
          ||||||||||||
Db  7840  CGCCACTCCACGTCGTCCTC-GGTGAGCTGCAGCTGCTGGGCAAGAGGCCCCACCGGC  7899

Qy   412  ----
Db  7900  GCTGACCTGTCCCTGCCCTCAGGACCAGAGGGCGGAAGCAACACCCACCGCTG  7959

Qy   413  --------GluGlnGluArgGluGlyGlyArgThrProThrLeu
                  |||||||||||||||||||||||||||||||
Db  7960  ...
```

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Qy   425  GluIleLeuLysSerHisIleSerGlyIlePheArgProLysPheSer----
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  7960  GAGATCCTTAAGAGCCACATCTCAGGAATCTTCCGCCCAAGTTCTGGTGAGTGGCGCC  8019

Qy   440  ----
Db  8020  CAGCCTCGGGCCCCCCTACTGTTGTGTTTAATCACTGGGATGTCCTAGAGAGGA  8079

Qy   440  ----
Db  8080  GGCTCTGCCCAGGCTGCTTGTATTGGGAAGTTCCTCTTCCCTGGGATTCCAGGCGTCA  8139

Qy   440  ----
Db  8140  GATGTCCCAGACCCTGCCCCTGTGACCCCTCCCTTTCCATCGCCCAGTGTGCTAAAGG  8199

Qy   440  ----
Db  8200  GACCAGCAACCTGACTATTCCATGGCTCTCCCGCTTCAGGAGCGGTTGGGGGCCTGTG  8259

Qy   440  ----
Db  8260  GCCTGAGGAGGAGGGCACCAGCTTGGTTGGGGTCTTCCTGCCTGGGCTTCCCTTCCCAG  8319

Qy   440  ----
Db  8320  CTCTGCCCAGGCGTGAGCCTGGGCCAGTCCACCTGCCACTCCAGGGGCCTGTGTGATGGCTC  8379

Qy   440  ----
Db  8380  TGCATGCCACTCCATGGTGTAAGGGCTGAGGGCATATAGGGGGGCAGAGAGAGACCCCG  8439

Qy   440  ----
Db  8440  GCTGCCCCACGGCCTCTTCAACAAGGTGGTTAAGTGACTCCTCCGATCCCCTTGC  8499

Qy   440  ----
Db  8500  CCAGCTCCCTCCACCGCTGCAGCTCATTCCGAGGTGCAGGAGCCCCTGCATGAGCAGCT  8559

Qy   440  ----
Db  8560  GTGGTACCACGGGGCCATCCCGAGGCAGAGGTGGCTGAGCTGCTGGTGGTCTGGGGA  8619

Qy   440  ----
Db  8620  CTTCCTGGTGCGGGAGCCAGGGCAAGCAGGAGTACGTGCTGTCGGCTGTGTGGGATGG  8679

Qy   440  ----
Db  8680  TCTGCCCCGGCCACTTCATCATCCAGTCCTTGGATGTGAGTGGGGCTGGGACCCGAGCCTT  8739

Qy   440  ----
Db  8740  CCAGGGCCTCACTCTTCCCCTCCCCTTCCCCAGGGAAATGGCCTTTCACGGTAGGG  8799

Qy   440  ----
Db  8800  GGTAGCTGCCAGTGTCTTGGATGCCTCCTAGCAGGGGCTGGCTGGAAGGGGCCACAGAGAC  8859

Qy   440  ----
Db  8860  CACCCTGTCCCTGCAACAAAATAGAGGCTTAAGTGTGAGTCCTCCCCTGGTGGGGCAGCA  8919

Qy   440  ----
Db  8920  GGATGTCATGTCCATCAGATGCCATCTTTTCTGGAGTCTCTCTGCCCTGTCCTGGG  8979

Qy   440  ----
Db  8980  CAGGCCCCTTTCTCCCCTGCTCCTCCCTTTCCCCTTCCCCCAGGGCTCACGCCCCCCCTCAGA  9039
```

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Qy            --------------------------AsnLeuTyrArgLeuGluGlyGlu  448
Db   9040 ATGGAGGCTGCTGCTCCCGGTCCCTGCCTGCAGAACCTGTACCGACTGGAAGAGGGGAA  9099

Qy    449 GlyPheProSerIleProLeuLeuIleAspHisGlnLeuSerThrGlnGlnProLeuThr  468
Db   9100 GGCTTCCTAGCATTCCTTTGCTCATCGACACACCTACTGAGCACCCAGCAGCCCTCACC  9159

Qy    469 LysLysSerGlyValValLeuHisArgAlaValProLys--------------------  481
Db   9160 AAGAAGAGTGGTGTGTCCTGCACAGGGCTGTGCCCAAGGTGAGCCTGCACCCAGCCTG  9219

Qy    481 ------------------------------------------------------------  481
Db   9220 CCCATGCCACCTGTGGCAGGGCTTGGGGAGTGTGGGTCAGGCCCACCCACCCGGTCTGAGCA  9279

Qy    481 ------------------------------------------------------------  481
Db   9280 GAAAGGGCTTTCCAGGCCCTCGTCTACATACAAGATGCAGAGTGAGTGACCCTCAGGGC  9339

Qy    481 ------------------------------------------------------------  481
Db   9340 CAGCCTTGCTCTAGGTTTGGAATGTCAGGGCCACTCCTATGCCATGGGTGTACACACCA  9399

Qy    481 ------------------------------------------------------------  481
Db   9400 GGTTGGTGCTTACCTGGTCAGGGCACCTGCCTGGACCCCGTAGTCATCTCAGTGTGCTCC  9459

Qy    481 ------------------------------------------------------------  481
Db   9460 CCACGTGGTCCACCCTGGTCACATGAGGCGCCAAAAATGGAGGACACAGCCCTT  9519

Qy    481 ------------------------------------------------------------  481
Db   9520 CTAAGGGCCCAGCACCCCTTTTCTTCAGACTTCCCCGTCCTTCTTCCCCAG  9579

Qy    482 AspLysTrpValLeuAsnHisGluHisAspLeuValLeuGlyGlnIleGlyArg------  499
Db   9580 GACAAGTGGGTGCTGAACCATGAGGAACCTGGTGTTGGGTGGTCAGATTGGACG-GGTGAG  9638

Qy    499 ------------------------------------------------------------  499
Db   9639 TGCGCCTCGCTGGCCTCCTTGTCGCTGGCGACTTCTTCTGAGTCGCGCCTGGGCCCCCT  9698

Qy    499 ------------------------------------------------------------  499
Db   9699 GCCCTACCACCCAGAGAACCTCCCACTGTACCCGACTCCCT  9758

Qy    499 ------------------------------------------------------------  499
Db   9759 GCCCCAGCCCCCCACCACACCATCCTCCAGGAAAACGGGACAGTACCTACGGCTGAAAACTC  9818

Qy    499 ------------------------------------------------------------  499
Db   9819 CCAGCAGACAGCTCTGCCAGCACCCTGACCTCATCACCCCACCCAGGCCGCGCCCATCG  9878

Qy    499 ------------------------------------------------------------  499
Db   9879 AGCTCTTGTGTGCACGGAGGAGACACCCTGTACTGTAAGCCATAAGATACCTGTTTAG  9938

Qy    499 ------------------------------------------------------------  499
Db   9939 GGAAGAGTCACTGTCCTAAAAATCAGAATGTCTTTTCAAACCCAAGGGAGTGATTTTT  9998

Qy    499 ------------------------------------------------------------  499
Db   9999 GGATTTCCATGTCACTTCTTCTCAGGAAGGGTGGCACATCGGAGGCAACTTTCCCTGCCTG  10058

Qy    499 ------------------------------------------------------------  499
Db  10059 CCCCATGTGCTCTCTAGGTTCCCCAGCGAGGGTCAAACTCCCAGAGAGCGCTGGGGTGAGG  10118
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Qy            ------------------------------------------------------------  499
Db  10119 GGTCCGAACACGGCGGGGCCCCTCACCCAGGGGTAGGAGGAAGCAGAAATGGGTAGGAAGCGGCGAGA  10178

Qy    500 --------------------------------------------------GlyAsnPhe  502
Db  10179 AGAGAACTGCGGGGACTGGGAGGGCCGTGGTAGGAGGCCCAGACCGTTTCAGGGGAACTTT  10238

Qy    503 GlyGluValPheSerGlyArgLeuArgAlaAlaAspAsnThrLeuValAlaValLysSerCys  522
Db  10239 GGCGAAGTGTTCAGCGAGCCGCCTGCGACGGCCGACAACACCCTGGTGGCGGTGAAGTCTTGT  10298

Qy    523 ArgGluThrLeuProProAspLeuLysAlaLysPheLeuGlnGluAla--------------  538
Db  10299 CGAGAGACCCTCCCACCTGACCTCAAGGCCAAGTTTCTACAGGAGCGAGGTGGGTGATA  10358

Qy    538 ------------------------------------------------------------  538
Db  10359 AACTAATGATCACCACCGGGTCCCGATACACAGAGGTTACACTGGCACAGTGTGAA  10418

Qy    538 ------------------------------------------------------------  538
Db  10419 GTGCTTGACCACCGTGGTCGTGTTTAGTCCTCGAGCCCCCCATTGCGGGTAGTACCCCC  10478

Qy    538 ------------------------------------------------------------  538
Db  10479 TTATAGTGCCGAAGGGTAGAGGCTGCCCCAGGTCACACGTCCGGGTCTCGCTGGCCTTGGA  10538

Qy    538 ------------------------------------------------------------  538
Db  10539 GGCCAAGCTCTTCTCCCATCATCCCTGGGGAGGGCCGGCCCTGGCCCACGTAG  10598

Qy    539 --------------------ArgIleLeuLysGlnTyrSerHisProAsnIleValArg  551
Db  10599 ATCCTGAGCAGCAGTGCCCTCCCAGGATCCTGAAGCAGTACAGCCACCCCAACATCGTGCG  10658

Qy    551 gLeuIleGlyValCysThrGlyGlnLysGlnGlyIleGlyArg--------------  570
Db  10659 TCTCATTGGTGTCTGCACCCAGAAGCAGCCCATCTACATCGTCATTGGAGCTTGTGCAGGG  10718

Qy    570 ------------------------------------------------------------  570
Db  10719 TGAGCGCGGGCGCGGCCGCTGAGCTTCCAGGTAGGGCGGCCGCCAGCCTTGGTCAGGTGGCAGCCTTACC  10778

Qy    571 -----------------------------------GlyGlyAspPheLeuThrPheLeuAr  579
Db  10779 TCAGGAGGCTCAGACAGGGGTTCCTCCCACCTGCAGGGGGGCACTTCCTGACCTTCCTCCG  10838

Qy    579 gThrGluGlyAlaArgValLysThrLeuLeuGlnMetValGlyAlaAlaAl  599
Db  10839 CACGGAGGGGGCCCGGGTGAAGACTCTGCTGCAGATGGTGGGGGATGCAGCTGC  10898

Qy    599 ------------------aGlyMetGluTyrLeuGluSerCysIleHisArg--------  612
Db  10899 TGGCATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCG--GTGAGTGGGCGGTGGCCACG  10957

Qy    612 ------------------------------------------------------------  612
Db  10958 GGCCCTGCCACACCCCGACCAGAGTCAAGAGGTACCTATACCCCTAGGGCCCCCGCT  11017

Qy    612 ------------------------------------------------------------  612
Db  11018 GGACCATCAGGCATCAGTCTCCAGAGGGGGAGTTGGCCTCTGTGGTAGACAGGGGTGCCCA  11077

Qy    612 ------------------------------------------------------------  612
Db  11078 GGGCCGGGAGCAGCTTTTGTCCTTGGCTTTCTAGAGTGTTCAGCCAGGTGCTGGGCAGGC  11137

Qy    613 ----------AspLeuAlaAlaArgAsnCy  619
Db  11138 TGGCATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGCTGCCTGTCTGCCCGGAACTG  11197

Qy    619 sLeuValThrGluLysAsnValLeuLysIleSerAspPheGlyMetSerArgGluGluAl  639
Db        GACTGTTGGCCAAATGAGCCCGTGCCCTGCCCAGGGACCTGCGCTGCCTCGGAACTG  11197
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Db  11198  CCTGGTGACAGAGAAGAATGTCCTGAGATCAGTGACTTTGGGATGTCCCGAGAGAAGC  11257
Qy    639  aAspGlyValTyrAlaAlaSerGlyIleGlyLeuArgGlnValProValLysTrpThrAlaPr  659
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  11258  CGATGGGGTCATGCAGCCTCAGCGGGCCTCAGACAAGTCCCGTGAAGTGACCGCACC  11317

Qy    659  oGluAlaLeuAsnTyr-  664
           ||||||||||||||
Db  11318  TGAGGCCCCTTAACTACCGGTACCTAGTCCCTGTCTCCCTGGACTCCATGGCCAGAGCCA  11377

Qy    664  -  664
Db  11378  GGCCTGGGTCCTGCCGGCTCGCCTGCCCCAGGGAGGGTGCACTCACGCTGCCTC  11437

Qy    665  -------GlyArgTyrSerGluSerGlyAspValTrpSerPheGlyI  678
           ||||||||||||||||||||||||
Db  11438  ACCTCCTCGCCTTCCTCGGCCGCTACTCCTCCGAAAGCACGGTGGGAGCTTTGGCA  11497

Qy    678  leLeuLeuTrpGluThrPheSerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnG  698
           |||||||||||||||||||||||||||
Db  11498  TCTTGCTCTGGGGAGACCCTTCAGCCTGGGGGCCCTCCCCCTATCCCAACCTCCAGCAATCAGC  11557

Qy    698  lnThrArgGluPheValGluLys------  705
           ||||||||||||||
Db  11558  AGACACGGAGGTTTGTGGAGAGGGGTAAGCACCCCTGTGATGACAGCAGCCTCAGGCTGCA  11617

Qy    705  -----  705
Db  11618  CCCTCCTTCCAGATGCTCCAGCCGGACTCTTCTAACTCCCTAATGCCAACCTTCCCACCA  11677

Qy    705  -----  705
Db  11678  GGCAGAATAAGAATAACCTGGCCAGTTGCTCACGCCTGTCATCCCAGCACTTTGGGAGGC  11737

Qy    705  -----  705
Db  11738  TGAGCTGGGTGGATCACTTGAGGTCAGGAGTTCAAGATCAGCTTGGACAACACAGTGAAA  11797

Qy    705  -----  705
Db  11798  CTCCATCGTGTACAAAAAATACAAAAATTAGACTGGGCACGGTGGCTCACACCTGTAATCCC  11857

Qy    705  -----  705
Db  11858  AGCACTTTGGGAGGCCGAGGCAGGCAGGATCATCGTGGTCAGGAGTTTGAGACCAGCCAG  11917

Qy    705  -----  705
Db  11918  ACCAACATGGTGAAACCCCATCTCTACTAAAAATACAAAAATTAGCCAGGCATGGTGGCA  11977

Qy    705  -----  705
Db  11978  CGTGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGTGGGAGAATTGCTTGAACCCAGGAG  12037

Qy    705  -----  705
Db  12038  GCGGAGGCTGCAGTGAGCCGAGATTGTGCCACTGCAGCCTCCAGCCTGGGCGACAAGAGTGA  12097

Qy    705  -----  705
Db  12098  AACTCCATCTCAAAAAACAAAAACCAAAAACAAAAAATTAGCTGGGTGTGGTGAC  12157

Qy    705  -----  705
Db  12158  ATGCGCCTGTAGTCCCTGCTACTCGGGAGGCTGAGGCTGAGGATCACTGGAGCCCGGGA  12217

Qy    705  -----  705
Db  12218  GGTGGAGGTTGCAGTGAGCTGAGATCATGCCACTGCACCCCAACCTGGGTGACAGAGAGA  12277

Qy    705  -----  705
Db  12278  GAGAGAGACCTTGACTCAGACCAGTGCGCCAGTGGCTCACGCCTGTAATT  12337

Qy    705  -----  705
Db  12338  TCAACATTTGGGAGGCTGAGGAAGGTGGATCACTTGAGGTCAGGAGTTTGACACTAGCC  12397

Qy    705  -----  705
Db  12398  TGGCCAACATGGCAAAACCTGTCTCTACTAAAAATACAAAAATTAGCCGAGGTGTAGTGG  12457

Qy    705  -----  705
Db  12458  TGCAAGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAACCTGGG  12517

Qy    705  -----  705
Db  12518  AGGTGGAGGTTGCAGTGAGCTGAGATCACACCACCACTGCATTCCAGCGTGGGTGACAGAGCA  12577

Qy    705  -----  705
Db  12578  AGACTCCATCTCAGAAAAAGAAAAAAAAAAATAGAATATCCCTGTAGCTACTACTACTGAGTG  12637

Qy    705  -----  705
Db  12638  AGCACCTGGTCTGTGCTGTAGGTCACATGTTATTTCATTTGCTCATCACATGTGTGTA  12697

Qy    705  -----  705
Db  12698  GGGATTAATATGTCCCTTTCTCAGATGGAAAAACAGGCTGGCAGAGGGGACACAGCTAGC  12757

Qy    705  -----  705
Db  12758  ACGTGGTAGGATTAGGATCAGAAGCCAGGCCACCAGGCCCTTGTTCCTTTGGGCCCTTGGTGGAGAA  12817

Qy    705  -----  705
Db  12818  CAGTGCATCCTTCAGACAGTGCATCTTAAGCAGCTCCTATGGCTCATCGTATCCCCCAG  12877

Qy    705  -----  705
Db  12878  AGTCTGCCGAGGACCCTCAAACTCCCTCGGTGTGCGTGTGCCTCCTCCACA  12937

Qy    706  GlyGlyArgLeuProCysProGluLeuCysProAspAlaValPheArgLeuMetGluGln  725
           ||||||||||||||||||||||||||||
Db  12938  GGGGGGCCTCTGCCCTGCCCCAGCAGCGTGTCCCCAGAGCCGTGTTCAGCGTCATGGAGCAG  12997

Qy    726  CysTrpAlaTyrGluProGlyGlnArgProSerPheSerThrIleTyrGlnIleTyrGlnLeuGln  745
           |||||||||||||||||||||||||||||||||
Db  12998  TGCTGGGCCTATGAGCCTGGGCAGCGGCCCCAGCTTCAGCACCACCATCTACCAGGAGCTGCAG  13057

Qy    746  SerIleArgLysArgHisArg  752
           |||||||||||||||||||
Db  13058  AGCATCCGAAAGCGGCATCGG  13078
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Alignment Scores:
Pred. No.:   2950
Score: 1.1e-165   Length: 376
Percent Similarity: 1853.00   Matches: 150
Best Local Similarity: 63.60%   Conservative: 217
Query Match: 45.47%   Mismatches: 84
DB: 47.77%   Indels: 9
                    21   Gaps:

US-10-660-763-2 (1-752) x US-10-887-553A-240 (1-2950)

Qy   1 MetGlyPheSerGluLeuCysSerProGlnHisGlyValLeuGlyHisGlnMetGln 20
            ||||||:||:::|:|:   :::|||:||
Db   385 ATGGGGTTTGGGAGTGACCTG------AAGAATTCACATGAAGCAGTGTTAAATTGCAA 438

Qy   21 GluAlaGlyLeuLeuGluGlyLeuGlyMetArgLysTrpMetAlaArgValLysSer 40
            ::: ||||||:||::|:::||||||:::||:|:||:::|:|||||:||
Db   439 GACTGGGAATTACGGGTTACTGGAAACAGTAGAGAAATTTATGGCCCTGAGAATAAAAGT 498

Qy   41 AspArgArgGluTyrAlaGlyLeuLeuHisHisMetSerLeuGlnAspSerGlyGlnSer 60
            ::: |||||:|||:||:::::|::::||:||| |||
Db   499 GATAAAGAATATGCATCTACTTTACAGAACCTTTGTAATCAAGTTGATAAGGAAGTACT 558

Qy   61 ArgAlaIleSerProAspSerProIleSerGlnSerTrpAlaGluIleThrSerGlnThr 80
            ::::: ||||:|| ||||| ||||||
Db   559 GTCCAAATGATTGAATTATGTCAGCAACGTATCCAAGTCTTGGCTACTTATGATTCAGACA 618

Qy   81 GluGlyLeuSerArgLeuLeuArgGlnHisAlaGluAsnLeuAsnSerGlyProLeuSer 100
            ||||||:|:::: ||:|:||:||| |:: |:|::|||
Db   619 GAACAACTTAGTAGGCTGTTAAGACACACATGGACACTAAATTCTGAACCTTTACAC 678

Qy   101 LysLeuSerLeuLeuLeuLeuIleArgGlnLeuArgLysThrTyrSerGluGlnTrp 120
            |||||:|| ||||||::|||:||||::|:::|:|||:::|
Db   679 AGGCTCACCATGATGATTAAGGACAAGCAGGGTGAAGAAAGTTACATAGGTGTTCAT 738

Qy   121 GlnGlnLeuGlnGlnLeuThrLysThrHisSerGlnAspIleGluLysLeuLysSer 140
            ||||||:||::|:|:   ::|:::||||||||||||||||||:||||||
Db   739 CAGCAGATAGAGCAGGATGATGATCAAGGTTACCAAGACAGAATTGGAGAAGTTAAAATGC 798

Qy   141 GlnTyrArgAlaLeuAlaArgAspSerAlaGlnAlaLysArgLysTyrGlnGluAla-- 159
            ||||||:::||||:||::::: ||:::|::::::||:
Db   799 AGCTATAGACAATTAACAATTAAAGAAAATGAATTCTGCCAAAGAGAAATTAAAGAAGCTTTA 858

Qy   160 SerLysAspArgAspLysAspLysAspLysTyrValArgSerLeuTrpLysLeu 179
            :::||:|:|:||:||:|||||:||:::||| ||::::||||:|:
Db   859 GCTAAAGGAAGGAAGAAACTGAAAGGTATACGAGAACGATCGACAAAGCCACATGAACTT 918

Qy   180 PheAlaHisHisAsnArgTyrValLeuGlyValArgAlaAlaLeuGlnLeuHisHisHis 199
            ||:::|||::::|:|:|::|||||||:||:::|:|::|:::||
Db   919 CATATATGTTGCACAATCAGTATTGGCGTTGAAAGGGGCCACAGCTTCCATCAGAATCAG 978

Qy   200 HisHisLeuGlnLeuLeuLeuProGlyLeuLeuArgSerLeuGlnAspLeuHisGluMet 219
            :::::   ::| |::|::||||::|:|:|||:::|:::::::||||||
Db   979 TATTATGATATCACACTTCCCCGTCTTCTGGACTCCTTACAAAGATGCAAGAAGAAATG 1038

Qy   220 AlaCysIleLeuLeuGluGlyIleLeuGluIleSerSerGluValGlnAsp 239
            |::|::: |:|||||||:|:||||:::|||:||:::|:::
Db   1039 ATAAAAGCACTCAAGGTATATTTGATGAATACAGCCAGTAACTAAGAACTCTGTCACAGAG 1098

Qy   240 GluValAlaAlaIleHisArgGluMetAlaAlaAlaAlaAlaLysArgIleGlnProGluAla 259
            ||:|::::|:||| |:||:|:|||:::|:|::|:|::::||
Db   1099 GAAGTAGTAGCAATTCATAGAGAGATGGCGGTGAACAGATAGATCCTAGTACA 1158

Qy   260 GluTyrGlnGlyPheLeuArgGlnTyrGlySerAlaProAspValProProCysValThr 279
            |||::|:|:|:||: ||:::|::::|:|||::|:::|:::
Db   1159 GAATACAATAATTTCATAGATGTTCACAGACAACAACGGCTGCTAAAGACAAGAAATAGAG 1218

Qy   280 PheAspGluSerLeuGluGluGluGlyProGlyLeuGluGlnLeuGlnLeuAsn 299
            ||::|:|::|||||::|:|:|:||::|:|||::::::|::
Db   1219 TTTGATACTTCCTTACTGGAAGAAGAAATTGAAAATGAAAAATCTCAGGCAAATGACGATCATGTGGAAT 1278

Qy   300 GluLeuThrValGluSerValGlnHisThrLeuThrSerValThrAspLeuAlaAlaVal 319

Qy   320 AlaThrGluMetValPheArgArgGlnMetValThrArgLysArgLysArgGlnLeuLeuArg 339
            :::|::||| |||| :::|||
Db   1339 ACACAGACAGATGCGTTTAAACAAGGAGGAGGCGTGTTTGGAGTAGAAGAAGAATTGAA 1398

Qy   340 AsnGluGluGlnAsnThrHisProArg---GluArgValGlnLeuLeuGlyLyLysArgGln 358
            :::::|:| ::::||:|||:::|||:|:|||||:|:::|:::||||||
Db   1399 GAATCTTCTGAAACTTGTGAGAGAAGAGTCTGATATTGTGCTTCTGCTAAGCCAAAAAACAG 1458

Qy   359 ValLeuGlnGluLeuGlnGlyLeuGlnValAlaLeuCysSerGlnAlaAlaLysLeuGln 378
            ::|:|::|:|||||:|:::::|:||:||:|:::
Db   1459 GCACTTGAAGAACTGAAACAGTCAGTCCAGCGATGCACTGAGACTGAAGCAAAGTTTTCA 1518

Qy   379 AlaGlnGlnLeuLeuGlnLnThrLeuGluHisLeuGluLeuProGlyGluGlnGlnProPro 398
            :::::|||::|::|| |:::|||::|:|:|::|::||||:||||
Db   1519 GCACAGAAGGAATTACTAGCAGAAAAAGTGCAAGAAAATGATGGAAGAGCCACCTCCA 1578

Qy   399 ValLeuLeuGlnAspAspArgHisSerThrSerSerGluGlnLeuGlnArgGluGlyGly 418
            ::|:|:|::|:|:::||||: ||:::||:::|::|:||||||
Db   1579 GTAGTAAATTATGAAGAAGATGCACGATCAGTTACATCTAGTGAAAGAAAAAGAG------ 1632

Qy   419 GlyArgThrProThrLeuGluIleLeuArgGlnSerHisIleSerGlyTyrIlePhe---Pro 437
            ||| |:::::|||||||:::|:::|:|:|:::   :::
Db   1633 --AGGCTCACCATGATGATTAAGGACAAGCAGGGTGAAGAAAGTTACATAGGTGTTCCTCCA 1689

Qy   438 Lys-------------------- 438
            |||
Db   1690 AAATCTCAGTGGGCTCTTCAGCACTTTCTGATATGATCTCCAGTGAGAAGCCTTTG 1749

Qy   438 ------------------------- 438
Db   1750 GCAGAAACAGGACTGGTACCATGGTGCAATCCCAGAATAGAAGCTCAAGAACTGTTAAAA 1809

Qy   438 ------------------------- 438
            |||
Db   1810 AAACAAGGAGGACTTTTTGGTGCGAGAGTCATGGGAAACCTGGTGAATATGTCCTTTCT 1869

Qy   439 ----------------------------------PheSerAsnLeuTyrArg 444
                                              :::::|:::|
Db   1870 GTATATTCTGATGGACAGAGAGACATTTTATCATACAATATGTTGATAACATGTATCGA 1929

Qy   445 LeuGluGlyGlyPheProSerIleProLeuLeuAspHisLeuLeuSerThrGln 464
            |||||:|:|:||||:::|:|::||:|:::||:::|::|:::|:||
Db   1930 TTCGAGGGCCACTGGGTTTCAAACATTCCTCAAACTTTATAGATCATCACTATACACAAAA 1989

Qy   465 GlnProLeuThrLysLysSerGlyValValLeuHisArgAlaValProLysAsp---Lys 483
            ||:|:::||:::::|:|:||||:::||:||:|:||::||:::|::|||
Db   1990 CAGGTCATCACTAAGAAATCAGGTGGTTCTGCTGAATCCATTCCTAAGGACAAGAAA 2049

Qy   484 TrpValLeuAsnHisGluAspLeuValLeuGlyValGluGlnIleIleGlyArgGlyAsnPheGly 503
            |||||:::||:|:|:||||:||:||:||:::|||:|::::|:::|||
Db   2050 TGGGATTCTCAGTCATGAAGATGTTCATTGGGAGAATTACTGGGCAAGGAAATTTTGGT 2109

Qy   504 GluValPheSerGlyArgLeuArgLeuAlaAspAsnThrLeuValAlaValLysSerCysArg 523
            ||||::|::|:||||::|::|:::||:::::: |||:::||:::|:::|
Db   2110 GAAGTAACTTCTGTGCTTAGAGCCCAAAATCTTCAAGCAA 2166

Qy   524 GluThrThrProProAspLeuProLysLysAlaLysPheLeuGlnGluLeuArgLeuLeuLysGln 543
            ||:|::|::   ::::|::|:|:|||::|:||:|||:::|::||||
Db   2167 GAAGATTTCCTCAGGAATTGAAAATAAAATTTTTACAAGGAGCCAAAATTCTCAAGCAG 2226

Qy   544 TyrSerHisProAsnIleValArgLeuIleGlyValCysThrGlnLysGlnProIleTyr 563
            ::|:::|:::||||:::|:::|:|::||:|::||::|:::||:::|:|:
Db   2227 TATGATCATCCAAATATTGTCAACTTATAGGAGTTTGCACACAAAAGCAGCCTGTCTAC 2286

Qy   564 IleValMetGluLeuValGlnGlyGlyAspPheLeuThrPheLeuArgThrGluGlyAla 583
            ::|::|:::||::|:|:|:|||::|||:||::|::|::|:|::|::
Db   2287 ATCATTATGGAACTGGTTCAGGGTGGTGATTTCCTACCTTTCTGAGGAAGGAAGGAT 2346

Qy   584 ArgLeuArgLysThrLeuThrLeuGlnMetValGlyAspAlaAlaAlaGlyMetGluTyr 603
            |||||||:||:|| |||||||||||||||||||:::::

```
Db  2347 GAACTAAAACTCAAACAGTTAGTGAAATTTCATTACGACGTGCTGCTGCTGGTATGTTGTAT 2406
              |||||||
Qy   604 LeuGluSerLysCysSerIleHisArgAspLeuAlaAlaAlaArgAsnCysLeuValThrGlu 623
              ||||||     |||||  |||
Db  2407 CTTCGAGAGTAAAAACTGTATACACAGGACCGACCTTGCTGCAAGAAACTGCCTGGTAGTGAA 2466

Qy   624 LysAsnValLeuLeuSerArgAspPheGlyMetSerArgGluGlnAlaAspGlyValTyr 643
              ||:::|||
Db  2467 AATAATGTTCTGAAAAATCAGTGACTTTGGAATGTCTCGTCAAGAGGATGGTGAGTGTAT 2526

Qy   644 AlaAlaSerGlyGlyLeuArgGlnValProValLysTrpThrAlaProGluAlaLeuAsn 663
              :::|||   |||||  |||
Db  2527 TCATCTTCT---GGCTAAAGCAGATTCCCATTAAATGGACAGCACCGGAAGCTCTTAAT 2583

Qy   664 TyrGlyTyrSerSerGluSerAspValTrpSerPheGlyIleLeuLeuTrpGluThr 683
              |||||||||    |||||  |||||||
Db  2584 TATGGGAGATACAGTTCAGAGAGTGACCGTGTGGAGCTTGGCCATCCTTCTCTGGGAGACC 2643

Qy   684 PheSerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnGlnThrArgGluPheVal 703
              |||
Db  2644 TTCAGCTTAGGGGTTTGTCCGTACCCCTGAAATGACAAATCAGCAAGCAAGAGCAGTA 2703

Qy   704 GluLysGlyGlyArgLeuProCysProGluLysCysProAspAlaValPheArgLeuMet 723
              |||||| ::: |||||||
Db  2704 GAAAGAGGATACCGGATGTCAGCTCCCCAGCACTGTTCCAGAGGATATTTCCAAAATCATG 2763

Qy   724 GluGlnCysTrpProAlaTyrGluTyrGlyGlnArgProSerPheThrIleTyrGlnGlu 743
              |||:::|    |||   ::: |||||
Db  2764 ATGAAGTGTTGGGGATTATAAACCTGAAAATCGCCCTAAGTTCAGTGAACTTCAGAAAGAG 2823

Qy   744 LeuGlnSerIleArgLysArg 750
              :::||||||||||:
Db  2824 CTCACTATCATCAAGAGAAAA 2844
```

```
Db   279 CTCCAAGTTGCTCAATTTCCAGTTGAGGCGTCCAAGCCGTGCAA----------ACA 326
              :::|||          |||
Qy   244 IleHisArgGluMetAlaAlaAlaAlaAla-ArgIleGlnProGluAlaGluTyrGlnIleGlnIle 263
              |||::::|||
Db   327 GTGCACCAGAG------------ACGTCGCATCCATCCGACGCAAAAGTGTCTTTGA 371
Qy   263 yPheLeuArgGlnTyr----------GlySerAlaProAsp------------ 273
              |||        |||
Db   372 TTTTGCCAAAGAGTTGGAGGTGGAACAACCGGCTGGTTCGGCGGCGATGAGCAATTCTG 431
Qy   274 ------------------ValProProCysValThrPheAspGluSerIle 284
                                   |||
Db   432 CAACTGTCCGCCAGCTCGTCAAAAGCCTGTTAAGCCATCCGTCCAAATATCCGGC------ 486
Qy   284 uLeuGluGluGlyGluProLeuGlu------ProGlyLeuGlnLeuAsn---GluLeu 301
              :::       |||
Db   487 ---CACAAAGATCACCCGTTCGAGTCCAGTTCTGGAGCGTCGGACGAGCGTCGGGATCG 542
Qy   301 uThrValGluSerValGlnHisThrLeuThrSerValThrAspGluLeuAlaValAlaAlaTh 321
              |||
Db   543 GGACATCGACAACGACGAGGAGGAGGAGGATAGCGCCAGTGACGACGTGCTCAGCATGAA 602
Qy   321 rGluMetValPheArgArgGlnGluMetValThrGlnIleuGlnIleGluLeuArgAsn-- 340
              :::          :::
Db   603 GGATCACTGCTATTGCGTGCCCAGCTGGCGGCCAGTATATCCGTCTCCACAAATCGTCC 662
Qy   341 ------GluGluGlnAsnThrHis----------ProArgGluArgValGlnLeuLeuLeuGl 355
                     :::
Db   663 GCTTTACAGGAGGAATGGTTCCATGGGGTTCTGCCGCGGCGGGAGGAAGTG--------- 711
Qy   355 yLysArgGlnValLeuGlnGluGlnLeuLeuLeuGlyLeuGlnValAlaLeuCysSerGlnAl 375
Db   711 --------------------------------------------- 711
Qy   375 aLysLeuGlnAlaGlnGluLeuLeuGlnThrLysLeuGluHisLeuLeuGlnThrLysLeuGluHisLeuLeuGlnGluHisLeuGlyProGlyGl 395
Db   711 ------------------------------------------- 711
Qy   395 uProProProValLeuLeuGlnAspAspArgHis-SerThrSerSerGluGlnGlnG 415
              ::::||
Db   712 --------------GTTCGATTGCTGAATAACGATGTGACTTCCTGGTCCGGAAACGATTCG 761
Qy   415 luArgGluGlyGlyArgThrProThrLeuGluGluIleLeuGluLysLysSerHisIleSerGlyIleP 435
              ||          :::|:::
Db   762 AAACGAGGAGAGCCAGATTGTGCTCAGTGTCTTGTTGGAATGGCCATAAGCACTTCATTGT 821
Qy   435 heArgProLysPheSerAsnLeuTyrArgLeuTyrArgLeuGlyGluGlyProSerIleProL 455
              |||||          |||
Db   822 CCAGACCACCGA-GAGGGTAATTTCCGGTTCGAGGACCACCATTTGCCAGCATCCAGG 880
Qy   455 euLeuIleAspHisLeuLeuSerThrGlnGlnProLeuThrLysLysSerGlyLyaValVal 475
              ::::          :::
Db   881 AGCTGATCATGCATCAGTATCACTCGGAATTGCAGTTGCACCGTGAAATCGGGAGCCCATAC 940
Qy   475 euHisArgAlaValProLysAspArgLysTrpValLeuAsnHisGluLeuValLeuGlyG 495
              |||  |||
Db   941 TCCGACGACCCGTTGCCGGGAGCGGCTGAGCAACGATGATGTGGTACTTCTCGG 1000
Qy   495 luGlnIleLeuGlyGlyArgGlyAsnPheGlyGluValPheSerGlyArgLeuArgAlaAspAsnT 515
              ||:::||||||          :::|:::
Db  1001 AGAGGATTGGTCGGGAGGGAAACTTTGGGGATGTCTACAAGGCCAAACTGAAGTCCACCAAAC 1060
Qy   515 hrLeuValAlaValLysSerCysArgGluThrLeuProProAspLeuProLysLysPheL 535
              |||||||||:::||:::
Db  1061 TGGATGTGGCTGTCAAAAGCTGTCGAGAAACCCTGCCCGACGAACAGAGGTAAAATTCC 1120
Qy   535 euGlnGluAlaArgIleLeuGlyGlnTyrSerHisProAsnIleValArgLeuIleGlyV 555
              ||||||||||||||||||:::
Db  1121 TACAGGAAGGGCGCCATCCTCAAGCAATACGATCATCCAAATATCGTAAAATTGATTGGCA 1180
Qy   555 alCysThrGlnLysGlnProIleTyrIleValMetGluLeuValGlnGlyGlyAspPheL 575
              :::|||
```

RESULT 7
US-10-280-576-19;
 Sequence 19, Application US/10280576
 Publication No. US20040044405A1
 GENERAL INFORMATION:
 APPLICANT: Wolff, Matthew R.
 TITLE OF INVENTION: VASCULAR STENT OR GRAFT COATED OR IMPREGNATED WITH PROTEIN
 FILE REFERENCE: 09820.189
 CURRENT APPLICATION NUMBER: US/10/280,576
 CURRENT FILING DATE: 2002-10-22
 PRIOR APPLICATION NUMBER: 60/343,732
 PRIOR FILING DATE: 2001-10-25
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 19
 LENGTH: 1779
 TYPE: DNA
 ORGANISM: Drosophila melanogaster
US-10-280-576-19

Alignment Scores:
Pred. No.:
Score: 1.78e-74
                        892.00
Percent Similarity: 51.35%   Length: 1779
Best Local Similarity: 37.37%   Matches: 222
Query Match: 23.00%   Conservative: 83
                        18   Mismatches: 185
                                      Indels: 105
                                      Gaps: 13

US-10-660-763-2 (1-752) x US-10-280-576-19 (1-1779)

```
Qy   197 HisGlnHisHis----------------------GlnLeuLeuPro 206
              |||  ||||||||
Db   159 CACGATCACCACCACCACCATAACGACTACCACCGACGCCGTCCAAGGAAAATTCAAG 218

Qy   207 GlyLeuLeuArgSerLeuGlnAspLeuHisGlu------GluMetAlaCysIleLeu 223
              :::||||||| ||||||:::  |||
Db   219 ACTGAAATTCAAAGTGCCCAAGATCCAGAAGAAATCAAAGGCCATCCGCAATACATTCCG 278

Qy   224 LysGluIleLeuLeuGlnLeuTyrLeuGluIleSerSerLeuValGlnAspGluValValAla 243
```

```
Qy   511 ArgAlaAspAsnThrLeuValAlaValLysSerCysArgGluThrLeuProProAspLeu 530
             ||||||||||||||||||||||||||||||||||
Db    39 CGAGCGGACAACACCCTGGTGCGGTGGGTGAAGTCTTGTCGAGAGACGCGTCCCACCTGACCTC  98

Qy   531 LysAlaLysPheLeuGlnGluAlaArgIleLeuLysGlnTyrSerHisProAsnIleVal 550
             |||       :::   |||||||
Db  1241 TAACTTATTTACGCAAGAAGTCCAATGGCCTCACCACTCCGCCACAAATGGGCATGTGCA 1300

Qy   595 lyAspAlaAlaAlaGlyMetGluTyrLeuGluSerLysCysCysIleHisArgAspLeuA 615
             |||||||:::|||||||||
Db   125 ----------------------------------------------------------- 125

Qy   551 ArgLeuIleGlyValCysThrGlnLysGlnProIleTyrIleValMetGluLeuValGln 570
             |||||
Db   125 ----------------------------------------------------------- 125

Qy   571 GlyGly-AspPheLeuThrPheArgThrGluArgAlaArgLeuArgValLysThrLe 590
               :::::  :::    ::||||||||||||||||||
Db   126 ---GGGCGGACTTCCTGACCTTCCTCCGCACGGAGGGGGCCCGCTGCGGGTGAAGACTCT 182

Qy   590 uLeuGlnMetValGlyMetGluTyrLeuGluSerLysCysCysI1 610
             ||||||||||||||||||||||||||||
Db   183 GCTCGCAGATGGTGGGGATGGAGTACCTGGAGTCTAAGTGCTGCAT 242

Qy   610 eHisArgAspLeuAlaAlaArgAsnCysLeuValThrGluLysAsnValLeuLysIleSe 630
             ::||||||||||||||||||||||||||||
Db   243 CCACCGGGACCTGGCTGCTCGGAACTGCCTGGTGACAGAGAAGAATGTCCTGAAGATCAG 302

Qy   630 rAspPheGlyMetSerArgGluGluGluAspGluValTyrAlaAlaSerGlyGlyLeuAr 650
             ::||||:||||||||||||||||||
Db   303 TGACTTTGGGATGTCCCGAGAGGAAGCCATGGGGTCTATGCAGCCTCAGGGGGCCTCAG 362

Qy   650 gGlnValProValLysTrpThrAlaProGluAlaLeuAsnTyrGlyArgTyrSerSerG1 670
             ::|||
Db   363 ACAAGTCCCGTGAAGTGGACCCCACCTGAGGCCCTTAACTACGGCCGCTACTCCTCCGA 422

Qy   670 uSerAspValTrpSerPheGlyIle 678
             ||||||:::
Db   423 AAGCGACGTGTGGAGCTTTGGCATC 447
```

RESULT 9
US-10-204-041-3

```
; Sequence 3, Application US/10204041
; Publication No. US20030176443A1
; GENERAL INFORMATION:
;  APPLICANT: STEIN-GERLACH, MATTHIAS
;  APPLICANT: SALASSIDIS, KONSTADINOS
;  APPLICANT: BACHER, GERALD
;  APPLICANT: MULLER, STEFAN
;  TITLE OF INVENTION: Pyridylpyrimidine Derivatives as Effective Compounds Against Prior
;  TITLE OF INVENTION: Infections and Prion Diseases
;  FILE REFERENCE: AXM-007.1P US
;  CURRENT APPLICATION NUMBER: US/10/204,041
;  CURRENT FILING DATE: 2002-08-16
;  PRIOR APPLICATION NUMBER: EP 01111858.5
;  PRIOR FILING DATE: 2001-05-16
;  PRIOR APPLICATION NUMBER: PCT/EP02/05420
;  PRIOR FILING DATE: 2002-05-16
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;  LENGTH: 3840
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-204-041-3
```

```
Alignment Scores:
Pred. No.:                          Length:            3840
Score:                   1.58e-48   Matches:            138
Percent Similarity:      624.50     Conservative:        68
Best Local Similarity:   53.79%     Mismatches:         128
Query Match:             36.03%     Indels:              49
DB:                      16.10%     Gaps:                10
```

US-10-660-763-2 (1-752) x US-10-204-041-3 (1-3840)

```
Qy   405 AspArgHisSerSerGluGluArgGluGlyArgThrProThrLeu 424
```

```
Db  1181 TTTGTGCAGAAGCAGCCATCATGATTGTTGCTGTCGGTGGTTCGCTT 1240

Qy   575 euThrPheLeuArgThrGluArgAlaArgLeuArgValLysThrLeuLeuGlnMetValG 595
             ||||||:::|||            :::   :::|||||||
Db  1241 TAACTTATTTACGCAAGAAGTCCAATGGCCTCACCACTCCGCCACAAATGGGCATGTGCA 1300

Qy   595 lyAspAlaAlaAlaGlyMetGluTyrLeuGluSerLysCysCysIleHisArgAspLeuA 615
             |||||||||||||||||||||||||||:::|||||||||||
Db  1301 GAGATGCGCGGCGGCAGGCATGCGAATATCTGGAGTCCAAAAACTGCATTCATCGCGATCTGG 1360

Qy   615 laAlaArgAsnCysLeuValThrGluLysAsnValLeuLysIleLeuLysIleSerAspPheGlyMetS 635
             ||||||||            :::::: |||::|||||||||
Db  1361 CGGCGGGTAATTGCTCGTTGACTTGGACGACCAGTGGAAGATCTCCGATTTCGGAATGT 1420

Qy   635 erArgGluGluAlaAspGluValTyrAlaAlaSerGlyGlyLeuArgGlnValProVall 655
             ::|||                                     ||||||||
Db  1421 CTCCGCGAGGAGGAGGA------TATATAGTTCCGATGGCATGAAACAAATACCTGTGA 1474

Qy   655 ysTrpThrAlaProGluAlaLeuAsnTyrGlyArgTyrSerSerGluSerAspValTrpS 675
             ::::::|||      |||||||         ::::::|||
Db  1475 AGTGGACAGCTCCCGAGGCCTTGAATTTCGGCAAGTACACTTCGTTGTGTGCGATGTGGGT 1534

Qy   675 erPheGlyIleLeuLeuTrpGluThrPheSerLeuGlyAlaSerProTyrProAsnLeuS 695
             |:::::||||||||||       :::||||||
Db  1535 CCTATGGCATACTGATGTGGGAGATCTTCTCCAAGGGCGACACCTTCTCCCGGCATGA 1594

Qy   695 erAsnGlnGlnThrArgGluPheValGluLysGlyGlyArgLeuProCysProGluProGlnArgP 715
             |||||||||        ::: |||||
Db  1595 CCAACTCCAGAGCCAGAGAGCCAGCATCGATACGGGATATCGTATGCCAACGCCGAAGAGCA 1654

Qy   715 ysProAspAlaValPheArgLeuMetGluGlnCysTrpAlaTyrArgGluProGlyGlnAsnArgP 735
             |||||||||||   |||     :::
Db  1655 CGCCGGAGGAGAGTTACCGACGTGATGCCTGCGGCAGCCGGCGCCCGAATCCCGAC 1714

Qy   735 roSerPheSerThrIleTyrGlnGluLeuGlnSerIle 747
             |||||:::           :::::::
Db  1715 CGCATTTCGATGAGATCTACAATGTGGTGGATGCACTG 1752
```

RESULT 8
US-09-918-995-1503

```
; Sequence 1503, Application US/09918995
; Publication No. US2003007363623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE: 2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1503
;  LENGTH: 449
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: (1)...(449)
;  OTHER INFORMATION: n = A,T,C or G
US-09-918-995-1503
```

```
Alignment Scores:
Pred. No.:                          Length:            449
Score:                   1.64e-53   Matches:            136
                         663.00     Conservative:         0
Percent Similarity:      80.47%     Mismatches:           0
Best Local Similarity:   80.47%     Indels:              33
Query Match:             17.09%     Gaps:                 1
DB:                      10
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US-10-660-763-2 (1-752) x US-09-918-995-1503 (1-449)

Db 1784 GCATGTTGGCAGTGGAATCCCTCTGACCGGCCGCCCTCCTTTGCTGAAATCCACCAAGCCTTT 1843

Qy 745 GlnSerIle 747
         :::|:::::
Db 1844 GAAACAATG 1852

RESULT 10
US-10-717-597-234
; Sequence 234, Application US/10717597
; Publication No. US20040110221A1
GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael E.
; APPLICANT: Twine, Natalie C.
; APPLICANT: Dorner, Andrew J.
; APPLICANT: Trepicchio, William L.
; APPLICANT: Slonim, Donna K.
; APPLICANT: Stover, Jennifer A.
TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS
; FILE REFERENCE: AM101080L
; CURRENT APPLICATION NUMBER: US/10/717,597
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/459,782
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/427,982
; PRIOR FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 4904
; SOFTWARE: PatentIn version 3.2
SEQ ID NO 234
; LENGTH: 3840
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-717-597-234

Alignment Scores:
Pred. No.:   Length: 3840
Score: 1.58e-48   Matches: 138
Percent Similarity: 624.50   Conservative: 68
Best Local Similarity: 53.79%   Mismatches: 128
Query Match: 36.03%   Indels: 49
DB: 16.10%   Gaps: 10
                        19

US-10-660-763-2 (1-752) x US-10-717-597-234 (1-3840)

Qy 405 AspArgHisSerThrSerSerGluGlnLysArgGluGlyGlyArgThrProThrLeu 424
            :::|:|||||| |||| |||
Db 731 GAGAAACACTCCTGGTACCATGGCCGTGTCCCGCAATGCCGTCGAGTATCCG------ 784

Qy 425 GluIleLeuLysSerHisIleSerGlyIleSerArgProLysPheSer---------- 440
            |||| :::|||
Db 785 ------CTGAGCAGCGGGATCAATGGCAGCTTCTTGGTGCGTGAGAGCAGTCCT 838

Qy 440   440

Db 839 AGCCAGAGGTCCATCTCGCTGAGATACGAAGGGAGGGTGTACCATTACAGGATCAACACT 898

Qy 441 ------------AsnLeuTyrArgLeuGluGlyLyGlyPheProSerIleProLeuLeu 456
                      |||||
Db 899 GCTTCTGATGGCAAGCTCTACGTCTCCTCCGAGACCCCTGGCCCCGAGTTG 958

Qy 457 IleAspHis-----------LeuLeuSerThr---GlnGlnProLeuThr 468
            :::| |:::|:::
Db 959 GTTCATCATCATCAACGGTGCCGACGGGCTCATCACCACGCTCCATTATCCAGCCCA 1018

Qy 469 LysLysSerGlyValValLeuHisArgAlaValProLys---AspTrpValLeuAsn 487
            ||||| :::   :::
Db 1019 AAGGCGAACAACAGCCCACTGTCTATGGTGTCCCCAACTACGACAAGTGGGAGATGGAA 1078

Qy 488 HisGluAspLeuValLeuGlyIleGlyLyArgGlyAsnPheGlyValPheSer 507
            ||:::| |||:||||||
Db 1079 CGCACGGACATCACCATGAAGCACAAGCTGGGCGGGCCAGTACGGGGAGGTGTACGAG 1138

Qy 508 GlyArgLeuArgAlaAspAsnThrLeuValAlaValLysSerCysArgGlu---ThrLeu 526
            ||:::   :::|::: |||
Db 1139 GGCGTGTGGAAGAAAATACGACCTGACGGTGGCGTGAAGACCTTGAAGGAGGACACCATG 1198

Qy 527 ProProAspLeuLysAlaLysPheLeuGlnLysGluLeuGluAlaArgIleLeuLysGlnTyrSerHis 546
            ::: |||||
Db 1199 GAGGTGGAA--------GAGTTCTTGAAAGAAGCTGCAGTCATGAAAGAGATCAAACAC 1249

Qy 547 ProAsnIleValArgLeuIleGlyValCysThrGlnLysGlnProIleTyrIleValMet 566
            |||||:::|||::: |||||
Db 1250 CCTAACCTAGTGCAGCTCCAGGGTCTGCACCCCGAGCCCGTTCTATATCATCACT 1309

Qy 567 GluLeuValGlnGlyGlyAspPheLeuThrPheLeuArgThrGluGlyAlaArgLeuArg 586
            :::|:::|||:|||||| ||:||:||
Db 1310 GAGTTGCAACCGGGAACCTCCTGGACTACCTGAGG---GAGTGCAACCGGCAGGAG 1366

Qy 587 ValLys------ThrLeuLeuGlnMetValGlyAspAlaAlaAlaGlyMetGluTyrLeu 604
            ||||:   :::|||||||
Db 1367 GTGAACGGCCGTGGTCGTGCTGTACATGGCCACTCAGATCTCGTCAGCCATGGAGTACCTA 1426

Qy 605 GluSerLysCysCysIleHisArgAspLeuAlaAlaArgAsnCysLeuValThrGluLys 624
            |||||:::|||::: ||:|||||||
Db 1427 GAGAAGAAAACTTCATCCACAGAGATCTTGCCTGCCGAAACTGCCTGGTAGGGGAGAAC 1486

Qy 625 AsnValLeuLysValIleSerAspPheGlyMetSerArgGluGlyAlaAspAspTyrTyrAla 644
            :::|::: |:::
Db 1487 CACTTGTGAAGGTAGCTGATTTTGGCCTGAGCAGGGTTGATGACACGGGAACCTACACA 1546

Qy 645 AlaSerGlyValLeuArgGlnValProValLysTrpThrAlaProGluAlaLeuAsnTyr 664
            ||| |||
Db 1547 GCCCATGCTGAGCCAAG---TTCCCCATCAAATGACTGCACCCGAGAGCCTGGCCTAC 1603

Qy 665 GlyArgTyrSerSerGluSerAspValTrpSerPheGlyIleLeuLeuTrpGluThrPhe 684
            |||||:::::: |:::||:::|||
Db 1604 AACAAGAAAACTTCTCATCCAAGTCCATCAGTCCCTGGGAGTATTGCTTTGGGAAATTGCT 1663

Qy 685 SerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnGlnThrArgGluHisValGlu 704
            :::|:::   :::
Db 1664 ACCTATGGCATGTCCCCCTTACCCGGGAATTGACCGTTCCCAGGTGTATGAGCTGCTAGAG 1723

Qy 705 LysGlyGlyArgLeuProGlnProGlyLeuCysProAspValPheArgLeuMetGlu 724
            :::|::: ||:::
Db 1724 AAGGACTACCGCATGAAGCACATGAACCTGGGGCCCAGTACGGGGAGGTGTACGAG 1783

Qy 725 GlnCysTrpAlaTyrGluProGlyGlnArgProSerPheSerThrIleTyrGlnGluLeu 744
            |||||:::   :::|||:::
Db 1784 GCATGTTGGCAGTGGAATCCCTCTGACCGGCCGCCCTCCTTTGCTGAAATCCACCAAGCCTTT 1843

us-10-660-763-2.rnpb

Wed Aug 10 16:17:25 2005

Alignment Scores:
Pred. No.:
Score: 1.58e-48   Length: 3840
Percent Similarity: 53.79%   Matches: 138
Best Local Similarity: 36.03%   Conservative: 68
Query Match: 16.10%   Mismatches: 128
DB: Indels: 49
                                            Gaps: 10

US-10-660-763-2 (1-752) x US-10-802-432-26 (1-3840)

```
Qy    405  AspArgHisSerSerSerGluSerGlnGluArgGluGlyGlyArgThrProThrLeu  424
Db    731  GAGAAACACTCCTGGTACCATGGCCGTCTGTGTCCGCAATGCCCGTCGAGTATCCG------  784

Qy    425  GluIleLeuLysSerHisIleSerGlyIlePheArgProLysPheSer------  440
Db    785  -----CTGAGCAGGGAGATCAATGCAGCTTCTTGGTGCCTGAGAGTTGAGAGCAGTGCT  838

Qy    440  ------  440
Db    839  AGCCAGAGGTCCATCTGCGTGAGGATACGAAGGAGGGTGTACCATTACGGATCAACACT  898

Qy    441  ------AsnLeuTyrArgLeuGluGlyGlyProSerIleProLeuLeu  456
Db    899  GCTTCTGATGCGCAAGCTCTACGTCTCCTCCGAGAGCCGCTTCAACACCCTGGCCGAGTTG  958

Qy    457  IleAspHis---  LeuLeuSerThr---GlnGlnProLeuThr  468
Db    959  GTTCATCATCATTCAACGGTGCCGACGGGCTCATCACCAGTCCCATTATCCAGCCCCA  1018

Qy    469  LysLysSerGlyIleValValLeuHisArgAlaValProLys---  AspLysTrpValLeuAsn  487
Db   1019  AAGCGCCAACAAGCCCACTGTCTATGGTGTCCCCAACTACGACAAGTGGGAGATGGAA  1078

Qy    488  HisGluAspAspTyrProAsnLeuSerArgAsnGlnThrLeuAlaAlaValLysSerCysArgGlu---ThrLeu  526
Db   1079  CGCACGGACATCACCATGAAGCAACAGCACTGGGGGCCGGGGGCAGTACGGGGGAGGTGTACGAG  1138

Qy    508  GlyArgLeuArgAlaAspAsnThrLeuAlaValLysSerCysArgGlu---ThrLeu  526
Db   1139  GGCGTGTGGAAGAAAATACAGCCTGGACGGTGGCCGTGGAAGACCTTGAAGCAGGAACACCATG  1198

Qy    527  ProProAspLeuLysPheAlaLysPheGlnLysLysPheGlnLysLysArgIleLeuArgIleLeuLysGlnTyrSerHis  546
Db   1199  GAGGTGGAA------  GAGTTCTTGAAAGAAGATCCAGTCATGAAAGAGATCAAAACAC  1249

Qy    547  ProAsnIleValArgLeuIleGlyValCysThrGlnLysGlnProIleThrIleValMet  566
Db   1250  CCTAACCTAGTGCAGCTCGTGGGGTCCGGGGAGCCCCCGTTCTATATCATCACT  1309

Qy    567  GluLeuValGlnGlyGlyAspPheLeuThrPheLeuArgThrGluGlyAlaArgLeuArg  586
Db   1310  GAGTTCATGACCTACGGGAACCTCCTGGACTACCTGAGG---GAGTGCAACCGGCAGGAG  1366

Qy    587  ValLys------  ThrLeuGlnMetValGlyAspAlaAlaAlaGlyMetGluTyrLeu  604
Db   1367  GTGTGGAAGCGCGTGGGTGCTGCTACATGGCCACTCAGAGTCGTCACGATCAGTGGAGTACCTA  1426

Qy    605  GluSerLysCysIleHisArgAspLeuAlaAlaArgAsnCysLeuValThrGluLys  624
Db   1427  GAGAGAGAAAAACTTCATCCACAGAGATCTTGCCGCCGAAACTGCCTGGTAGGGGGAGAAC  1486

Qy    625  AsnValLeuLysIleSerAspPheGlyMetSerArgGluGluAlaAspGlyValTyrAla  644
Db   1487  CACTTGGTGAAGGTAGCTGATTTTGGCCTGAGCAGGTTGGATGACAGCGGGCACACCTACACA  1546

Qy    645  AlaSerGlyGlyLeuArgGlnValProValLysTrpThrAlaProGluAlaLeuAsnTyr  664
Db   1547  GCCCATGCTGCTGAGCCAAG---TTCCCCATCAAATGGACTGCACCCGAGAGCCTGGCCTAC  1603

Qy    665  GlyArgTyrSerSerGluSerAspIleTrpSerPheGlyIleLeuLeuTrpGluThrPhe  684
Db   1604  AACAAGTTCTCCATCAAGTCCGACGTTTGGAGTATTGCTTTGGGAAATTGCT  1663
```

```
Qy  457 IleAspHis-----------------LeuLeuSerThr---GlnGlnProLeuThr 468
             ::  :                       ||::::||         |||:||
Db  649 GTTCATCATCATTCAACGGTGCCGACGGGCTCATCACCACCTCCATTATCCAGCCCCA 708

Qy  469 LysLysSerGlyValValLeuHisArgAlaValProLys---AspLysTrpValLeuAsn 487
             ||:::::        ::||     ::::          ||::
Db  709 AAGCCGCAACAAGCCCACTGTCTCATGGTGGTGTCCCCAACTACGACAAGTGGGAGATGGAA 768

Qy  488 HisGluAspLeuValLeuGlyGlnIleGlyValGlyAsnPheGlyValPheSer 507
             |||::         |||::     ||
Db  769 CGCACGGACATCACCATGAAGCACAAGCTGGCGGGGCCAGTACGGGGAGGTGTACGAG 828

Qy  508 GlyArgLeuArgAlaAspAsnThrLeuAlaValAlaValValSerCysArgGlu---ThrLeu 526
             :::          ||:||::        |||||||
Db  829 GGCGTGTGGAAGAAATACAGCCTGACGGTGGCCGTGAAGACCTTGAAGGAGGACCACATG 888

Qy  527 ProProAspLeuLysAlaLysPheLeuGlnLeuGlnGluAlaArgIleLeuLysGlnTyrSerHis 546
             ::          ::||||||:::||:||     :::||||||
Db  889 GAGGTGGAA---------GAGTTCTTGAAAGAAGCTGCAGTCATGAAAGAAGATCAAACAC 939

Qy  547 ProAsnIleValArgLeuIleGlyValCysThrGlnLysGlnProIleTyrIleValMet 566
             |||||||:::||||:::|||||     ::||:::||||||
Db  940 CCTAACCCAGTGCAGTCTCCTTGGGGTCTGCACCCGGGAGCCCCGTTCTATATCATCACT 999

Qy  567 GluLeuValGlnGlyGlyAspPheLeuThrPheLeuArgThrGluGlyAlaArgLeuArg 586
             |||:::        |||::     ||
Db 1000 GAGTTCATGACCTACCGGGAACCTCCTGGACTACCTGAGG---GAGTGCAACCGGCAGGAG 1056

Qy  587 ValLys------ThrLeuGlnMetValGlyAspAlaAlaAlaGlyMetGluTyrLeu 604
             |||||         :::                    |||
Db 1057 GTGAACCGCCGTGGTACCATGGCCACTCAGATCTCGTCAGCCATGGAGTACCTA 1116

Qy  605 GluSerLysCysIleHisArgAspLeuAlaAlaArgAsnCysLeuValThrGluLys 624
             |||          :::::||                 ::
Db 1117 GAGAAGAAAACTTCATCCACAGAGATCTTGCTGCCCGAAACTGCCTCGTAGGGGAGAAC 1176

Qy  625 AsnValLeuLysIleSerAspPheGlyMetSerArgGluGluAlaAspGlyValTyrAla 644
             :::||||:::||:::||||||||:::        |||
Db 1177 CACTTGGTGAAGGTAGCTGATTTTGGCCTGAGCAGGGTTGATGACAGGGACACACACA 1236

Qy  645 AlaSerGlyGlyLeuArgGlnValProValLysTrpThrAlaProGluAlaLeuAsnTyr 664
             |||   ::                    :::::|||
Db 1237 GCCCCATGCTGGAGCCAAG---TTCCCCATCAAATGACTGACCCGGAGAGCCTGGCCTAC 1293

Qy  665 GlyArgTyrSerSerGluSerAspValTrpSerPheGlyIleLeuLeuTrpGluThrPhe 684
             :::::          ||:::||||||:::||
Db 1294 AACAAGTTCTCCATCAAGTCCGACGTCGGGCATTTGGAGTATTGCTTTGGGAAATTGCT 1353

Qy  685 SerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnGlnThrArgGluPheValGlu 704
             :::                      :::   |||:||||||
Db 1354 ACCTATGGCATGTCCCCTTACCCGGAATTGACCGTTCCCAGGTGTATGAGCTGCTAGAG 1413

Qy  705 LysGlyGlyArgLeuProGluProCysProGluLeuProCysProGluAspGlyAspAspAspArgLeuMetGlu 724
             |||:::                            :::         |||
Db 1414 AAGGACTACCGCCATGAAGCCCATGAAGAAGCTGCCCAGAGAGGTCTATGAACTCATGCGA 1473

Qy  725 GlnCysTrpAlaLeuTyrGluProGlyGlnArgProSerPheThrIleTyrGlnLeuLeu 744
             |||         :::   :::||||||
Db 1474 GCATGTTGGCAGTGGAATCCCTGCCGCCCCCTTCCTTGCTGAAATCCACCAAGCCTTT 1533

Qy  745 GlnSerIle 747
             :::::::
Db 1534 GAAACAATG 1542
```

RESULT 13
US-10-439-703-5
; Sequence 5, Application US/10439703
; Publication No. US2004001527A1
; GENERAL INFORMATION:
; APPLICANT: Chang, Jenny
; APPLICANT: O'Connell, Peter
; TITLE OF INVENTION: Differential Patterns of Gene Expression that Predict for Docetax

---

```
Qy  685 SerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnThrArgGluPheValGlu 704
             :::                      :::   |||:||||||
Db 1664 ACCTATGGCATGTCCCCTTACCCGGGAATTGACCGTGCCCAGGTGTATGAGCTGCTAGAG 1723

Qy  705 LysGlyGlyArgLeuProGluProCysProGluLeuProCysProGluAspGlyAspAspAspArgLeuMetGlu 724
             |||:::                            :::         |||
Db 1724 AAGGACTACCGCCATGAAGCCCATGAAGAAGCTGCCCAGAGAGGTCTATGAACTCATGCGA 1783

Qy  725 GlnCysTrpAlaTyrArgGluProGlyGlnArgProSerPheThrIleTyrGlnLeuLeu 744
             |||         :::   :::||||||
Db 1784 GCATGTTGGCAGTGGAATCCCTGCCGCCCCCTTCCTTGCTGAAATCCACCAAGCCTTT 1843

Qy  745 GlnSerIle 747
             :::::::
Db 1844 GAAACAATG 1852
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RESULT 12
US-10-170-385-182
; Sequence 182, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 53268200100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 182
; LENGTH: 5434
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-170-385-182

Alignment Scores:

Pred. No.:	
Score:	624.50
Percent Similarity:	53.79%
Best Local Similarity:	36.03%
Query Match:	16.10%
DB:	

	2.58e-48
Length:	5434
Matches:	138
Conservative:	68
Mismatches:	128
Indels:	49
Gaps:	10

US-10-660-763-2 (1-752) x US-10-170-385-182 (1-5434)

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Qy  405 AspArgHisSerThrSerSerGluGlnGluArgGluGlyGlyArgThrProThrLeu 424
             :::||:::                               ||
Db  421 GAGAAACACTCCTGGTACCATGGCCTGTGTCCCGCAATGCCGCTGAGTATCCG------ 474

Qy  425 GluIleLeuLysSerHisIleSerGlyIlePheArgProLysPheSer---------- 440
             |||   :::||||:::::||  ::|||   |||   ||
Db  475 ------CTGAGCAGCGGGATCAATGGCAGCTTCTTGGTGCGGTGAGAGCAGTCCT 528

Qy  440 ------------------------------ 440

Db  529 AGCCAGAGGTCCATCTCGCTAGATACGAAGGGAGGGTGTACCATTACAGGATCACACT 588

Qy  441 ------AsnLeuTyrArgLeuGluGlyGluGlyPhePheProSerIleProLeuLeu 456
                   :::||                        :::
Db  589 GCTTCTGATGCAAGCTCTACGTCTCCTCCGAGACCCGCTTCAACACCCCTGGCCGAGTTG 648
```

Wed Aug 10 16:17:25 2005

TITLE OF INVENTION: Chemosensitivity and Chemoresistance
FILE REFERENCE: HO-P2482US1/10205813
CURRENT APPLICATION NUMBER: US/10/439,703
CURRENT FILING DATE: 2003-05-16
PRIOR APPLICATION NUMBER: US 60/381,141
PRIOR FILING DATE: 2002-05-17
NUMBER OF SEQ ID NOS: 91
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 5744
TYPE: DNA
ORGANISM: Human
US-10-439-703-5

Alignment Scores:
Pred. No.:
Score: 624.50
Percent Similarity: 53.79%
Best Local Similarity: 36.03%
Query Match: 16.10%
DB:

Length: 5744
Matches: 138
Conservative: 68
Mismatches: 128
Indels: 49
Gaps: 10

2.79e-48

17

US-10-660-763-2 (1-752) x US-10-439-703-5 (1-5744)

```
Qy     405 AspArgHisSerThrSerSerGluGlnGluArgGluGlyArgGlyGlyArgThrProThrLeu 424
               :::::::||||||   |||||
Db     731 GAGAAACACTCCTGGTACCATGGGCCTGTCCCGCAATGCGCTGAGTATCCG--------- 784

Qy     425 GluIleLeuLysSerHisIleSerGlyIlePheArgProLysPheSer 440
               |||||   :::||    :::     ::: |||
Db     785 -----CTGAGCAGCGGGATCAATGGCAGCTTCTTGTGGTGCGTGAGAGTGAGAGCAGTCCT 838

Qy     440 ---------------------------------- 440
Db     839 AGCCAGAGGTCCATCTCGCTGAGATACGAAGGAGGGTGTACCATTACAGATCAACACT 898

Qy     441 AsnLeuTyrArgLeuGluGluGlyIleGlyIlePheProSerIleProLeuLeu 456
               |||||              :::::  |||
Db     899 GCTTCTGATGGCAAGCTCTACGTCTCCAGACCGGCTTCAACACCCTGGCCGAGTTG 958

Qy     457 IleAspHis------------LeuLeuSerThr---GlnGlnProLeuThr 468
               ::: |||           ||||||||                ||||||||
Db     959 GTTCATCATCATTCAACGGTGCCGACGGGCTCATCACCACGCTCCATTATCCAGCCCCA 1018

Qy     469 LysLysSerGlyValValValHisArgAlaValProLys---AspLysTrpValLeuAsn 487
               ||||||           :::::            |||||||  :::
Db    1019 AAGGCCAACAAGCCCACTGTCTATGGTGTGTCCCCAACTACGACAAGTGGGAGATGGAA 1078

Qy     488 HisGluAspLeuValLeuGlyIleGlnIleGlyLysArgGlyValAsnPheGlyValPheSer 507
               ||||:::  ::          :::::::: ||||
Db    1079 CGCACGGACATCACCATGAAGCACAACCTCCTGGACTGGGCGGGGCCAGTACGGGAGGTGTACGAG 1138

Qy     508 GlyArgLeuArgAlaAspAsnThrLeuValAlaValLysSerCysArgGlu---ThrLeu 526
               |||||              :::::||| |||              :::||::::
Db    1139 GGGCGTGTGGAGAAATACAGCGCTGGCCGTGGCCGTGAAGAGACCTTGAAGGAGGACACCATG 1198

Qy     527 ProProAspLeuLysArgAlaAlaPheLeuGlnGluLysArgIleLeuLysGlnTyrSerHis 546
               ||||||||||||||      :::::::                   |||
Db    1199 GAGGTGGAA---------GAGTTCTTGAAAAGAAGCGCTCAGTCAGTCATGATGAGATCAAACAC 1249

Qy     547 ProAsnIleValArgLeuIleGlyValCysThrGlnLysGlnProIleLeuTyrIleLeuValMet 566
               ||||||::::::||||||||||||||||:::
Db    1250 CCTAACCTAGTGCAGTTCGGCTTCCTTGGGGTTCTGCACCCCGGAGCCCCCGGTTCTATATCATCACT 1309

Qy     567 GluLeuValGlnGlyGlyAspPheLeuThrPheLeuArgThrGluGlyAlaArgLeuArg 586
               |||||||||              |||::::::::  |||
Db    1310 GAGTTCATGACCTACGGGAAACCTCCTGGACTACCTGAGG---GAGTGCACCGGCAGCAGGAG 1366

Qy     587 ValLys------ThrLeuGlnMetValGlyAspAlaAlaLeuAlaGlyMetGluTyrLeu 604
               ||||       ||||||
Db    1367 GTGAACGGCCGTGGTGTCGTGTACATGGCCACTCAGATCTCTGTCAGCAGTGAGTACCTA 1426

Qy     605 GluSerLysLysCysCysIleHisArgAspLeuAlaAlaArgAsnCysLeuValThrGluLys 624
               |||
```

Db   1427 GAGAGAAAAAACTTCATCCACCAGAGATCTTGCTGCCCGAAACTCCTGCTGAGGGGAGAAC 1486

Qy   625 AsnValLeuLysIleSerArgAspPheGlyMetSerArgGluGlnAlaAspGlyValTyrAla 644
                  :::::|||| ::: |||||
Db   1487 CACTTGGTGAAGTAGTCAGTTGGCCTGAGCAGGTTGATGCAGGGAGACACCTACACA 1546

Qy   645 AlaSerGlyLeuArgGlnValProValLysTrpThrAlaProGluAlaLeuAsnTyr 664
               ||||||||| ||| ::: |||
Db   1547 GCCCATGCTGGAGCCAAG---TTCCCCATCAAATGACTGACCAGCCTGGCCTAC 1603

Qy   665 GlyArgTyrSerSerGluSerAspValTrpSerPheGlyIleLeuLeuTrpGluThrPhe 684
               |||||| |||::: ||||||||||||||
Db   1604 AACAAGTTCTCCATCAAGTCCGACGTCTGGGCATTTGGAGTATTGCTTTGGGAAATTGCT 1663

Qy   685 SerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnGlnThrArgGluPheValGlu 704
               ::: ||| :::|||| |||::::: |||
Db   1664 ACCTATGGCAGTGTCCCCTTACCCGGAATTGACCGTTCCCAGGTGTATGAGCTGCTAGAG 1723

Qy   705 LysGlyGlyArgLeuProCysProGluLeuCysProAspAlaValPheArgLeuMetGlu 724
               ||||||||| ::: |||::::::
Db   1724 AAGGACTACCGCATGAAGCCGCCAGAAGGCTCATGAACTCATGCGA 1783

Qy   725 GlnCysTrpAlaTyrGluProGlyGlnArgProSerPheThrGlnTyrGlnLeuLeu 744
               ||||||||
Db   1784 GCATGTTGGCAGTGGAATCCCTGCAGTGGAAATCCACCAAGCCTTT 1843

Qy   745 GlnSerIle 747
               |||
Db   1844 GAAACAATG 1852

RESULT 14
US-10-457-954-5
; Sequence 5, Application US/1045954
; Publication No. US20040005623A1
; GENERAL INFORMATION:
; APPLICANT: Longley, B. Jack
; TITLE OF INVENTION: Method of determining tumor sensitivities to therapeutic drugs
; FILE REFERENCE: 960296.98890
; CURRENT APPLICATION NUMBER: US/10/457,954
; CURRENT FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/387,370
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/387,406
; PRIOR FILING DATE: 2002-06-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 5
; LENGTH: 3450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3447)
; FEATURE:
; NAME/KEY: misc structure
; LOCATION: (730)..(765)
; OTHER INFORMATION: encode amino acids 244-255 for forming the sides of the enzymatic
; OTHER INFORMATION: pocket
; FEATURE:
; NAME/KEY: misc structure
; LOCATION: (931)..(1077)
; OTHER INFORMATION: encode amino acids 311-359 for forming the sides of the enzymatic
; OTHER INFORMATION: pocket
; FEATURE:
; NAME/KEY: misc structure
; LOCATION: (1141)..(1206)
; OTHER INFORMATION: encode amino acids 381-402 for forming the enzymatic pocket's
; OTHER INFORMATION: activation loop
; US-10-457-954-5

Alignment Scores: 1.89e-48
Pred. No.:

Length: 3450

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Score:                   623.00      Matches:         158
Percent Similarity:      48.21%      Conservative:     84
Best Local Similarity:   31.47%      Mismatches:      150
Query Match:                         Indels:          110
DB:                                  Gaps:             17

US-10-660-763-2 (1-752) x US-10-457-954-5 (1-3450)

Qy    341  GluGluGluAsnThrHisProArgGluArgValGlnLeuGlyLysArgGlnValLeu   360
                :::||||   :::         :::  :||    :||
Db     85  AAGGAATCATCGAGGCATGGGGGTCCACACTGCAATGTTTTTGTGAACATGAAGCCCTT  144

Qy    361  GlnGluAlaLeu----------------GlnGlyLeuGlnValAlaLeuCysSerGln   374
                ::::|||            ||||||
Db    145  CAGCGGCCGCAGTAGCATCTGACTTGACCCTCAGGGTCTGAGTGAAGCC----------  192

Qy    375  AlaLysLeuGlnAlaGlnGlnAlaGlnGlnThrLysLeuGluHisLeuGlyLeuGlyProGly   394
                :::::::|    ||||||
Db    193  GCTCGTTGGAACTCAAGGAGAAAACCTTCTC----------------GCTGGACCCAGT   234

Qy    395  GluProProValLeuLeuGln----------------------------AspAsp-----   405
                |||   ||| :::                                ||| :|
Db    235  GAAAATGACCCCAACCTTTTCGTTGCACTGTATGATTTGTGGCCAGTGAGATAACACT   294

Qy    406  ----------------------------ArgHisSerThrSerSer   411
                                            |||:|:|
Db    295  CTAAGCATAACTAAAGGTGAAAAGTTCCGGGTCTTAGGCTATAATCACAATGGGAATGG  354

Qy    412  SerGluGlnGluArgGluGlyLyArg--------------ThrPro-----   422
                ||||   :::|||    ||||||               |||||
Db    355  TGTGAGGCCAAACCAAAATGGCCAAGGCTGGGTCCAAGCAACTACATCACGCCAGTC  414

Qy    423  --ThrLeuGlu-------------------------------------   425
                ::|||||
Db    415  AACAGTCTGGAGAAAACACTCTGGTACCATGGGCCTGTGTCCGCAATGCCGCTGAGTAT   474

Qy    426  IleLeuLysSerHisIleSerGlyIleProPheArgProLysPheSer-----   440
                :::|||||:   :|||
Db    475  CTGCTGAGCAGGGGGATCAATGCAGCTTCTTGGTCGTCCGTGAGAGTGAGAGCAGTCCTGGC  534

Qy    440  --------------------------------------   440
Db    535  CAGAGGTCCATCTCGCTGAGATACGAAGGAGGGGTGTACCATTACGGATCCAACACTGCT  594

Qy    441  --------AsnLeuTyrArgLeuGluGlyLyGlyPheProSerIleProLeuLeuIle   457
                            ||||         |||:::       |||||
Db    595  TCTGATGGCCAAGCTCTCACGTCTCCTCCGAGACCCGCTTCAACACCCTGGCCAGTTGGTT  654

Qy    458  AspHis-------------LeuLeuSerThr---GlnGlnProLeuThrLys   469
                |||              ||:::::|||    |||   ||||||
Db    655  CATCATCATTCAACGGTGGCCGCACGGGCTCATCACCACCATATCCAGCCCCAAAG   714

Qy    470  LysSerGlyValValLeuHisArgAlaValProLys---AspLysTrpValLeuAsnHis   488
                :::|   |||   :::   ||| :|||           ||| :|:
Db    715  CGCAACAAGCCCACTGTCTATGGTGTGTCCCCAACTACGACAGTGGGAGATGGAACGC   774

Qy    489  GluAspV)LeuValLeuGlyGlnIleGlyArgGlyAsnPheGlyValPheSerGly   508
                ||:::|   |||   :::       ::|||||||||   ||||||||||
Db    775  ACGGACATCACCATGAAGCACCATGAGCTGGGCGGGGAGGGTTACGGAGGGGC   834

Qy    509  ArgLeuArgAlaAspAsnThrLeuValAlaValLysSerArgGlu---ThrLeuPro   527
                :::        :::   |||::::|||      ||||||      ||||||
Db    835  GTGTGGAAGAAAATAACAGCCTGACGGTGGCCGTGAAGAGCACCATGGAG   894

Qy    528  ProAspLeuValLeuGlyAlaLysPheAlaLysGluGluLysIleLeuLysLysTyrSerHisPro   547
                |||   |||||||||   :::       |||||||      |||||||||
Db    895  GTGGAA--------GAGTTCTTGAAAGAAGCTGCAGTCATGAAAGAGATCAAACCCCT  945

Qy    548  AsnIleValArgLeuIleGlyValCysThrGlnLysGlnProIleGluTyrIleValMetGlu   567
                :::|||:|||||||||
Db    946  AACCTGGTGCAGCTCCGTTGGGGTTCGGGAGCCCCCGGTTCCTATATCATCACTCGAG  1005

Qy    568  LeuValGlnGlyGlyAspPheLeuThrPheLeuArgThrGluGlyAlaArgLeuArgVal   587
                |||||||||   |||:::
Db     73  CTGGAAGAAGAGCCCTTCAGGCGGCCAGTAGCATCTGACTTTGAGCCTCGAGTGAA   132
```

```
Db   1006  TTCATGACCTACGGAGACCTCCTGGACTACCTGAGG---GAGTGCAACCGGCAGGAGGTG  1062
                :::         |||       ||| |||
Qy    588  Lys------ThrLeuGluGlnMetValGlyAspAlaAlaAlaAlaGlyMetGluTyrLeuGlu   605
                            |||||| :::   :::
Db   1063  AACGCCCGTGGTGCTGCTGTACATGCGGCCACTCCAGATCTCGTCAGCCATGGAGTACCTGGAG  1122

Qy    606  SerLysCysCysIleHisArgAspLeuAlaAlaAlaArgAsnCysLeuValThrGluLysAsn   625
                |||   :::||||   ::|||      ||||||||||||||
Db   1123  AAGAAAAACTTCATCCACAGAGATCTTGCTGCCCGAAACTGCCTGGTAGGGGAGAACCAC  1182

Qy    626  ValLeuLysIleSerAspPheGlyMetSerArgGluGlnLeuAspGlyValTyrAlaAlaAla   645
                :::::||||||   ||||||:::||||||
Db   1183  TTGGTGAAGGTAGCCGATTTTGGCCTGAGCAGGGAGCAGCTTGATGGAGTACACAGCC  1242

Qy    646  SerGlyGlyLeuArgValProValLysProGluAlaProGluAlaLeuAsnTyrGly   665
                :::|||       :::  |||   ::::|||
Db   1243  CATGCTGGAGCCAAG---TTCCCATCAAATGACTGCACCCGAGCTGCCTACAAC  1299

Qy    666  ArgTyrSerSerGluSerAspValTrpSerPheGlyValIleLeuLeuTrpGluTrpPheSer   685
                :::|||   ::::|||   ::||||||   :::
Db   1300  AAGTTCTCCATCAAGTCCGACGTTGGGCATTTGGAGTATTGCTTTGGGGAAATTGCTACC  1359

Qy    686  LeuGlyAlaSerProTyrProCysProGluLeuValCysProAlaValPheArgLeuMetGluGln   705
                ||||||         :::
Db   1360  TATGGCATGTCCCCTTACCCGGGAATTGACCTGTCCCAGTGTATGAGCGTGTAGAGAAG  1419

Qy    706  GlyGlyArgLeuProGluLeuCysProLeuGlnArgProSerProAlaValPheArgLeuMetGluGln   725
                ||||||:::      :::      ||||||||||||||
Db   1420  GACTACCGCCATGAGCCCCAGAGGGTCTCATGAACTCATGCGAGCA  1479

Qy    726  CysTrpAlaTyrAlaTyrGluProGlyGlnArgProSerPheSerThrIleTyrGlnLeuGluGln   745
                |||||||||   :::|||||||||
Db   1480  TGTTGGCAGTGGAATCCCTGACCGGCCCCTCCTTTGCTGAAATCCACCAAGCCTTTGAA  1539

Qy    746  SerIle  747
                ::::|:
Db   1540  ACAATG  1545
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RESULT 15
US-10-263-480-1
; Sequence 1, Application US/10263480
; Publication No. US20030170851A1
; GENERAL INFORMATION:
;   APPLICANT: NO. US2003017085lAlartis AG
;   TITLE OF INVENTION: Organic Compounds
;   FILE REFERENCE: Case 4-32175P1/PROV
;   CURRENT APPLICATION NUMBER: US/10/263,480
;   CURRENT FILING DATE: 2002-10-03
;   NUMBER OF SEQ ID NOS: 2
;   SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
;   LENGTH: 3393
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(3393)
US-10-263-480-1

Alignment Scores:
Pred. No.:                2.29e-48      Length:        3393
Score:                    622.00       Matches:        158
Percent Similarity:       48.67%       Conservative:    79
Best Local Similarity:    32.44%       Mismatches:     136
Query Match:                           Indels:         114
DB:                                    Gaps:            17

US-10-660-763-2 (1-752) x US-10-263-480-1 (1-3393)

Qy    360  LeuGlnGluAlaLeu---------------------GlnGlyLeuGlnVal  369
                |||:::|||||||||
Db    73   CTGGAAGAAGAGCCCTTCAGGCGGCCAGTAGCATCTGACTTTGAGCCTCGAGTGAA   132
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us-10-660-763-2.rnpb

Wed Aug 10 16:17:25 2005

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Qy   641 GlyValTyrAlaAlaSerGlyGlyLeuArgGlnValProValLysTrpThrAlaProGlu 660
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Db  1171 GACACCTACACAGCCACCATGCTGGAGCCAAG---TTCCCCATCAAATGGACTGCACCCGAG 1227

Qy   661 AlaLeuAsnTyrGlyArgTyrSerSerGluSerAspValTrpSerPheGlyIleLeuLeu 680
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Qy   681 TrpGluThrPheSerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnGlnThrArg 700
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Search completed: August 10, 2005, 14:28:11
Job time : 1701 secs

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Qy   407 HisSerThrSerSerGluGlnInGluArgGluGlyGlyGlyArg------------ 420
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Qy   421 ------ThrLeuGlu----------ThrPro 425
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Qy   426 ----IleLeuLysSerHisIleSerGlyIleLeuPheArgProLysPheSer 440
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Qy   440 --------------------- 440
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Qy   441 -------AsnLeuTyrArgLeuGluLeuGlyLeuGluGlyGluGlyPheProSer 452
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Qy   453 IleProLeuLeuAspHis----------LeuLeuSerThr---Gln 464
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Qy   465 GlnProLeuThrLysLysSerGlyTyrValValLeuHisArgAlaValProLys---AspLys 483
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Db   643 TATCCAGCCAAAGCGCAACAAGCCACTGTCTATGGTGTGTCCCCAACTACGACAAG 702

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Db   703 TGGGAGATGGAACGCACGGACATCAACACCATGAAGACAACAGCTGGCGGCGGGCCAGTACGGG 762

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                    GenCore version 5.1.6
            Copyright (c) 1993 - 2005  Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:    August  9, 2005, 21:16:47 ; Search time 428 Seconds
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Searched:        1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters:        2405568

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES
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Result No.	Score	Query Match	Length	DB	ID	Description
1	3879	100.0	2674	3	US-09-817-180-1	Sequence 1, Appli
2	3879	100.0	2674	4	US-10-003-295-1	Sequence 1, Appli
3	2137	55.1	15297	3	US-09-817-180-3	Sequence 3, Appli
4	2137	55.1	15297	4	US-10-003-295-3	Sequence 3, Appli
5	624.5	16.1	3623	1	US-08-306-691B-35	Sequence 35, Appl
6	624.5	16.1	5434	4	US-09-949-016-927	Sequence 927, App
7	622	16.0	5763	3	US-09-949-016-3759	Sequence 3759, Ap
8	607.5	15.7	1521	2	US-08-604-989A-10	Sequence 10, Appl
9	607.5	15.7	1713	3	US-09-741-154-1	Sequence 1, Appli
10	605.5	15.6	1942	2	US-08-604-989A-11	Sequence 11, Appli
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15	598.5	15.4	2572	3	US-09-949-016-5357	Sequence 5357, Ap
16	598	15.4	2574	3	US-09-142-529-2	Sequence 2, Appli
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18	597	15.4	3650	4	US-09-949-016-454	Sequence 454, App
19	596.5	15.4	3622	4	US-09-949-016-5518	Sequence 5518, Ap
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                                         ALIGNMENTS

RESULT 1
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; Patent No. 6340584
; GENERAL INFORMATION:
;  APPLICANT: GAN, Weiniu et al.
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION: THEREOF
;  FILE REFERENCE: CL001183
;  CURRENT APPLICATION NUMBER: US/09/817,180
;  CURRENT FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;  LENGTH: 2674
;  TYPE: DNA
;  ORGANISM: Human
US-09-817-180-1

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Best Local Similarity:  100.00%                          Mismatches:       0
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Qy  561  ProIleTyrIleValMetGluLeuValGlnGlyGlyAspPheLeuThrPheLeuArgThr  580
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Db  621  ValThrGluLysAsnValLeuValIleLeuSerAspPheGlyMetSerArgGluGluAlaAsp  640
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1932  GTGACAGAGAAGAATGTCCTGGTCATCAGTGACTTTGGAATGTCCCGAGAGGAAGCCGAT  1991

Db  641  GlyValTyrAlaAlaSerGlyGlyLeuArgGlnValTrpProValLysTrpThrAlaProGlu  660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1992  GGGGTCTATGCGGCCTCAGGGGGCCCTCAGAGCAAGTCCCCGTGAAGTGGACCGCACCTGAG  2051

Qy  661  AlaLeuAsnTyrGlyArgTyrTyrSerSerGluSerAspValTrpSerPheGlyIleLeuLeu  680
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2052  GCCCTTAACTACGGCCGCTACTACTCCTCCGAAAGCGACGTGTGGAGCTTTGGCATCTTGCTC  2111

Qy  681  TrpGluThrPheSerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnGlnThrArg  700
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2112  TGGGAGACCTTCAGCCTTGGGGCGTCCCCATCCCAACCTCAGCAATCAGCAGACACGG  2171

Qy  701  GluPheValGluLysGlyGlyArgLeuProGluCysProGlyLysValGlnArgProSerThrIle  720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2172  GAGTTTGTGGAGAAGGGGGGGCGGCTGCCGGAGTGTCCTGGGAAAGTGTCCCGATGCCGGTTC  2231

Db  721  ArgLeuMetGluGlnCysTrpThrAlaTyrProGlyGlnArgProSerPheThrIle  740
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2232  AGGCTCATGGAGCAGTGCTGGGCCTATCCGGGCCAGAGCTTGTCTCCAGCACCATC  2291

Qy  741  TyrGlnLeuGlnSerIleArgLysArgHisArg  752
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2292  TACCAGGAGCTCCAGAGCATCCGAAAGCGCCATCGG  2327
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RESULT 2
US-10-003-295-1
; Sequence 1, Application US/10003295
; Patent No. 6686187
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001183DIV
; CURRENT APPLICATION NUMBER: US/10/003,295
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 1
; LENGTH: 2674
; TYPE: DNA
; ORGANISM: Homo sapiens
; SOFTWARE: FastSEQ for Windows Version 4.0
US-10-003-295-1

Alignment Scores:
Pred. No.:   0   Length: 2674
Score: 3879.00   Matches: 752
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: Gaps: 0

US-10-660-763-2 (1-752) x US-10-003-295-1 (1-2674)

Qy   1 MetGlyPheSerSerGluPheSerProGlnGlyHisGlyValLeuGlnGlnMetGln 20
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   72 ATGGGCTTCTCTTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG 131

Qy   21 GluAlaGluLeuArgLeuGluGlyMetAlaArgLysTrpMetAlaArgValTyrSer 40
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   132 GAGGCCGAGCTTCGTCTACTGGAGGGCATGGCATGGGAAAAGTGGATGGCCAGCGGGTCAAGAGT 191

Qy   41 AspArgGluTyrAlaGlyLeuLeuHisHisMetSerLeuGlnGlnSer 60
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   192 GACAGGGAGTATGCAGGACTGCTTCACCACCATGTCCCTGCAGCAGAGC 251

Qy   61 ArgAlaIleSerProAspSerProIleSerGlnSerTrpProAlaGluIleThrSerGlnThr 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   252 CGGGGCCATCAGCCTGACAGCCCCATCAGTCAGTCCTGGCCTGAGATCACCAGCCAAACT 311

Qy   81 GluGlyLysLeuSerArgLeuLeuArgGlnHisAlaGluAspAsnSerGlyProLeuSer 100
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   312 GAGGGCCTGAGCCGCTTGCTGCGGCAGCACGCAGAGGATCGAACTCAGGGCCCCTGAGC 371

Qy   101 LysLeuSerLeuLeuIleArgGluArgGlnLeuArgLeuArgLysTyrSerGluGlnThrTrp 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   372 AAGCTGAGCCTGCTCATCCGGGAACGGCAGCTTCGCAGAAGAGACCTACAGCGAGCAGTGG 431

Qy   121 GlnGlnLeuGlnLeuGluThrLysSerThrHisSerGlnHisAspIleGluLysLeuLysSer 140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   432 CAGCAGCTGCAGCAGGAGACCAAGAGCACCCACAGCCAGCATTGAGAAGCTGAAGAGC 491

Qy   141 GlnTyrArgAlaLeuArgAspAspSerAlaGlnAlaLysAspTyrGlnGluAlaSer 160
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   492 CAGTACCGAGCTCTGCGACACGGACAGTGCCCAAGCGCCAAGTACCAGGAGGCCAGC 551

Qy   161 LysAspLysAspArgAspLysAlaLysAspTyrValArgSerLeuTyrLysLeuLeuPhe 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   552 AAAGACAAGGACCGTGACAAGGCCAAGGACTATGTGCGCAGCCTGTACAAGCTCCTTT 611

Qy   181 AlaHisHisAsnArgTyrValLeuGlyValArgAlaAlaGlnLeuHisHisGlnHisHis 200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   612 GCTCACCACAACCGCTATGTGCTGGGCGTGCGGGCTGCACAGCTACACCACCAGCACCAC 671

Qy   201 HisGlnLeuLeuLeuProGlyLeuLeuLeuArgSerLeuGlnAspLeuHisGluGluMetAla 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   672 CACCAGCTCCTGCTGCCCGGCCTGCTGCTGCGGTCACTGCAGGACCTGCACGAGGAGATGGCT 731

Qy   221 CysIleLeuLysGluLeuLysGlnIleLeuSerSerValGlnGlnAspGlu 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   732 TGCATCCTGAAGGAGATCCTGCAGGAATACCTGGAGATTAGCAGCGTGCAGGGATGAG 791

Qy   241 ValAlaAlaIleHisArgGluMetAlaAlaAlaAlaAlaAlaAlaArgIleGlnProGluAlaGlu 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   792 GTGGTGGCCATTCACCGGGAGATGGCTGCTGCAGCTGCAGCTGCGCCGCATCCAGCCTGAGGCTGAG 851

Qy   261 TyrGlnGlyPheLeuArgGlnTyrGlySerAlaProAspValProProCysValThrPhe 280
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   852 TACCAAGGCTTCCTGCGACAGTATGGGTCCGCACCTGACGTCCCACCCTGTGTCACCGTTC 911

Qy   281 AspGluSerLeuLeuGluGluGluGlyGluProGlyGluLeuGlnLeuAsnGlu 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   912 GATGAGTCACTGCTTGAGGAGGGTGAACCGGCTGGAGCTCCAGCTGAACCAG 971

Qy   301 LeuThrValGluSerValGlnHisThrLeuThrSerValThrArgAspGluLeuAlaValAla 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   972 CTGACTGTGGAGAGCGTGCAGCACACGCTGACCTCAGTGACCAGAGATGAGCTGGCTGTGGCC 1031

Qy   321 ThrGluMetValPheArgGlnMetValThrGlnLeuGluLeuArgAsn 340
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1032 ACCGAGATGGTGTTCAGGCAGATGGTTACGCAGCTGGAGCTGCGGAAT 1091

Qy   341 GluGluGlnAsnThrHisProArgGluArgValGlnLeuGlnLeuLeuGlyLysArgGlnValLeu 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1092 GAAGAGGAGAACACCCACCCCGGGAGCCGGGTGCAGCTGCTGGGCAAGAGGCAAGTGCTG 1151

Qy   361 GlnGluAlaLeuGlnIleGlyLeuGlnValAlaLeuCysSerGlnAsnAlaLysLeuGlnAlaGln 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1152 CAAGAAGCACTGCAGATCGGCCTGCAGGTAGCGCTGTGCAGCCAGAGCTGCAGGCCCAG 1211

Qy   381 GlnGluLeuGlnThrLysLeuGluHisGluLysProGlyValProProValLeu 400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1212 CAGGAGTTGCTGCAGACCAAGCTGGAGCACGAGAAGCCTGGGGTCCCGCCTGTCTG 1271

Qy   401 LeuLeuGlnAspAspArgHisSerSerGluGluArgGlnGluGlyGlyArg 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1272 CTCCTGCAGGATGACCGGCACTCCAGTGTCCTCCGGGAGGAGAGGGGGAAGG 1331

Qy   421 ThrProThrLeuGluIleLeuLysSerHisIleSerGlyIleLeuSerGlyIleProPheSer 440
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1332 ACACCCACGCTGGAGATCCTGAAGAGCCACATCTCAGGAATCTTCCGCCCAAGTTCTCG 1391

Qy   441 AsnLeuTyrArgLeuGlyLyGluGlyPheProSerIleProSerLeuLeuAspHisLeu 460
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1392 AACCTGTACCGACTGGAAGGGGAAGGCTTCCTGAGCATTCCTTGCTCATCGACCACCTA 1451

Qy   461 LeuSerThrGlnGlnProLeuThrLyeSerSerGlyLeuValLeuHisArgAlaValPro 480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1452 CTGAGCACCCAGCAGCCCCTCACCAAGAAGAGTGGTGTTCTGCACAGGGCTGTGCCC 1511

Qy   481 LysAspLysTrpLeuAsnHisGluAsnGluGluLysLysSerGlyIleLeuGlyArgGly 500
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1512 AAGGACAAGTGGCTGCTGAACCATGAGAATGAAGAGAAGAAGTCAGGGATTGGACGGGGG 1571

Qy   501 AsnPheGlyValPheSerGlyArgLeuArgAlaAspAsnThrLeuValAlaValLys 520
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1572 AACTTTGGCGAAGTGTTCAGCGGACGCCTGCGAGCCGACAACACCCTGGTGGCGGTGAAG 1631

Qy   521 SerCysSerArgGluThrArgLeuProProAspLeuLysSerPheGlnGluAlaArgIle 540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1632 TCTTGTGTCAGGGAGACGCGTCTCCCACCTGACCTCAAGAGCTTCCAGGAAGCGAGGATC 1691

Qy   541 LeuLysGlnTyrSerHisProAsnIleValArgLeuIleGlyValCysThrGlnLysGln 560
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1692 CTGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCCAGAAGCAG 1751

Qy   561 ProIleTyrIleValMetGluLeuValGlnGlyGlyAspPheLeuThrPheLeuArgThr 580
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1752 CCCATCTACATCGTCATGGAGCTTGTGCAGGGGGGGGACTTCCTGACCTTCCTCCGCACG 1811

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Qy   581 GluGlyAlaArgLeuArgValyLysThrLeuLeuGlnMetValGlyAspAlaAlaAlaGly 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1812 GAGGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGATGCAGCTGCTGGC 1871

Qy   601 MetGluTyrLeuGluSerLysCysCysIleHisArgAspLeuAlaAlaArgAsnCysLeu 620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1872 ATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACCTGGCTGCTCGGAACTGCCTG 1931

Qy   621 ValThrGluLysAsnValLeuLysIleSerAspPheGlyMetSerArgGluGluAlaAsp 640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1932 GTGACAGAGAAGAATGTCCTGAAGATCAGTGACTTTGGGATGTCCCGAGAGGAAGCCGAT 1991

Qy   641 GlyValTyrAlaAlaSerGlyGlyLeuArgGlnValProValyTrpThrAlaProGlu 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1992 GGGGTCTATGCAGCCTCAGGGGGCCTCAGACAAGTCCCGTGAAGTGGACCGGACCCTGAG 2051

Qy   661 AlaLeuAsnTyrGlyArgTyrSerSerGluSerAspValTrpSerValTrpPheGlyValIleLeuLeu 680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2052 GCCCTTAACTACGGCCGCTACTCCTCCGAAAGCGACGTGTGGAGCGTTTGGCATCTTGCTC 2111

Qy   681 TrpGluThrPheSerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnGlnThrArg 700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2112 TGGGAGACCTTCAGCCTGGGGGCCTCCCCATCCCAACCTCAGCAATCAGCAGACACGG 2171

Qy   701 GluPheValGluLysGlyGlyArgLeuProCysProGluLeuCysProAspAlaValPhe 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2172 GAGTTTGTGGAGAAGGGGGGGCCGTCTGCCCTGCCCCAGAGCTGTGTCCTGATGCCGTGTTC 2231

Qy   721 ArgLeuMetGluGlnCysTrpAlaTyrArgAlaTyrArgGluProGlyGlnArgProSerPheSerThrIle 740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2232 AGCTCATGGAGCAGTGCTGGGCCTATCGAGCCTGGGCAGCCGCCCAGCTTCAGCACCATC 2291

Qy   741 TyrGlnLeuGlnSerIleArgLysArgHisArg 752
             ||||||||||||||||||||||||||||||||||
Db  2292 TACCAGGAGCTGCAGAGCATCCGAAAGCGGCATCGG 2327
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RESULT 3
US-09-817-180-3
; Sequence 3, Application US/09817180
; Patent No. 6340584
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001183
; CURRENT APPLICATION NUMBER: US/09/817,180
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15297
; TYPE: DNA
; ORGANISM: Human
US-09-817-180-3

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Alignment Scores:
Pred. No.:
Score:                   2.55e-198        Length:        15297
                         2137.00          Matches:       747
Percent Similarity:      21.28%           Conservative:  0
Best Local Similarity:   21.28%           Mismatches:    5
Query Match:             55.09%           Indels:        2764
DB:                      3                Gaps:          16
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US-10-660-763-2 (1-752) x US-09-817-180-3 (1-15297)

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Qy     1 MetGlyPheSerSerGluLeuCysSerProGlnGlyHisGlyValLeuGlnHisGlyValLeuGlnHisMetGln 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2563 ATGGGCTTCTCTTCTGAGCTGTGCAGCCCCAGGGGCCACGGGGTCCTGCAGCAAATGCAG 2622

Qy    21 GluAlaGluLeuArgLeuLeuGlyMetGlyTrpMetAlaAlnArgValvalLysSer 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2623 GAGGGCCGAGCTTCGTCTACTGAGGGCATGAGAAAGTGGATGGCCCCAGCGCGGGTCAAGAGT 2682

Qy    41 AspArgGluTyrArgAlaGlyValyLeuHisHisMetSerLeuGlnAspSerGlyGlyGlnSer 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2683 GACAGGGAGGATGTCAGGAGACTGCTTCACCCATGTCCCTGCAGGACAGTGGGGGCCAGAGC 2742

Qy    61 ArgAlaIleSerProAspSerProIleSerGlnSer 72
             ||||||||||||||||||||||||||||||||||||
Db  2743 CGGGCCATCAGCCCTGACAGCCCCATCAGTCAGT-GGGTCTCTATGGGACTTGGTGGG 2801

Qy    72 -------------------------------------------------------------
Db  2802 TGCTGGCGTATCTGCTTCCTTCCTTCCTCCTCCTGGGGCACTGGCTGGAGA 2861

Qy    72 -------------------------------------------------------------
Db  2862 TCTGGCAGGCCAATGCTTGGGAGCCATTGTGCCCCCTCCCTGCTCCCCATCTGTGCT 2921

Qy    73 ---TrpAlaGluIleThrSerGlnThrGluGlyLeuSerArgLeuLeuArgGln 89
                |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2922 GTATAGTTCCTGGCTGAGATCACCAGCCAAACTGAGGGCCTGAGCCGCCTTGCTGCGGCAG 2981

Qy    90 HisAlaGluAspSerLeuAsnSerGlyTyrProLeuSerLysLeuSerLeuLeuIleLeuArgGluArg 109
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2982 CACCGAGGGATCTGAACTCAGGGCCCCTGAGCAAGCTGAGCCTGCTCATCCCGGAACGG 3041

Qy   110 GlnGlnLeuArgLysThrTyrSerGluLeuTrpGlnGlnLeuGlnLeuGluThrLys 129
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3042 CAGCAGCTTCGCAAGACCTACAGCGAGCAGTGCCAGCCAGGAGCTCACCAAG 3101

Qy   129 -------------------------------------------------------------
Db  3102 GTGAGCGGGCAGCACTGGGCTTCGGTCATTTCTGTCATTTCTGTCTAAATTTGAGCCTCGAAGGGGT 3161

Qy   129 -------------------------------------------------------------
Db  3162 TGTTTGCACAAGAGGCCCTGGATTCACTGGGAAGTGAAGTCCCTGACCCGCAGGCCTG 3221

Qy   129 -------------------------------------------------------------
Db  3222 GCTTGCTCTAACCTTGATGTAGCTTCCTCCTTCCTTCCTTCCCTACGTTGAGCTGCTTGCA 3281

Qy   129 -------------------------------------------------------------
Db  3282 GCAAGGCCCTCTCTGTGCTTTTTCTGTGCCTGGGCAAAGTGCTGGGAGTGTAAGGATGAGT 3341

Qy   129 -------------------------------------------------------------
Db  3342 GACCGGTCACGTGCCTGGGAGAAGTCAGAATCGGTACTCGCCTCCCACTGTGCCCATCT 3401

Qy   129 -------------------------------------------------------------
Db  3402 GGCTTCTGGGTTCTGAGAGTCAGGAGGGAATGAGGGTCAGTCTGTTTGGCCTTCGACCTA 3461

Qy   129 -------------------------------------------------------------
Db  3462 TGCAGCCTCCTCTCAGGGCCCCAGAGACTGGGCAGCAGCATGGCCCCGAAGGTCGAGG 3521

Qy   129 -------------------------------------------------------------
Db  3522 ACTCGGGCCGTGAAGTCAGCCTGCCTAGGTTTGAATCCCACCAGCTTCCTCAGTCTAGAG 3581

Qy   129 -------------------------------------------------------------
Db  3582 GCTGTGTGATTTGGAACTATTTATCTGGGAGCCTAGTGCCCCATTCAGTGTGCTGGTCA 3641

Qy   129 -------------------------------------------------------------
Db  3642 CCCTCCCTGCACCACCACCCCTTCCTCAGTGCAGAGCCCAGCCTTGCCATGACCACCACAG 3701

Qy   129 -------------------------------------------------------------
Db  3702 CGGGCCCCTGGTGGCCACCCTGGCCACCCTGGCCCCCAAAAGATCATCATCGATTCAAGGG 3761
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Qy   129 -- 129

Db   4842 GCTGCGGTCACTGCAGGACCTGCGACGAGGAGATGCGTTGCATCCTGTAAGCCCGCAGCCC 4901
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   129 -- 129

Db   4902 CGTCCCCTGGCCCCACCCTTGAGCAGCCCTAAGCCCAGCCATCAGGCCCAGAGGCAGGA 4961

Qy   129 -- 129

Db   4962 CCCAGAAATCCATTGCTGGGAAGGTGCTGGCCATGTAACCACATGAGAACGGGACCTGG 5021

Qy   129 -- 129

Db   5022 GCCAAGGATTGGAAACAGGCAACTTACCTCTGAATTACACTATTCCAGGGTCTCATTATT 5081

Qy   129 -- 129

Db   5082 CCAGGGTTTTATTACATTCATTGAGCACTGTTCTGGGCTCTGGATTATACCAGAGAACGA 5141

Qy   129 -- 129

Db   5142 TGGTAGACAAAAACATCTGTCCTCAGGGATCTTTCGTGTTAGTGGAGTGAGAATGTGAGG 5201

Qy   129 -- 129

Db   5202 AGCACTAAGAGCCATGAGAAAAATAAAGCAAGAAGAGTGATCGGGACCTGGGAGCACG 5261

Qy   129 -- 129

Db   5262 GAGGCAAGGGAGGAGGTGACAGTTGTCATAGAGTGATCTGGGAAAGCCTCTTGAGAGGT 5321

Qy   129 -- 129

Db   5322 GACATTCAAAGAGCCCCTGAGAGGGGTACGGGAGTGAATCATGGGCTATTTGGAGAAA 5381

Qy   129 -- 129

Db   5382 GACCATTCCAGAAAGGAGGACAGCAATTACACAGGCCTTGAGGTAGGAGAGTACCAGGGA 5441

Qy   129 -- 129

Db   5442 CTAATAGCCAGGAACCAGTGGTGCCCTGAGAGTGAGGGAGGGGGAGTCATACACGAG 5501

Qy   129 -- 129

Db   5502 GCTGGAGGAGGCAGGCGTCAAGGGCTACTGGGTGATAGAAGGTCTAGCAGGGCCATGGTG 5561

Qy   129 -- 129

Db   5562 AGGACTTTGGCTCTGGGTGAACAAGAGATGGCATGATCTGACCTCGTTGTTTTTTGTTCAT 5621

Qy   129 -- 129

Db   5622 TTTGTTTTAACTTTTTTTGAGTCAGAGTCTCGCTCTGCGCCCCAGGCTAGAGTGCAGTGG 5681

Qy   161 -- 161

Db   5682 CATGATCTCGGCTTACTGCAACCTCCGCCTCCCAGGTTCAAGTGATTCCCCTGCCTCAGC 5741

Qy   162 --------------------------------AspLysAspArgAspLysAl 168

Db   5742 CTCCCGAGTAGCTGAAAACTACGGCATGCGCCACCACCACACCCGACTAATTTTTGTATTTTT 5801

Qy   168 aLysAspLysTyrValArgSerLeuTrpLysPheAlaHisHisAsnArgTyrValLe 188

Db   5802 AGTAGAGACGGGGTTTCACCATGTTGCCCAGGCTGGTCTCTAATTCCTGGGCTCAAAGCG 5861

Qy   188 uGlyValArgAlaAlaGlnLeuHisHisGlnHisHisGlnLeuLeuLeuProGlyLe 208

Db   5862 ATTTGCCTGCCTCGCCTCCCAAAGTGCCGGGATTACAGGCATGAGCCACCACATGCCCAGC 5921

Qy   208 uLeuArgSerLeuGlnAspLeuHisGluHisGluMetAlaCysIleLeu---------- 223

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277 ysValThrPheAspGluSerLeuLeuGluGluGlyGluProLeuGlyGluLeuG 297
Qy
Db  7062 GTGTCACGTTCGATGAGTCACTGCTTGAGGAGGGTGAACCGCTGGGGGAGCTCC 7121

297 lnLeuAsnGluLeuThrValGluSerValGlnHisThrLeu 310
Qy
Db  7122 AGCTGAACGAGCTGACTGTGGAGAGCGTGCAGCACACGTG-GGTGGTGGCTTTGCACCTG 7180

310 ---- 310
Qy
Db

310 ---- 310
Qy
Db  7181 GGCTGCGGCGGGGGGCTCCCAGCAGACCACCAGAGTGTTTATGTAGGCAGGGGTCGTGTGGA 7240

310 ---- 310
Qy
Db

310 ---- 310
Qy
Db  7241 GACTGTCCACAGAGCTGTCACCAGGTGGCCGGGCTTGCTTGGCTCTACAGGGATGGCAC 7300

310 ---- 310
Qy
Db

310 ---- 310
Qy
Db  7301 TGGGACCTGGGTTGAGGGGGTGAGGAGGGGTCCGGTTCTAATGCTGCCCTTCTCTTGGGTGCA 7360

329 ---ThrSerValThrAspGluAlaValAlaAlaThrGluMetValPheArgGlnG 329
Qy
Db  7361 GGCTGACCTCCAGTGACAGATGAGCTGCGTGTGGCCACCGAGATGGTGTTCAGGCGGCGCAGG 7420

329 luMetValThrGlnLeuGlnGlnLeuLeuArgAsnGluGluAsnThrHisProArgG 349
Qy
Db  7421 AGATGGTTACGGAGCTGCAACAGGAGCTCCGAAATGAAGAGGAGAACACCCCACCCCCGGG 7480

349 lu 349
Qy
Db  7481 AGCGGTGAGGTGGGGCCCTGCCCCCTGCTGCCAGCCCTCCTGCCCTCCCTCCCTCCTACCC 7540

349 ---- 349
Qy
Db

365 ----ArgValGlnLeuLeuGlyLysArgGlnValAlaLeuGlnG 365
Qy
Db  7541 TAACTGCTCTGGCTAGCCGCCGCCCAGACCGGCCCCTTATTCTTCATCCACCCTCCACCC 7600

385 GlyLeuGlnValAlaLeuCysSerGlnAlaAlaLysLeuGlnGlnGluGlnLeuLeuGln 385
Qy
Db  7601 GCCCCTGCCTGCCAGGGTGCTGCTGGCCAAGGAGCTGCAAGAGCAGCACTGCAG 7660

385 ---- 385
Qy
Db  7661 GGGCTGCAGTAGCGGTGTGTGCAGCCCAAGCTGCAGCCCAGCGAGAGTTGCTGCAG 7720

405 ThrLysLeuGluHisGluGlyLeuProGluProProValLeuLeuGluLeuGlnAspAsp 405
Qy
Db  7721 ACCAAGCTGGAGCACCTGGGCCTGCCTGAGCCCCGCCTGTGCTGCCTGCCAGGATGAC 7780

412 ArgHisSerThrSerSer---- 412
Qy
Db  7781 CGCCACTTCCACGTGCTGTCCTC-GGTGAGCTGCCCCATCCGCGGCCGCCGCTGCCCACCGGC 7839

412 ---- 412
Qy
Db  7840 CTGCCCACCTCGGGGGGTTCGCGCTCCCATTTTCGCCCTCCCCCTCCCTAAGCCTGGCCACCCC 7899

424 ----GluGlnLeuArgGluGlyGlyTyrArgThrProThrLeu 424
Qy
Db  7900 GCTGACGTCGTCCCTGCCCTGGCTCCCAGGAGCAGGACACCCCACGCTG 7959

440 GluIleLeuLysSerHisIleSerHisGlyIlePheArgProLysPheSer---- 440
Qy
Db  7960 GAGATCCTTAAGCACCCACCATCTCCAGGAATCTTCCGGCCCCAAGTTCTCGGTGAGTGGCGCC 8019

440 ---- 440
Qy
Db

440 ---- 440
Qy
Db  8020 CAGCCTGGGCCCCCCTACTGTTGTGTTTAATCACTGGAGTTAATCACTGGGATGTCCTAGAGAGGA 8079

440 ---- 440
Qy
Db

440 ---- 440
Qy
Db  8080 GGCTCTGCCCAGGCTGCTTGTATTGGGAAGTTCCTCTTCTTCCCTGGGATTCCAGGCTGCA 8139
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Db  5922 CCTGACCTCTGTTTAATAAGGCCACTCTGGCTGCTGCTGTGCTGCAAATAGACTTCAGGGAG 5981
Qy       --------------------------------------------------------------- 223
Db  5982 CAAGGACAGAAGCTGGGAGGAGCAGAGAGCAGGCTGCTTGCCATAATCCAGATCCAAGCTT 6041
Qy       --------------------------------------------------------------- 223
Db  6042 TTGGCCAGTAGGACGCGGGAGGTAGCAATGGAGGTGAGGCGCGGTCAGGTCCTGGGGCAG 6101
Qy       --------------------------------------------------------------- 223
Db  6102 GTCCTGGAAGGTGAAGCCAGTGGGATTTCCCTATGGAGTTCCCTATGGAGTGGGCGTGAAATAGA 6161
Qy       --------------------------------------------------------------- 223
Db  6162 GGAGTCAGGGGTCACTCTGGGGATTTGGCTGCTGAGCAGCTGGAAGAGATGGAGTGGCTGTTA 6221
Qy       --------------------------------------------------------------- 223
Db  6222 ACTTATGTAGGGGAAGGCTGTGGGAAGAAGAGGTTTAGAGACAAGAAGTAGCAGTTCATTT 6281
Qy       --------------------------------------------------------------- 223
Db  6282 ATTTATTTATTTATTTATTTATTTATTTATTTATTTAGAGATGTAGTCATTCTTTCGC 6341
Qy       --------------------------------------------------------------- 223
Db  6342 CAGGCTGGAGTGCAGTGGCGCGATCTTGGCTCACTGCAACCTCCACCTCCCAGGCTCAAG 6401
Qy       --------------------------------------------------------------- 223
Db  6402 CGATTCTCTTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCATGTGCCAC 6461
Qy       --------------------------------------------------------------- 223
Db  6462 CATGCCTGGCTAATTTTTGTATTTTGCTTTTCAGTAGAGATGGGGTTTCACCACGTTAGC 6521
Qy       --------------------------------------------------------------- 223
Db  6522 CAGGCTGGTCTCGAACTGACCTCAGGCAATCACCGCTCGACCTCCCAGTGTTGGTAT 6581
Qy       --------------------------------------------------------------- 223
Db  6582 TATAGGCGTGAGCCACTGCCTGGCCCACTGGATCCTTATTACAACTGCCAGTGTCCCT 6641
Qy       --------------------------------------------------------------- 223
Db  6642 CTTATATATATCAGGAAATAGAAGATTAGGGAGAGGTTAAATAATTTGCCTAGAGTTGGCA 6701
Qy       --------------------------------------------------------------- 223
Db  6702 TGGCTAGCTCGAAGTGAGTGAGCGCAGGGGTCAACCCCAGACTCCAAAACCCAGGGTCCTA 6761
Qy       --------------------------------------------------------------- 223
Db  6762 GGCCTGAACTGACCCTGCCCAGCCTGCCCCTGAGGCTCCCCTGACTCCTCGG 6821
Qy       --------------------------------------------------------------- 223
Db  6822 GGGCAGGAGGAGATCCTGCAGGAATACCTGGAATTAGCAGCCTGGTGCAGGATGAGGT 6881
Qy   224 -----LysGluIleLeuGlnGluTyrLeuGluIleSerSerLeuValGlnIleAspArgGluVa 241
Db  6882 1ValAlaAlaIleHisArgGluMetAlaAlaAlaLaAlaAlaArgIleGlnProGlyAlaGluTy 261
Qy   241 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6942 CCAAGGCTTCCCTGCGACAGTATGGGTAAGCCCCGTCCTTGCTCCTGGGCCCCAGGGGCT 7001
Qy   261 rGlnGlyPheLeuGlnArgGlnTyr-Gly                            269
Db  6942 GGTGGGCCATTCAACCCGGGAGATGGCTGTGCTGCCCGATCCCAGGCCTGGAGGCTGAGTA 6941
Qy   261 |||||||||||||||||||||||||                              269
Db  7002 GCTGGCCTCTGCCACTGACGCGGGGCGCGTGTCCCCCACAGTGCCGCACCTGACCTCCCACCCT 7061
Qy   270 -----SerAlaProAspValProProC 277
```

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Qy    440                                                                                             440
Db   8140 GATGTCCCAGAGACCTGCCCCTGACCCCTCCTTTCCATCGCCCCAGTGTGTAAAGG 8199
Qy    440                                                                                             440
Db   8200 GACCAGCAACCTGACTATTCGACTTCTCCCTGCTTCAGGAGCCGGTTGGGGGCTGTG 8259
Qy    440                                                                                             440
Db   8260 GCCTGGAGGAGGAGGCACCAGCTTGGTTTGGGGTCTTCCTGCCTCCGGCTTCCCTTG 8319
Qy    440                                                                                             440
Db   8320 CTCTGCCCAGCCTGAGCCTGGGCCAGTCCAGTGCCCACTCCAGGGGCCTGTCGATGGCTC 8379
Qy    440                                                                                             440
Db   8380 TGCATGCCACTCCATGTTGTAAGGGCTGACGGCATATAGGGGGAGAGAGACACCCCG 8439
Qy    440                                                                                             440
Db   8440 GCTGCCCCACGGCCCTCTTCAACAAGTGGTTAAGTGACTCCTCCTGATCCTCCCCTGC 8499
Qy    440                                                                                             440
Db   8500 CCAGCTCCCTGCAGCTCATTCCGAGAGGTGCAGAAGCCCTGCATGAGCAGCT 8559
Qy    440                                                                                             440
Db   8560 GTGGTACCACGGGGCCATCCCGAGGGGCAGAGGTGGCTGAGCTGCGTGCACTCTGGGGA 8619
Qy    440                                                                                             440
Db   8620 CTTCCTGGTGCGGGGAGAGCCAGGGGCAAGCAGGAGTACGTGCTGCTGTCGGGGATGG 8679
Qy    440                                                                                             440
Db   8680 TCTGCCCCGGCACTTCATCATCCAGTGTGATGTGGGGCTGGGACCCGAGCCTT 8739
Qy    440                                                                                             440
Db   8740 CCAGGGCCTCACTCTTCTCCCCTTCCCCTTCCCAAGGGAAATGGCCTTTCAGGGTAGGG 8799
Qy    440                                                                                             440
Db   8800 GGTAGCTGCCCAGGTCTTGGATGCCTCCCTAGCAGGGGCTGGCTGGAAGGGGCCACAGAGAC 8859
Qy    440                                                                                             440
Db   8860 CACCCTGTCCCTGCAACAAAATAGAGGCTTAAGTGTGAGTCCTCCCCTGGTGGGGCAGCA 8919
Qy    440                                                                                             440
Db   8920 GGATGTCATGTGCCATCAGATGGCATCTTTTCTGAAGGTCTCTTCTCTGCCCCTGGTCTGGG 8979
Qy    440                                                                                             440
Db   8980 CAGGGCCCTTTCCCCTGCTCTCCCCTTTCCCCTTCCCCAGGGGCTCAGCCCCCTCAGA 9039
Qy    441            AsnLeuTyrArgLeuGluGlyGlu 448
Db   9040 ATGGGAGGCTGCTGACCCCGGGTCCCCTGCCCTGCCAGGAACCTGTACCGACTGGAAGGGGAA 9099
Qy    449 GlyPheProSerIleProLeuLeuIleAspHisLeuSerThrGlnProLeuThr 468
Db   9100 GGCTTTCCTAGCATTCCTTTGCTCATCGACCACCTACTGAGCACCCAGCCCCTCACC 9159
Qy    469 LysLysSerGlyValValLeuHisArgAlaValProLys 481
Db   9160 AAGAAGAGTGGTGTTGTCCTGCACAGGGCTGTGCCCAAGGTGAGCCTGCACCCAGCCTGG 9219
Qy    481                                                                                             481
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Qy    440                                                                                             440
Db   9220 CCCATGCCACCTGTGGGACGGCTTGGGGAGTGTGGGGTCAGGGCCCACCCAGCGCTCTGAGCA 9279
Qy    481                                                                                             481
Db   9280 GAAAGGGGTTTCCAGGCCCTCCGTCTACATACAGATGCAGAGTGAGTGACCCTCAGGGC 9339
Qy    481                                                                                             481
Db   9340 CAGCCTTGCTCTAGGTTTGGAATGTCAGGGCCACTCCTATGCCATGGCTGTACACACCA 9399
Qy    481                                                                                             481
Db   9400 GGTTGGTGCTTACCTGGTCAGGGCACCTGCCTGGACCCCGTAGTCAGTCAGTGCTGTGTGCTCC 9459
Qy    481                                                                                             481
Db   9460 CCACGTGTCCCACCCCTGGTCACATATGGAGGGCGCCAAAAAATGGAGGACACAGCCCTT 9519
Qy    481                                                                                             481
Db   9520 CTAAGGGCCCAGCACCCCTTTCTTCAGACTTCTGATCCCTGTCTCCTGTCTCTTCCCCAG 9579
Qy    482 AspLysTrpValLeuAsnHisGluTyrGluGlnIleLeuGlyArg------ 499
Db   9580 GACAAGTGGGTGCTGAACCATGAGGACGACCTGGTCGTTGGGTGAGCAGATTGGACG-GGTGAG 9638
Qy    499                                                                                             499
Db   9639 TGCGCCTGCTGGCCTTCCTGTGCTGGCGACTTCTCCGAGTCGCGCCTGGGCCCCCT 9698
Qy    499                                                                                             499
Db   9699 GCCCTACCACCCAGGAGAAACCTCCCGCCCATCGATTCCCCACTTGTACCCCGACTCCCT 9758
Qy    499                                                                                             499
Db   9759 GCCCAGCCCCCACCACCACACCATCCTCCAGGAAAACGGACAGCAGTACTACCTGCTGAAAACTC 9818
Qy    499                                                                                             499
Db   9819 CCAGCAGACAGCTCGCCAGGAGACACCCTGTTACTGTAAGCCATAAGATACCTGTTTAG 9938
Qy    499                                                                                             499
Db   9939 GGAAGAAGTCACTGTGTCCTAAAAATCAGAAATGCTTTCAAACCCAGGAGGAGTGATTTTT 9998
Qy    499                                                                                             499
Db   9999 GGATTTCCATGTGTCACTTCTCCTCAGGAAGGGTGCACATCGGAGGCAACTTCCCTGCCTG 10058
Qy    499                                                                                             499
Db  10059 CCCCATGTGCTCCTCTAGGTTCCCAGCGAGGGTCAAACTCCCAGAGAGCCTGGGTGGAGG 10118
Qy    499                                                                                             499
Db  10119 GGTCCGAACACGGGGCCCCCCTCACCCAGGGGTAGGGAGCAGAATGGGTAGGAAGCGGAGA 10178
Qy    500                                                                                  GlyAsnPhe 502
Db  10179 AGAGAACTGCGGGACTGGGAAGCGCGTTGGTAGGGACGCGTTTCAGGGGAACTTT 10238
Qy    503 GlyGluValPheSerGlyArgLeuArgAlaAspAsnThrLeuValAlaValLysSerCys 522
Db  10239 GGCGAAGTGTTCAGCGGACGCCTGCGCGAGCCGACAACCCCTGGTGGCGGTGAAGTCTTGT 10298
Qy    523 ArgGluThrLeuProAspLeuLysAlaLysPheLeuGlnGluLeuAla------ 538
```

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Qy    665  ------GlyArgTyrSerSerGluSerAspValTrpSerPheGlyI                678
Db  11438  ACCTCCTCGCCTCCTCTGCCAGGCCGCTACTCCTCCGAAAGCGACGTGTGGAGCTTTGGCA 11497
Qy    678  leLeuLeuTrpGluThrPheSerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnG  698
Db  11498  TCTTGCTCTGGGAGACCTTCAGCCTGGGGGCCTCCCCGTACCCCCCAATCCCAGCGAATCAGC 11557
Qy    705  ------                                                        705
Db  11558  AGACACGGGAGTTTGTGAGAGAAGGGTAAGCACCCCTGTGATGACAGCAGCCTCAGGCTGCA 11617
Qy    705  ------                                                        705
Db  11618  CCCTCTTCCAGATGCTCCAGCCGGACTCTTCTAACTCCCTTAATGCCAACTTCCCACCA   11677
Qy    705  ------                                                        705
Db  11678  GGCAGAATAAGAATAACCTGGCCAGTTGCTCACGCCTGTCATCCCAGCACTTTGGGAGGC  11737
Qy    705  ------                                                        705
Db  11738  TGAGCTGGGTGGATCACTTGAGCCCAGGAGTTCAAGATCAGCTTGGACAACACAGTGAAA  11797
Qy    705  ------                                                        705
Db  11798  CTCCATCTGTACAAAAATACAAAAATTAGCTGGGCACGGTGGCTCACACCTGTAATCCC   11857
Qy    705  ------                                                        705
Db  11858  AGCACTTTGGGAGGCCGAGGCAGGCAGATCAGGTGATCACCTGTCGAGGAGTTTGAGACCAGCCAG 11917
Qy    705  ------                                                        705
Db  11918  ACCAACATGGTGAAACCCCATCTCTACTAAAAATACAAAAATTAGCCAGGCATGGTGGCA  11977
Qy    705  ------                                                        705
Db  11978  CGTGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGTGGGAGGAGAATTGCTTGAACCCAGGAG 12037
Qy    705  ------                                                        705
Db  12038  GCGGAGGCTGCAGTGAGCCGAGATTGTGCCACTGCACTCCAGCCTGGGCGACAAGAGTGA  12097
Qy    705  ------                                                        705
Db  12098  AACTCCATCTCAAAAAAACAAAAATACAAAAATTAGTCGGGTGTGGTGAC            12157
Qy    705  ------                                                        705
Db  12158  ATGCGGCCTGTAGTCCCTGCTACTCGGAGGCTGAGGTGGGAGGATCACTGGAGCCCGGGA  12217
Qy    705  ------                                                        705
Db  12218  GGTGGAGGTTGCAGTGAGCTGAGATCATGCCACTGCACCCCAACCTGGGTGACAGAGAGAGA 12277
Qy    705  ------                                                        705
Db  12278  GAGAGAGACCTTGACTCAGAAAAAGAAAAACCTGGGCGCAGTGGCTCACGCCTGTAATT   12337
Qy    705  ------                                                        705
Db  12338  TCAACATTTTGGGAGGCTGGAGGTGGATCACTTGAGTCTAGGAGTTTGACACTAGCC     12397
Qy    705  ------                                                        705
Db  12398  TGGCCAACATGGCAAAACCTGTCTCTACTAAAAATACAAAAATTAGCGAGGTGAGTGG    12457
Qy    705  ------                                                        705
Db  12458  TGCAAGCCTGTAATCCCAGCTACTTCGGGAGGCTGAGGCACAGAATCCCTTGAACCTGGG  12517


Db  10299  CGAGAGACGCTCCCACCTGACCTCAAGGCCAAGTTTCTACAGGAAGCGAGGTGGGTGATA  10358
Qy    538  ------                                                        538
Db  10359  AACTAATGATCACCACGGGTCCCGCATACACAGAGGTTACACTGGCACAGTGTGAA      10418
Qy    538  ------                                                        538
Db  10419  GTGCTTGACCACCGTGGTGTGTTTAGTCCTGAGGCCCCCATTGCGGGTAGTACCCCC     10478
Qy    538  ------                                                        538
Db  10479  TTATAGTGCCGAAGGGTAGAGGGCTGCCCCAGTCACACGTCCGGGTCTCTGCCCTTGA    10538
Qy    538  ------                                                        538
Db  10539  GGCCAAGCTCTTCTTCCCATCATCCCTGGGGGGCCCTGGGGAGGCGGGGCCTGGCCACGTAG 10598
Qy    539  ------ArgIleLeuLysGlnTyrSerHisProAsnIleValAr                  551
Db  10599  ATCCTGAGCAGCAGTGCCCTCCAGGATCCTGAAGCAGTACGCCACCCCAACATCGTGCG   10658
Qy    551  gLeuIleGlyValCysThrGlnLysGlnProIleTyrIleValMetGluValGln--    570
Db  10659  TCTCATTGGTGTCTGCGACCCAGAGCAGCCCCATCTACATCGTGTCATGGAGCTTGTGCAGGG 10718
Qy    570  ------                                                        570
Db  10719  TGAGCCGGGGCCTGAGCTCCAGGTAGGGCGCCGAGCCTGGTCAGGTGGCAGCCTTACC    10778
Qy    571  ------GlyGlyAspPheLeuThrPheLeuAr                              579
Db  10779  TCAGGAGCTCAGCAGGGGGTCCTCCCAGGGGGGACTTCCTGGACCTTCCTCCG         10838
Qy    579  gThrGlyAlaArgLeuArgValLysThrLeuThrGlyMetValGlyMetValGlyAspAlaAlaAl 599
Db  10839  CACCGGAGGGGGCCCGCCCGGTGAAGACTCTGCTGCAGATGGTGGGGGATGCAGCTGC    10898
Qy    599  aGlyMetGluTyrLeuGluSerLysCysCysIleHisArg                     612
Db  10899  TGGCCATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCG-GTGAGTGGGCCGGTGGCCACG 10957
Qy    612  ------                                                        612
Db  10958  GGCCCTGCCAACACCCCGACCAGAGTCAAGAGGTACCTATACCCCTAGGGCCCCCGCT    11017
Qy    612  ------                                                        612
Db  11018  GGACCATCAGGCATCAGCTCAGAGGGGGGAGTTGGCCTTCGTGTGGTAGACAGGGGTGCCCA 11077
Qy    612  ------                                                        612
Db  11078  GGGCGGGAGCAGCTTTGTCCTGGCTTTCCTTGCCTTTCCTGTTCCACGGCTGGGCAGGC   11137
Qy    613  ------AspLeuAlaAlaArgAsnCy                                    619
Db  11138  GACTGTTGGCCAAATGAGCCCCTGCCCGTCTCACCAGGGAACCTGCCTGCTCCGGAACTG  11197
Qy    619  sLeuValThrGluLysLysAsnValLeuLysIleSerAspPheGlyMetSerArgGluGluuA 639
Db  11198  CCTGGTGACAGAGAAGAATGTCCTGAAGATCAGTGACTTTGGGATGTCCCGAGAGGAAGC  11257
Qy    639  aAspGlyValTyrAlaAlaSerGlyValGlyLeuArgGlnValProValTyrTrpThrAlaPr 659
Db  11258  CGATGGGGTGTATGCAGCCTCAGGCGTGGGCCTCAGACAAGTCCCCGTGAAGTGGACCGCACC 11317
Qy    659  oGluAlaLeuAsnTyr-                                             664
Db  11318  TGAGGCCCTTAACTACGGTACCTAGTCCCTGTCTACCCTGGACTCCATGGCCAGGAGGCCA 11377
Qy    664  ------                                                        664
Db  11378  GGCCTGGGTCCTGCCGCTGCCTCGCCCTGCCCCAGGAGAGGGTGCACTCCAGCTTCACGCGCCTC 11437
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Qy    21 GluAlaGluLeuArgLeuLeuGluGlyMetArgLysTrpMetAlaGlnArgValLysSer   40
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2623 GAGGCCGAGCTTCGTCACTGCAGCGATGAGTCTGAGATCACACCACTGCATTCCAGCCGTGGGTGACAGAGT  2682

Qy    41 AspArgGluTyrAlaGlyLeuLeuHisHisMetSerLeuGlnAspSerGlyGlnSer      60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2683 GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGAGACAGTGGGGCCAGAGC  2742

Qy    61 ArgAlaIleSerProAspSerProIleSerGlnSer---------------------     72
         |||||||||||||||||||||||||||||||||||
Db  2743 CGGGCCATCAGCCCTGACAGCCCCATCAGTCAGGT-GGTTCTCTATGGGACTCTGGTGGG  2801

Qy    72 -------------------------                                      72
Db  2802 TGCTGGGTATCTGCCTTCTCCTCCTCCTGGGGGCCCTGTGGGGCAGTGGCTGGAGA  2861

Qy    72 -------------------------                                      72
Db  2862 TCTGGCAGGCCAATGCTGGAGGACTCCATCGTGCCCCCTCCCTGCTCCCCATCTGTGCT  2921

Qy    73 -------TrpAlaGluIleThrSerGlnThrGluGlyLeuGlySerArgLeuLeuArgGln   89
                 ||||||||||||||||||||||||||||||||||||||||||||||
Db  2922 GTATAGTCCTGGGCTGAGATCACCAGCCAAACTGAGGGCCGTTGCTGCGGCAG  2981

Qy    90 HisAlaAspLeuAsnSerGlyProLeuSerLysSerLeuSerLeuLeuIleArgGluArg  109
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2982 CACGCAGAGGATCTGAACTCAGGGCCCCTGAGCAAGCTGAGCCTGCTCATCCGGGAACGG  3041

Qy   110 GlnGlnLeuArgLysThrTyrSerGluGlnTrpGlnLeuGlnLeuThrLys           129
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  3042 CAGCAGCTTCGCAAGACCTACAGCGAGCAGTGGCAGCTGCAGAGCTCACCAAG  3101

Qy   129 ---------                                                     129
Db  3102 GTGAGCGGCAGCACTGGGCTTCGGTCATTTCTGTCTAAATTTGAGCCTGAAGGGGT  3161

Qy   129 ---------                                                     129
Db  3162 TGTTTGCACAAGAGGCCCTGATTCACTGGGGAAGTGTAAGTCCCTGACCCGAGGCCTG  3221

Qy   129 ---------                                                     129
Db  3222 GCTTGCTCTAACCTTGATGTAGCTTCCTCCTCTTCCCTACGTGGTCTGAGCTGCCTTGCA  3281

Qy   129 ---------                                                     129
Db  3282 GCAAGGCCTCTCTGTGCTTTTCTGTGCCTGGCAAAGTGTGGGAGTGTAAGGATGAGT  3341

Qy   129 ---------                                                     129
Db  3342 GACCGGTCACGTGCCTGGGAGAAGCTCAGAATCGGTACTCGCCTCCACTGTGCCATCT  3401

Qy   129 ---------                                                     129
Db  3402 GGCTCTGGGTTCTGAGAGTCAGGAGGAGGAATGAGGGTCAGTCGTTGTTTGCCTTCGACCTA  3461

Qy   129 ---------                                                     129
Db  3462 TGCAGCCTCCTCTCAGGCCTCAGGGACAGCTGGGCAGCAGACTGGCCACGCCCCCGAGG  3521

Qy   129 ---------                                                     129
Db  3522 ACTCGGGCCGTGAAGTCAGCCTGCTAGGTTTGAATCCACCCAGCTCCTCAGTCTCAGAG  3581

Qy   129 ---------                                                     129
Db  3582 GCTGTGTGATTTGGAACTATTTATCTGGGAGGCCTAGTGCCCCCATTCAGTGTGCTGGTCA  3641

Qy   129 ---------                                                     129
Db  3642 CCCTCCCTGCCACCACCACCCCCTTCCTCAAGTGCAGAGCCAGCCTTGCCATGACCCCACAG  3701
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Qy   705 ----------                                                    705
Db 12518 AGGTGGAGGTTGCAGTGAGCTGAGATCACACCACTGCATTCCAGCCGTGGGTGACAGAGCA 12577

Qy   705 ----------                                                    705
Db 12578 AGACTCCATCTCAGAAAAGAAAAAAAAAAAATAGAATATCCCTGTAGCTACTACTGAGTG 12637

Qy   705 ----------                                                    705
Db 12638 AGCACCTGGTCTGTGTCTAGGTCACATGTTATTTGCTCATCACTACACATGTGTGGTA 12697

Qy   705 ----------                                                    705
Db 12698 GGGATTAATATGTCCCTTTCTCGAGATGGAAAAACAGCTGGCAGAGGGGACACAGCTAGC 12757

Qy   705 ----------                                                    705
Db 12758 ACGTGGTAGGATTAGGATCAGAAGCCAGGCCTCTTTGTCCTTTGGTCCCCTTGGTGGAGAA 12817

Qy   705 ----------                                                    705
Db 12818 CAGTGCATCCTTCAGAACAGTGCATCTTAAGCAGCTCCTATGGCTCATGGTATCCCCCAG 12877

Qy   705 ----------                                                    705
Db 12878 AGTCTGCCGAGGACACCCTCAAACTCCCTCCTCATGCCTGGTGTGCTCCTCCTCACA 12937

Qy   706 GlyGlyArgLeuProCysProGluLeuCysProAlaAspAlaValPheArgLeuMetGluGln  725
Db 12938 GGGGGGCCGTCGCCCTGCCCCAGAGCTGTGTCCTGCCGTGTTCAGGCTCATGGAGCAG 12997

Qy   726 CysTrpAlaTyrGluProGlyTyrGlnArgPheSerThrIleTyrGlnGluLeuGln      745
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 12998 TGCTGGGCCTATGAGCCTGGGTACCGGCGCCCAGCTTCAGCACCATCTACCAGGAGCTGCAG 13057

Qy   746 SerIleArgLysArgHisArg                                         752
         |||||||||||||||||||||
Db 13058 AGCATCCGAAAGCGGCATCGG 13078
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RESULT 4
US-10-003-295-3

; Sequence 3, Application US/10003295
; Patent No. 6686187
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001183DIV
; CURRENT APPLICATION NUMBER: US/10/003,295
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15297
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-003-295-3

Alignment Scores:
Pred. No.:   129
Score: 2137.00   Length: 15297
Percent Similarity: 21.28%   Matches: 747
Best Local Similarity: 21.28%   Conservative: 0
Query Match: 55.09%   Mismatches: 5
DB: 4   Indels: 2764
                                      Gaps: 16

US-10-660-763-2 (1-752) x US-10-003-295-3 (1-15297)

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Qy     1 MetGlyPheSerGluLeuCysSerProGlnGlyValHisGlyValLeuGlnGlnMetGln   20
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2563 ATGGGCTTCTCTTCTGAGCTGTGCAGCCCCCAGGGCCACGCGGGGTCCTGCAGCAAATGCAG  2622
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Qy        129 -------------------------------------------------------------- 129
                                                                              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4782 GGGCGTGCGGGCGCTGCGCAGCTACACCACCACCAGCACCACCAGCTTCCTGCTGCCGGCCT 4841

Db       3702 CGGCCCCTGGTGGGCCACCCTGGCCCCATTCCTCGCCCCAAAAAGATCATCTGATTCAAGGG 3761   Qy        208 uLeuArgSerLeuGlnAspLeuHisGluGlnMetAlaCysIleLeu-- 208
                                                                                            |||
Qy        129 -------------------------------------------------------------- 129   Db       4842 GCTGCGGTCACTCGACCTGCACGAGGAGATGGCTTGCATCCTGTAAGCCCGCAGCCC 4901

Db       3762 TGGGCCCATTTTTATAAGTTTGCTGGAACAGCTATGCCCCTTTGTTTGTTTCATATTGT 3821   Qy        223 --------------------------------------------------- 223

Qy        129 -------------------------------------------------------------- 129   Db       4902 CGTCCCCTGGCCCCACCCTTGAGCAGCCCTAAGCCCAGCCATCAGGCCCAGAGGCAGGA 4961

Db       3822 CTGTGACTACAACATGACAGAGTTGAGTAATTGTGACAGAGGCTCTATGGCCTACAAGCCTA 3881   Qy        223 --------------------------------------------------- 223

Qy        129 -------------------------------------------------------------- 129   Db       4962 CCCAGAAAATCCATTGCTGGGAAGGTGCTGGCCATGTAACCACATGAGAACGGGGACCTGG 5021

Db       3882 AAATATTTATTTACTATCTGGCCCTTTAAGAAAAAGACTGATCTAGTCGAGGAATCTAGC 3941   Qy        223 --------------------------------------------------- 223

Qy        129 -------------------------------------------------------------- 129   Db       5022 GCCAAGGATTGGAAACAGGCAACTTACCTCTGAATTACACTTATTCCAGGGTCTCATTATT 5081

Db       3942 TCAGTTACAGATGGGGAAACTGAGGTTGGGCGCTTGCCCAACATATCCCAGCACACATAAAC 4001   Qy        223 --------------------------------------------------- 223

Qy        129 -------------------------------------------------------------- 129   Db       5082 CCAGGGGTTTATTACATTCATTGAGCACTGTTCTCGGGCTCTGGATTATACCAGAGAACGA 5141

Db       4002 AGGAGAACTGGGACGAGAGACTCTCGGGCTGTCATCTATTCCTACTGCCAAGAACA 4061   Qy        223 --------------------------------------------------- 223

Qy        129 -------------------------------------------------------------- 129   Db       5142 TGGTAGACAAAAACATCTGTCCTCAGGGATCTTTCGTGTTGTTAGTGGAGTGAGAATGTGAGG 5201

Db       4062 TAATTTGCAGGACCCAGTGCAAAGTGAAATTGTGGGGGTCTTTGTTAAAAGATTGCTAGG 4121   Qy        223 --------------------------------------------------- 223

Qy        129 -------------------------------------------------------------- 129   Db       5202 AGCACTAAGACCATGAGAAAAATAAAGCAAGAGAAGTGATCGGGACCTGGGAGCACG 5261

Db       4122 AATTTCCAGGTGCAATAATGGAGAATGAAACCAAGCACAGGGCCCTTCTACATGTGGAG 4181   Qy        223 --------------------------------------------------- 223

Qy        129 -------------------------------------------------------------- 129   Db       5262 GAGGCAAGGAGGAGGAGTGACAGTTGTCCATAGATGATCTGGAAAGCCTCTTGAGAGGT 5321

Db       4182 CCCCGTGTGACTGCACAGGCCGTGCACACCTGCCAACTGGCCCTGCCGCCACCCAGCTAC 4241   Qy        223 --------------------------------------------------- 223

Qy        129 -------------------------------------------------------------- 129   Db       5322 GACATTCAAAGAGGCCCCTGAGACGGGGTACGGGAGTGAATCATGGGCTATTCGGAGAAA 5381

Db       4242 CACTGTCAGTCCAAGGAGGGACCGGTTGTAGCCGTTGTACCCTCTTTGCCTCCCCAAGG 4301   Qy        223 --------------------------------------------------- 223

Qy        129 -------------------------------------------------------------- 129   Db       5382 GACCATTCCAGAAAGGAGGACAGCAATTACACAGGCCTTGAGGTAGGAGAGTACCAGGGA 5441

Db       4302 GGTCTGTCTTCAACAGGCTCTCTGATCTTTGACTCTCACGTCAGCAGCCAGCTTTCCCAG 4361   Qy        223 --------------------------------------------------- 223

Qy        129 -------------------------------------------------------------- 129   Db       5442 CTAATAGCCAGAACCAGTCGTGTGCCTCGAGTGAGTGAGAGGGGGAGAGTCATCACGAG 5501

Db       4362 AAGTCTCCAGGTGCTCCTTGCCTGACGACAGAGACCTTTCACCCCAGGCAAG 4421   Qy        223 --------------------------------------------------- 223

Qy        130 ----------------------------------------------------ThrHi 131   Db       5502 GCTGAGGAGGCAGGCGTCAAGGCGTCTAGCAGGGCCATGGTG 5561

Db       4422 AATCTTCCAACTGGGGACCTGCTGCCCCACACTGGCCTCTCTCTCCCCACCCA 4481   Qy        223 --------------------------------------------------- 223

Qy        131 sSerGlnAspIleGluLyLeuLysSerGlnTyrArgAlaLeuAlaArgAspSerAlaGl 151   Db       5562 AGGACTTTGGCTCTGGTGAACAAGAATGCATGAAATGATCTGACCTCGTTTGTTTTTTGTTCAT 5621

Db       4482 CAGCCAGGACATTGAAGAGCTGAAGAGCCAGTACCGGAGCTCGGCACGGGACAGTGCCCA 4541   Qy        223 --------------------------------------------------- 223

Qy        151 nAlaLysArgLysTyrGlnGluAlaSerLys-------- 161   Db       5622 TTTGTTTTAACTTTTTTTGAGTGAGACGAGTCTCGCTCTGCGCCCAGGCTAGAGTGCAGTGG 5681

Db       4542 AGCCAAGCGCAAGTACCAGGAGGCCAGCAAAGGTTCGTGGCTTCCCTTGCTGCAGGGAG 4601   Qy        223 --------------------------------------------------- 223

Qy        161 -------------------------------------------------------------- 161   Db       5682 CATGATCTCGGCTTACTGCAACCTCCGCCTCCCAGGTTCAGTGATTCCCGTGCCTCAGC 5741

Db       4602 GGAATCCGAAGCCGGAGCCAGTGTCCTGACCTGTCCTTGGGTACCCAGAGAGTGGGGCTGCTGGGC 4661   Qy        223 --------------------------------------------------- 223

Qy        162 ----------------AspLysAspArgAspLysGlyAl 168   Db       5742 CTCCCGAGTAGCTGAAACTACGGGCATGCGCCACCACCCACGCTAATTTTTGTATTTTT 5801

Db       4662 CTCCATGCTGTCATCTATACCCCCTTGCTCAGACAGAGACGGTGACAAGGC 4721   Qy        223 --------------------------------------------------- 223

Qy        168 aLysAspLysTyrValArgSerLeuTrpLysLysPheAlaHisHisAsnArgTyrValLe 188   Db       5802 AGTAGAGACGGGGTTTCACCATGTTGCCCAGGCTAGTCTCAAATTCCTGGGCTCAAAGCG 5861

Db       4722 CAAGGACAAGTATGTGCGCAGCCTGTGGAAGCCTCTTTGCTCACCACAACCGCTATGTGCT 4781   Qy        223 --------------------------------------------------- 223

Qy        188 uGlyValArgAlaAlaGlnHisLeuHisHisGlnHisHisGlnHisHisGlnHisLeuLeuLeuProGlyLeu 208
```

```
Qy   270 ---------------------------------------------------------- 270
Db  5862 ATTTGCCTGCCTCTGCCTCCCAAAGTGCCGGGATTACAGGCATGAGCCACCATGCCCAGC 5921
         
Qy   270 -----------------------------------------SerAlaProAspValProProC 277
Db  5922 CCTGACCCTCTGTTTAATAAGCCACTCTGGCTGCTGCTGCTGCAAATAGACTTCAGGGAG 5981
Db  7002 GCTGGCCTGTCCACTGACGGGCGCTGTCCCCACCAGGTCCGACGTCCGACCTCCACCCT 7061

Qy   277 yrValThrPheAspGluSerLeuLeuGluGluGlyLysGluProLeuGluProGlyGluLeuG 297
Db  5982 CAAGGACAGAGAGCTGGAGGCCAGAGAGCAGGCTGCTTGCCATAATCCAGATCCAAGCTT 6041
Db  7062 GTGTCACGTTCGATGAGTCACTGCTTGCTGCTGGAGGGTGAACCGCTGGGGAGAGCTCC 7121

Qy   297 lnLeuAsnGluThrValGluSerValGlnHisThrLeu-------------------- 310
Db  6042 TTGGCCAGCTAGGACGGGGAGGTAGCAATGAGGTGAGGCGGGTCAGGTCCTGGGGCAG 6101
Db  7122 AGCTGAACGAGCTGACTGTGGAGAGCGTGCAGCACACGTG-GGTGGTGCTTTGCACCTG 7180

Qy   310 ---------------------------------------------------------- 310
Db  6102 GTCCTGGAAGTGAAGCCAGTGGGATTCCCTATGGATTGGAAGTGGGGGCTGAAATAGA 6161
Db  7181 GGCTGCGGCGGGGGCTCCCAGAGACCACGAGTGTTTATGTAGGCAGGGCTAGGTCGTGA 7240

Qy   310 ---------------------------------------------------------- 310
Db  6162 GGAGTCAGGGGTCACTCTGGGGATTGGCCTGGAGCAGCTGGAGAGATGGAGTGGCTGTTA 6221
Db  7241 GACTGTCCACACAGAGCTGTCACCAGTGGCCCGGGCTTGGCTCTTACAGGGATGGAC 7300

Qy   310 ---------------------------------------------------------- 310
Db  6222 ACTTATGTAGGGAAGGCTGTGGGAAGAAGAGGTTTAGGAGACAAGGATAGCAGTTCATTT 6281
Db  7301 TGGACCTGGGTTGAGGGGCAGGAGGGCTCGGTTCTAATGTGCCCTTCTCTTGGGTGCA 7360

Qy   311 -----ThrSerValThrAspGluLeuAlaValAlaAlaThrGluMetValPheArgArgGlnG 329
Db  6282 ATTTATTTATTTATTTATTTATTTATTATTATTATTAGAGATGTAGTCTCATTCTTTCGC 6341
Db  7361 GGCTGACCTCAGTGACAGATGAGCTGGCTGTGGCCACCGAGATGGTGTTCAGGCGGCAGG 7420

Qy   329 luMetValThrGlnLeuGlnLeuGluArgAsnGluGluAsnThrHisProArgG 349
Db  6342 CAGGGCTGGAGTGCAGTGGCGCGATCTTGGCTCACTGCAACCTCCACCTCCCAGGGCTCAAG 6401
Db  7421 AGATGGTTACGCAGCTGCAACAGAGCTCCGAATGAGAGGAGAACACCCCACCCCGGG 7480

Qy   349 lu-------------------------------------------------------- 349
Db  6402 CGATTCTTCTTGCCTCAGCCTCCCGAGTAGCCAAGTAGCTGGGACTACAGGCCATGTGCCAC 6461
Db  7481 AGCGGGTGAGTGGGCCCCTGCCTGCCAGCAGCCTCCTGGCCTCCCCTCCCTACCTACCC 7540

Qy   349 ---------------------------------------------------------- 349
Db  6462 CATGCCTGGCTAATTTTTGTATTGCTTTTTCAGTAGAGATGGGGTTTCACCAGGTTAGC 6521
Db  7541 TAACTGCTGCTAGCCGCCGCAGACCGAGCCCTTATTCTTCATCCACCCTCCCACCC 7600

Qy   350 -----ArgValGlnLeuLeuGlyLysArgGlnValLeuGlnValLeuAlaLeuGln 365
Db  6522 CAGGGCTGGTCTCGAACTGACCTCAGGCAATCCACCCGCCTCGACCTCCCAGTGTTGTAT 6581
Db  7601 GCCCCTGCCTGCAGCTGCGTGCTGGCCAAGAGGCAAGTGCTGCAAGAGAAGCACTGCAG 7660

Qy   366 GlyLeuGlnValAlaLeuCysSerGlnAlaAlaLysGlnAlaGlnGluGluLeuLeuGln 385
Db  6582 TATAGGCGTGAGCCACTGTGCCTGGCCCACTGGATCCTTATTACAACTGCCAGTGTCCCT 6641
Db  7661 GGGCTGCAGGTAGCGCTGTGCAGCCAGCCGCCAAGCAGGCCCAGCAGGAGTTGCTGCAG 7720

Qy   386 ThrLysLysGluHisLeuLeuGlyLysProGlyProProProValLeuLeuLeuGlnAspArgAsp 405
Db  6642 CTTATATATATCAGGAAATAGAAGATTAGGGAGAGGTTAAATAATTTGCCTAGAGTGGCA 6701
Db  7721 ACCAAGCTGGAGCACCTGGGCCTGCCGCCCCCGCGCCCGTGCTGCTGCTGCAGGATGAC 7780

Qy   406 ArgHisSerSerSer--------------------------------------- 412
Db  6702 TGGCTAGCTCGAAGTGAGGCAGCAGGGTCAACCCCAGCCTCCAAACCCAGGGTCCTA 6761
Db  7781 CGGCCACTCCACGTCGTCCTC-GGTGAGCTGCCCATCCGGCGGCCGCTGCCCACCGGC 7839

Qy   412 ---------------------------------------------------------- 412
Db  6762 GGGCTGAACTGCCCAGCCTTGCCCAGCCTGAGGCTCCCACTGGGGATCCGGTCTCCGG 6821
Db  7840 CTGCCCACCTGGGGCTGCGCTCCTCATTTCGCCTCCCCTCCCCCCTCCTAAGCCTCGG 7899

Qy   413 ------GluGlnGluArgGluGlyGlyTyrArgThrProThrLeu 424
Db  6822 ------LysGluIleuGluGlnTyrLeuGlnIleuSerSerLeuValGlnHisAspGluVa 241 (Qy 224)
Db  7900 GCTGACGTCTGTCCCTGGCCTCCAGGAGCAGCAGGAGGGGGGAAGGAACACCCACGCTG 7959

Qy   425 GluIleuLysSerHisIleSerGlyIlePheArgProLysPheSer------------- 440
Db  6882 GGTGGCCATTCACCGGGAGATGGCTGCTGCGCAGCTGCTGCCCATCCAGCCTGAGGCTGAGTA 6941
Db  7960 GAGAGCCTTAAGAGCCACATCTTCAGGAATCTTCCGCCCCAAGTTCTCCGTGAGTGGGCC 8019

Qy   440 ---------------------------------------------------------- 440
Db  6942 CCAAGGCTTCCTGCGACAGTATGGGTAAGCCCCGTCCTTGCTCCTGCTGGGCCCAGGGCT 7001
Db  8020 CAGCCTGGGCCCCCCACTGTTGTGTTTGTGAGTTTAATCACTGGGATGTCCTAGAGACGA 8079
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Left alignment column (protein translations):

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Qy   223 ---------------------------------------------------------- 223
Qy   224 ------LysGluIleuGluGlnTyrLeuGlnIleuSerSerLeuValGlnHisAspGluVa 241
Qy   241 lValAlaIleHisArgGluMetAlaAlaAlaAlaLysArgIleGlnProGluAlaGluTy 261
Qy   261 rGlnGlyPheLeuArgGlnTyr-Gly------------------------------- 269
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Qy    440 ---------------------------------------------------------------  440
Db   8080 GGCTCTGCCAGGCTGCTTGTATTGGGAAGTTCCTCTCTTCCCTGGGATTCCAGGCTGCA   8139

Qy    440 ---------------------------------------------------------------  440
Db   8140 GATGTCCCAGACCCTGCCCCTGTGACCCCTCCCTTTCCATCGCCCCAGTGTGCTAAAGG   8199

Qy    440 ---------------------------------------------------------------  440
Db   8200 GACCAGCAACCTGACTATTCCATGGCTCTCCCTGCTTCAGGACGCGGTTGGGGGCCTGTG   8259

Qy    440 ---------------------------------------------------------------  440
Db   8260 GCCTGGAGGAGGAGGCCACCAGCTTGGTTTGGGGTCTTCCTGCCTGGGCTTCCCTTCCCAG   8319

Qy    440 ---------------------------------------------------------------  440
Db   8320 CTCTGCCCAGCGTGAGCCTGGCCCAGTCCACTCCAGGGCCTGTGATGGCTC   8379

Qy    440 ---------------------------------------------------------------  440
Db   8380 TGCATGCCACTCCATGGTTGTAAGGGCTGAGGGCATATAGGGGGAGAGAGAGACCCCCG   8439

Qy    440 ---------------------------------------------------------------  440
Db   8440 GCTGCCCCCAGGGCCTCTTCAACAAGGTGGTTAAGTGACTCCTCCCTTTGC   8499

Qy    440 ---------------------------------------------------------------  440
Db   8500 CCAGCTCCCTCCACCCGCTCAGCTCATTCCCGGAGGTGCAGAAGCCCCTGCATGAGCAGCT   8559

Qy    440 ---------------------------------------------------------------  440
Db   8560 GTGGTACCACGGGGCCATCCCGAGGGGCAGAGGGTGGCTGAGCTGCTGGTGCACTCTGGGGA   8619

Qy    440 ---------------------------------------------------------------  440
Db   8620 CTTCCTGTGTGCGGGAGAGCCAGGCCAAGCAGGAGTACGTGCTGTCGTGCTGTGGGATGG   8679

Qy    440 ---------------------------------------------------------------  440
Db   8680 TCTGCCCCGGCACTTCATCATCCAGTCCTTGGATGTGAGTGGGCTTGGGACCCGAGCCTT   8739

Qy    440 ---------------------------------------------------------------  440
Db   8740 CCAGGCCTCACTCTTCCCCCTTCCCCTTCCCCAAGGGAAATGGCCTTTCAGGGTAGGG   8799

Qy    440 ---------------------------------------------------------------  440
Db   8800 GGTAGCTGCCAGGTCTTGGATGCCTCCCCTAGCAGGGGCTGGCTGGAAGGGCCACAGAGAC   8859

Qy    440 ---------------------------------------------------------------  440
Db   8860 CACCCGTGTCCCTGCAACAAAATAGAGGCTTAAGTGTGAGTCCTCCCCTGGTGGGCAGCA   8919

Qy    440 ---------------------------------------------------------------  440
Db   8920 GGATGTCATGTGCCATCACGATGGCATCTTTTCTGGAGGTCTCTCTGCCCCTGTCCTGGG   8979

Qy    440 ---------------------------------------------------------------  440
Db   8980 CAGGGCCCTTTCTCCCCGTCGCTCTCCCCTTTCCCCCTCCCAGGGCTCACGCCCCCTCAGA   9039

Qy    441 -----------------AsnLeuTyrArgLeuGluGlyGlu   448
                                   ||||||||||||||||||||
Db   9040 ATGGAGGCTGCTGACCCCGGGTCCCCTGCCCTGCCGACCTGTACCGACTGGAAGGGGAA   9099

Qy    449 GlyPheProSerIleProLeuLeuIleAspHisLeuLeuSerThrGlnGlnProLeuThr   468
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9100 GGCTTTCCTAGCATTCCTTTGCTCATCGACCACCTACTGAGCACCCAGCAGCCCCTCACC   9159

Qy    469 LysLysSerGlyValValLeuHisArgLeuHisArgAlaValProLys------------   481
```

```
Qy   9160 AAGAAGAGTGGTGTGTCCTGCCACAGGGCTGTGCCCAAGGTGAGCCTGCACCCAGCCTGG   9219
                                                                        |||||||
Db    481 ---------------------------------------------------------------  481

Qy   9220 CCCATGCCACCTGTGGCAGGGCTTGGGAGTCGTGGGTCAGGCCCACCCAGCCTCTGAGCA   9279
Db    481 ---------------------------------------------------------------  481

Qy   9280 GAAAGGGCTTTCAGGCCCTCCGTCTACATACAAGATGCAGAGTGAGTGACCCTCAGGGC   9339
Db    481 ---------------------------------------------------------------  481

Qy   9340 CAGGCCTTGCTCTAGGTTGGAATGTCAGGGCCACTCCTATGCCATGGGCTGTACACCA   9399
Db    481 ---------------------------------------------------------------  481

Qy   9400 GGTTGGTGCTTACCTGGTCAGGGCACCTGCCTGGACCCCTGAGTCATCTCAGTGTGCTCC   9459
Db    481 ---------------------------------------------------------------  481

Qy   9460 CCACGTGGTCCCACCCCTGGTCACATATGGAGGCGCCAAAAAAATGGAGGACACAGCCCTT   9519
Db    481 ---------------------------------------------------------------  481

Qy   9520 CTAAGGGCCCAGACACCCTTTTCTCAGACTTCTGATCCCGTCTCCTCTTCCCAG   9579
Db    482 AspLysTrpValLeuAsnHisGluGlnIleIleGlyArg------   499

Qy   9580 GACAAGTGGGTGCTGAACCATGAGCAGATTGGGTGGTGAGACG-GGTGAG   9638
          ||||||||||||||||||||||||||||||||||||||||||
Db    499 ---------------------------------------------------------------  499

Qy   9639 TGGCCCTCTGCTGGCCTCCTTGTCGCTGGCGACTTCTCTCGAGTCGCGCTGGGCGCCCCT   9698
Db    499 ---------------------------------------------------------------  499

Qy   9699 GCCCTACCACCCAGAAACCTCCCTGCCCCATCTGATTCCCCACTTGTACCCCGACTCCCT   9758
Db    499 ---------------------------------------------------------------  499

Qy   9759 GCCCAGCCCCCACCACCATCTCCAGGAAACGGGACAGTACCTACGCTGAAAACTC   9818
Db    499 ---------------------------------------------------------------  499

Qy   9819 CCAGCAGACAGCTCTGCCAGCACCCTGACCTCATCACCCCGCCGCCCCCATCG   9878
Db    499 ---------------------------------------------------------------  499

Qy   9879 AGCTCTTGTGTGCACGCAGGAGACACCCTGTTACTGTAAGCCATTAAGATACCTGTTTAG   9938
Db    499 ---------------------------------------------------------------  499

Qy   9939 GGAAGAAGTCACTGTCCTAAAATCAGAATGCTTTTCAAACCCAGGGAGAGTGATTTTT   9998
Db    499 ---------------------------------------------------------------  499

Qy   9999 GGATTTCCATGTCACTTCTTCTTCCGAGGAGGGTGGCCATCGGAGGCAACTTTCCCCTGCTG  10058
Db    499 ---------------------------------------------------------------  499

Qy  10059 CCCCATGTGCTCTCTAGGTTCCCAGCAGGGTCAAACTCCCGAGGGTCGGGTGGAGG  10118
Db    499 ---------------------------------------------------------------  499

Qy  10119 GGTCCGGAACACGGGGGCCCCTCACCCAGGGTAGGGAGGCAGAATGGGTAGGAAGGCGGAGA  10178
Db    500 ----------------------------------------------------GlyAsnPhe   502

Qy  10179 AGAGAACGTGGGGACTGGGAAGGCCGTTGGTAGGAGGCCCAAGACCGTTTCAGGGGAACTTT  10238
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    503 GlyGluValPheSerGlyArgLeuArgAlaAspAsnThrLeuValAlaValAlaValSerCys   522
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Db   10239 GGCGAAGTGTTCAGCGGAGCGCTGCGAGCCGACAACACCCTGGTGCGGGTGAAGTCTTGT 10298
Qy   523 ArgGluThrLeuProProAspLeuLysAlaLysPheLeuGlnGluAla------------ 538
Db   10299 CGAGAGACGGCTCCCACCTGACCTCAAGGCCAAGTTTCTACAGGAAGCGAGGTGGGTGATA 10358

Qy   538 -- 538
Db   10359 AACTAATGATCACCACGGGTCCCGCATACACAGAGGTTACACTGCACACAGTGAA 10418

Qy   538 -- 538
Db   10419 GTGCTTGACACCGTGGTGGTGTTAGTCCTCGAGGCCCCCCCATTGCGGGTAGTACCCCC 10478

Qy   538 -- 538
Db   10479 TTATAGTGCCGAAGGGTAGAGGCTAGCACGTCCGGGTCGTCTGTGGCCTTGGA 10538

Qy   538 -- 538
Db   10539 GGCCAAGCTCTTCTCCATCATCCCTGGGGAGGCGGCCTGGCCACGTAG 10598

Qy   539 ---------ArgIleLeuLysGlnTyrSerHisProAsnIleValAr 551
Db   10599 ATCCTGAGCAGCAGTGCCCTCCAGGATCCTGAAGCAGTACAGCCACCCCAACATCGTGCG 10658

Qy   551 gLeuIleGlyValCysThrGlnLysGlnProIleTyrIleValMetGluGluValGln-- 570
Db   10659 TCTCATTGGTGTCTGCACCCAGAAGCAGCCCATCTACATCGTCATGGAGCTTGTGCAGGG 10718

Qy   570 -- 570
Db   10719 TGAGCCGGGGCGCTGAGCTCAGGTAGGGCGGCCGAGCCTGTCAGTGGCAGCCTTACC 10778

Qy   571 -----------GlyGlyAspPheLeuThrPheLeuAr 579
Db   10779 TCAGGAGGCTCAGCAGGGGTCCTCCCCACCTGCAGGGGCGACTTCCTGACCTTCCTCCG 10838

Qy   579 gThrGluGlyAlaArgValLysThrLeuLeuGlnMetValGlyMetValGlyAspLeuAl 599
Db   10839 CACGGGAGGGGGCGCCCGGGTGAAGACTCTGCTGCAGATGGTGGGGATGGCAGCTGC 10898

Qy   599 aGlyMetGluTyrLeuGluSerLysCysCysIleHisArg--------------- 612
Db   10899 TGGCATGGAGTACCTTGGAGAGCAGAAGTGCTGCATCCACCG-GTGAGTGGGCCGTGGCCACG 10957

Qy   612 -- 612
Db   10958 GGCCCTGCCAACACCCCGACCCAGAGTCAAGAGGTACCCTATACCCCTAGGGGCCCCCGCT 11017

Qy   612 -- 612
Db   11018 GGACCATCAGGCATCAGCTCCAGAGGGAGTGGCCTCTGGGTAGACAGGGGTGCCCCA 11077

Qy   612 -- 612
Db   11078 GGGGCCCGGAGCAGCTTTGTCCTTGGCTTTCCTAGAGTGTTCCAGCCAGGGCTGGGCAGGC 11137

Qy   613 ----------------AspLeuAlaAlaArgAsnCy 619
Db   11138 GACTGTTGGCCAAATGAGCCCTGCCCTGCGCTGCTTCCGGAACTG 11197

Qy   619 sLeuValThrGluLysAsnValLeuLysIleSerAspPheGlyMetSerArgGluLysAl 639
Db   11198 CCTGGTGACAGAGAAGAATGTCCTGAAGATCAGTGACTTTGGGATGTCCCGAGAGGAAGC 11257

Qy   639 aAspGlyValTyrAlaAlaSerGlyGlyLeuArgGlnValProValLysTrpThrAlaPr 659
Db   11258 CGATGGGGTCTATGCGGCCTCAGGGGGCCTCAGACAAGTCCCCGTGAAGTGGACCGCACC 11317

Qy   659 oGluAlaLeuAsnTyr--------------------------------------- 664
Db   11318 TGAGGCCCTTAACTACGGGTACCTAGTCCCGTCTACTAAAATACACAAAAATTAGCGAGGTGTAGTGG 11377

Qy   664 -- 664
Db   11378 GGCCTGGGTCCTGCCGCCGTCGCCCTGGCCCCTGGCCCCAGGGAGGGGTGCACTCACGTCGCTCCTC 11437

Qy   665 -------------GlyArgTyrSerGluSerAspValTrpSerPheGlyI 678
Db   11438 ACCTCCTCGCCTCCTCCTCGCAGGCCGACTCCTCCAGGAAAGCGACGTGTGGAGCTTTGGCA 11497

Qy   678 IeLeuLeuTrpGluThrPheSerLeuLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnG 698
Db   11498 TCTTGCTCTGGGAGACCTTCAGCCTGCTGGGGGCCTCCCCATCCCAACCTCAGCAATCAGC 11557

Qy   698 lnThrArgGluPheValGluLys--------------------------------- 705
Db   11558 AGACACCGGAGTTTGTGGAGAAGGGTAAGCACCCTGTGATGACAGCAGCCCTCAGGCTGCA 11617

Qy   705 -- 705
Db   11618 CCCTCTTCCAGATGCTCCAGCCGGACTCTTCTAACTCCCTTAATGCCAACCTTCCCACCA 11677

Qy   705 -- 705
Db   11678 GGCAGAATAAGAATAACCTGGCCAGGTGCAGTGGCTCACGCCTGTCATCCCAGCACTTTGGGAGGC 11737

Qy   705 -- 705
Db   11738 TGAGCTGGTGATCACTTGAGGTCAGGAGTTCAAGATCAGCTTGGACAACACAGTGAAA 11797

Qy   705 -- 705
Db   11798 CTCCATCTGTACAAAAATACAAAAATAGACTGGGCACGGTGGCTCACACCTGTAATCCC 11857

Qy   705 -- 705
Db   11858 AGCACTTTGGGAGGCCGAGGCAGGTGGATTGCTTGAGCTGTGTCAGGAGTTTGAGACCAGCCAG 11917

Qy   705 -- 705
Db   11918 ACCAACATGGTGAAACCCATCTCTACTAAAAATACAAAAATTAGCCAGGCATGGTGGCA 11977

Qy   705 -- 705
Db   11978 CGTGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGCTGGGAGAATTGCTTGAACCCAGGAG 12037

Qy   705 -- 705
Db   12038 GCGGAGGCTGCAGTGAGCCGAGATTGTGCCACTGCACTCCAGCCTGGGCGACAAGAGTGA 12097

Qy   705 -- 705
Db   12098 AACTCCATCTCAAAAAAAACAAAAAATACAAAAATTAGTGGGTGTGGTGAC 12157

Qy   705 -- 705
Db   12158 ATGCGCCTGTAGTCCCTGCTACTCGGGAGGCTGAGGTGGGAGGATCACTGGAGCCCGGGA 12217

Qy   705 -- 705
Db   12218 GGTGAGGTTGCAGTGAGCTGAGATCATGCCACCCACCTGGGTGACAGAGAGA 12277

Qy   705 -- 705
Db   12278 GAGAGAGACCTTGACTCGAAAGAAAAGAAAAAACCTGGGCGGTGGCTCACGCCTGTAATT 12337

Qy   705 -- 705
Db   12338 TCAACATTTGGGAGGCTGAGGAGGTGGATCGATCCATGAGGTCAGGAGTTTGACACTAGCC 12397

Qy   705 -- 705
Db   12398 TGGCCAACATGCAAAACCTGTCTCTACTAAAAATACAAAAAATTAGCGAGGTGTAGTGG 12457

```
ATTORNEY/AGENT INFORMATION:
  NAME: Monaco, Daniel A.
  REGISTRATION NUMBER: 30,480
  REFERENCE/DOCKET NUMBER: 8321-8
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (215) 568-8383
  TELEFAX: (215) 568-5549
  TELEX: NO. 5734039e
INFORMATION FOR SEQ ID NO: 35:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 3623 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: double
    TOPOLOGY: linear
US-08-306-691B-35
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Alignment Scores:                          Length:        3623
  Pred. No.:            9.85e-51            Matches:        138
  Score:               624.50              Conservative:    68
  Percent Similarity:   53.79%             Mismatches:     128
  Best Local Similarity: 36.03%            Indels:          49
  Query Match:          16.10%             Gaps:            10
  DB:
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US-10-660-763-2 (1-752) x US-08-306-691B-35 (1-3623)

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Qy    405 AspArgHisSerThrSerSerGluGlnGluArgGluGlyGlyArgThrProThrLeu 424
              ::::||||||||                            |||
Db    514 GAGAAACACTCCTGTACCATGGGCTCCATGCCCGCCAATGCCGTGTCCCAGTATCCG------ 567

Qy    425 GluIleLeuLysSerHisIleSerGlyIlePheArgProLysPheSer------------ 440
                                     :||::|||        |||:|:|:::
Db    568 ------CTGAGCAGCGGGATCAATGGCACGACTTCTTGGTCGTGAGAGTGAGCAGTCCT 621

Qy    440 ---------------------------------------------------------- 440
Db    622 AGCCAGAGGTCCATCTCGCTGAGATACGAAGAGGAGGGTGTACCATTACAGGATCAACACT 681

Qy    441 ------------AsnLeuTyrArgLeuGluGlyPheSerIleProLeuLeu 456
                          :::::||:||||||||:::::::
Db    682 GCTTCTGATGCGCAAGCTCACGTCGTCTCCTCCGAGACCCGCTTCAACACCCTGGCCAGTTG 741

Qy    457 IleAspHis------LeuLeuSerThr---GlnGlnProLeuThr 468
              ||:                        |||
Db    742 GTTCATCATCATCAACGTGGCCGACGGGCTCATCACCACGCGCTCCATTATCCAGCCCCCA 801

Qy    469 LysLysSerGlyValValLeuHisArgAlaValPro Lys---AspLysTrpValLeuAsn 487
              ||:|:||:|||::                      ||||||||          ::
Db    802 AAGCCGCAACAACAGCCCACTGTTCATGGTGTGTCCCCAACTACGACAAGTGGGAGATGGAA 861

Qy    488 HisGluAspLeuValLeuGlyLysGlnIleGlyTyrAsnPheGlyValPheSer 507
              ||||:    ::::              ::::|||||:|:||:
Db    862 CGCACGGACATCACCAGAGCACAAGCTGGCGCGGGCCCAGTACCGGGAGGGTGTACGAG 921

Qy    508 GlyArgLeuArgAlaAspAsnAsnThrLeuValAlaValLysSerCysArgGlu---ThrLeu 526
              ||||          :::            ||||||||||:||||:||||
Db    922 GGCGTGTGGAAGAATACAGCCTGACGTGCCGTGAAGACCTTGAAGGAGGACCAATG 981

Qy    527 ProProAspLeuLysAlaLysPheLeuGlnLeuGlnLeuAlaArgIleLeuLysGlnTyrSerHis 546
                     :::             ::|||                  :::|||
Db    982 GAGGTGAA---------GAGTTCTTGAAGAAGCTGCAGTCATGAAAGAGATCAAACAC 1032

Qy    547 ProAsnIleValArgLeuIleGlyValCysThrGlnLysGlnProIleTyrIleValMet 566
              ::                 :::|||||                |||
Db    1033 CCTAACCTAGTCGACGTCGCAGCTCCTTGGGTCGTGCACCGGGAGCCCCGTTCTATATCATCACT 1092

Qy    567 GluLeuValGlnGlyGlyAspPheLeuThrPheLeuArgGluTyrAlaArgLeuArg 586
                     ::::||:|||:||||:::            ::::|||
Db    1093 GAGTTCATGACCTACGGAACCTTCCTGAGG---GAGTACGCAGGAGAGGAG 1149

Qy    587 ValLys------ThrLeuLeuGlnMetValGlyAspAlaAlaAlaGlyMetGluTyrLeu 604
                     |||                                    |||
Db    1150 GTGAACGCCCTGGTGCTGCTGCAGATGGTGGGTGACGCCACTGCAGATCTCGTGCTGCGGCAGGAGTACCTA 1209
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Qy    705 ------------------------------------------------------------- 705
Db  12458 TGCAAGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGCCACAAGAGAATCGCTTGAACCTGGG 12517

Qy    705 ------------------------------------------------------------- 705
Db  12518 AGGTGGAGGTTGCAGTGAGCTGAGATCACACCACTGCACTCCAGCCTGGGTGACAGAGCA 12577

Qy    705 ------------------------------------------------------------- 705
Db  12578 AGACTCCATCTCAGAAAAGAAAAAAAATAGAATATCCCTGTAGCTACTACTGAGTG 12637

Qy    705 ------------------------------------------------------------- 705
Db  12638 AGCACCTGGTCTGTCGTGCTAGGTCACATGTTATTGCTCATCACTACACATGTGTGGTA 12697

Qy    705 ------------------------------------------------------------- 705
Db  12698 GGGATTAATATGTCCCTTTCTCAGATGGAAAAACAGGCTGGCAGAGGGGACACAGCTAGC 12757

Qy    705 ------------------------------------------------------------- 705
Db  12758 ACGTGGTAGGATTAGGATTAGGATCAGAAGCCAGGCCTCTTTGTCCTTTGGGCCCTTGGTGGAGAA 12817

Qy    705 ------------------------------------------------------------- 705
Db  12818 CAGTGCATCATCCTTAAGCAGTCCTATGGCTTCATGGTAATCCCCCAG 12877

Qy    705 ------------------------------------------------------------- 705
Db  12878 AGTCTGCCGAGGACCCTCAAACTCCCCTCCGTGTGCGTGCCTCCTCCACA 12937

Qy    706 GlyGlyArgLeuProCysProGluLeuProLysProAspAlaValPheArgLeuMetGluGln 725
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  12938 GGGGGCCGTCTGCCCTGCCCAGAGCTGTGTCCTCGATGCCGTGTTCAGGCTCATGGAGCAG 12997

Qy    726 CysTrpAlaTyrGluProGlyGlnArgProSerPheSerThrIleTyrGlnGluLeuGln 745
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  12998 TGCTGGGCCTATGAGCCTGGGCAGCGGCCCAGCTTCAGCACCATCTACCAGGAGCTGCAG 13057

Qy    746 SerIleArgGlyLysArgHisArg 752
          ||||||||||||||||||||||||
Db  13058 AGCATCCCGAAAGGGGGCATCGG 13078
```

RESULT 5
US-08-306-691B-35

```
; Sequence 35, Application US/08306691B
; Patent No. 5734039
GENERAL INFORMATION:
  APPLICANT: Calabretta, Bruno
  APPLICANT: Skorski, Tomasz
  TITLE OF INVENTION: ANTISENSE
  TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
  NUMBER OF SEQUENCES: 55
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
    STREET: Two Penn Center, Suite 1800
    CITY: Philadelphia
    STATE: Pennsylvania
    COUNTRY: U.S.A.
    ZIP: 19102
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
    COMPUTER: IBM PS/2
    OPERATING SYSTEM: MS-DOS
    SOFTWARE: WordPerfect 5.1
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/306,691B
    FILING DATE: September 15, 1994
    CLASSIFICATION: 514
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:
    FILING DATE:
```

```
Qy   605  GluSerLysCysCysIleHisArgAspLeuLeuAlaAlaAlaArgAsnCysLeuLeuValThrGluLys 624                Qy   475  ------CTGAGCAGCGGATCAATGGCAGCTTCTTCGGTGCTGAGGAGTGAGAGCAGTCCT 528
          ||||     ||| ||                                 |||||                                         |||  |||           :::  |||
Db  1210  GAGAGCAAAAACTTCATCCACAGATCTTGCTGCCCGAAACTGCCTGGTAGGGGAGAAC 1269               Db   440  --------                                                  440

Qy   625  AsnValLeuLysIleSerArgAspPheGlyMetSerArgGluGluAlaAspGlyValTyrAla 644               Db   529  AGCCAGAGGTCCATCTGCTGAGATACGAAGGAGGGTGTACCATTACAGGATCAACACT 588
          :::::   ||| |||      ||||||  |||     ||||||                                               |||
Db  1270  CACTTGGTGAAGTAGCTGATTTGGCTGAGCAGGTGATGATGACAGGGACACCTACACA 1329              Qy   441  ------AsnLeuTyrArgLeuGluGlyGluGlyPheProSerIleProLeuLeu 456

Qy   645  AlaSerGlyLyValProValLysTrpThrThrAlaProGluAlaLeuAsnTyr 664                Db   589  GCTTCTGATGGCAAGCTCAGTGTCTCCGAGAGCGCTTCAACACCCTGGCCGAGTTG 648
          :::       |||||                    |||  ::: :||||||                                       ||
Db  1330  GCCCATGCTGGAGCCAAG---TTCCCCATCAAATGGACTGCACCCGAGAGCCTGGCCTAC 1386              Qy   457  IleAspHis------                    -LeuLeuSerThr--GlnGlnProLeuThr 468
                                                                                                        :::                            ||   |::|||
Qy   665  GlyArgTyrSerSerGluSerAspValTrpSerPheGlyIleLeuLeuTrpGluThrPhe 684               Db   649  GTTCATCATTCAACCGTGCCGACCACGTCCATCACCACGTCCATTATCCAGCCCCA 708
          ||||||          :::  :::  ||||||                    |||||::|
Db  1387  AACAAGTTCTCCATCAAGTCCGACGTCTGGGCATTTGGAGTATTGCTTTGGGAAATTGCT 1446              Qy   469  LysLysSerGlyValValLeuValHisArgAlaValProLys---AspLysTrpValLeuAsn 487
                                                                                                       :::::::    ||||||                    :::  |||||||||
Qy   685  SerLeuGlyAlaSerProTyrProAsnLeuSerArgAsnGlnIleThrArgGluPheValGlu 704              Db   709  AAGCGCAACAAGCCACTGTCTATGGTGTCCCCAACTACCAACAGTGGGAGATGGAA 768
          ::: ||| |||::||||||                    |||  :::|||||
Db  1447  ACCTATGCCATGTCCCCTTACCCGGAATTGACCCGTTCCGGGTATGAGCTGCTAGAG 1506              Qy   488  HisGluAspLeuValLeuGlyGluGlnIleIleGlyArgGlyAsnPheGlyGluValPheSer 507
                                                                                                       ||||||               ||||||
Qy   705  LysGlyGlyLyProCysProGluLeuProAspAlaValPheArgLeuMetGlu 724               Db   769  CGCACGGACATCACCATGAAGCACCAAGCTGGGCGGGGGCCAGTACGGGGGAGGTGTACGAG 828
          ::: ::: |||||  |||||||                    ||||||
Db  1507  AAGGACTACCGCAGTGGAGTTGATCCTCGACGCGCCCAGAGAGGTCTATGAACTCATGCGA 1566              Qy   508  GlyArgLeuArgAlaAspAsnThrLeuValAlaValLysSerCysArgGlu--ThrLeu 526
                                                                                                       :::                            |||
Qy   725  GlnCysTrpAlaTyrAlaTyrProGlyGlnArgProSerPheSerThrIleTyrGlnLeu 744               Db   829  GGCGTGGAAGAAATACGACGGTGGCCGTGAAGACCTTGAAGGAGGACACCATG 888
          :::::: ||||||||||                    |||:::||
Db  1567  GCATGTTGGCAGTGAAGTCCTGACAATCCCTCGACCGGCCCTCCTTTGCTGAAATCCACCAAGCCTTT 1626              Qy   527  ProProAspLeuLysAlaLysPheGlnLeuGlnLeuAlaArgIleLeuLysGlnTyrSerHis 546
                                                                                                       :::||||::                    ::: :||::::
Qy   745  GlnSerIle 747                Db   889  GAGGTGGAA--------                    -GAGTTCTTGAAGAAGAGCTGCAGTCATGATGAAAGATCAAAACAC 939
          ::::::::
Db  1627  GAAACAATG 1635              Qy   547  ProAsnIleValArgLeuIleGlyValCysThrGlnLysGlnProIleTyrIleValMet 566
                                                                                                       ||||||::                    |||||| ::
                                                                                       Db   940  CCTAACCTAGTGCAGCTCTCCTTGGGGTCTGCACCCGGAGCCCCGTTCTATATCATCACT 999

RESULT 6                                                                             Qy   567  GluLeuValGlnGlyGlyAspPheLeuThrPheLeuThrArgGluGlyAlaArgLeuArg 586
US-09-949-016-927                                                                             ||| |||:::                    :||||||
; Sequene 927, Application US/09949016                                          Db  1000  GAGTGTCATGACCTACGGGAACCTTCCTGACTACCTGAGG--GAGTTGCAACCCGCAGGAG 1056
; Patent No. 6812339
; GENERAL INFORMATION:                                                                   Qy   587  ValLys------                    ThrLeuGlnMetValGlyValAspAlaAlaAlaGlyMetGluTyrLeu 604
; APPLICANT: VENTER, J. Craig et al.                                                                ||| |||
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED                     Db  1057  GTGGAACGCGTGGTGCTGTACATGGCCACTCGATCTCGTCAGCCAGTAGTACCTA 1116
; TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307                                                               Qy   605  GluSerLysCysCysIleHisArgAspLeuLeuAlaAlaAlaArgAsnCysLeuLeuValThrGluLys 624
; CURRENT APPLICATION NUMBER: US/09/949,016                                                         ||| |||   ||
; CURRENT FILING DATE: 2000-04-14                                               Db  1117  GAGAGCAAAAACTTCATCCACAGATCTTGCTGCCCGAAACTGCCTGGTAGGGGAGAAC 1176
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20                                                         Qy   625  AsnValLeuLysIleSerAspAspPheGlyMetSerArgGluGluArgGlyValTyrAla 644
; PRIOR APPLICATION NUMBER: 60/237,768                                                              :::::::||||                    ||||||
; PRIOR FILING DATE: 2000-10-03                                                 Db  1177  CACTTGGTGAAGTAGCTGATTTGGCTGAGCAGGTTGATGACAGGGACACCTACACA 1236
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08                                                         Qy   645  AlaSerGlyLeuGlyArgGlnValProValLysTrpThrAlaProGluAlaLeuAsnTyr 664
; NUMBER OF SEQ ID NOS: 207012                                                                      :::                            ||||||::
; SOFTWARE: FastSEQ for Windows Version 4.0                                      Db  1237  GCCCATGCTGAGCCAAG---TTCCCCATCAAATGGACTGCACCCGAGAGCCTGGCCTAC 1293
; SEQ ID NO 927
; LENGTH: 5434                                                                          Qy   665  GlyArgTyrSerSerGluSerAspValTrpSerPheGlyIleLeuLeuTrpGluThrPhe 684
; TYPE: DNA                                                                                         ||||||                            :::  :::  ||||||
; ORGANISM: Human                                                               Db  1294  AACAAGTTCTCCATCAAGTCCGACGTCTGGGCATTTGGAGTATTGCTTTGGGAAATTGCT 1353
US-09-949-016-927
                                                                                       Qy   685  SerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnIleThrArgGluPheValGlu 704
Alignment Scores:                                                                                  :::                            :::
Pred. No.:          1.87e-50                Length:        5434                  Db  1354  ACCTATGCCATGTCCCCCTTACCCGGGAATTGACCGTTCCCAGTGTATGAGCTGCTAGAG 1413
Score:              624.50                  Matches:        138
Percent Similarity: 53.79%                  Conservative:   68                          Qy   705  LysGlyGlyLysArgLeuProCysProGluLeuProAspAlaValPheArgLeuMetGlu 724
Best Local Similarity: 36.03%               Mismatches:     128                                     :::::::                            |||||| :::
Query Match:        16.10%                  Indels:         49              Db  1414  AAGGACTACCGCAGTGGAGTTGATCCTCGACGCGCCCAGAGAGGTCTATGAACTCATGCGA 1473
DB:                                         Gaps:           10
                                                                                       Qy   725  GlnCysTrpAlaTyrAlaTyrProGlyGlnArgProSerPheSerThrIleTyrGlnLeu 744
US-10-660-763-2 (1-752) x US-09-949-016-927 (1-5434)                                                 :::::                           |||
                                                                               Db  1474  GCATGTTGGCAGTGGAATCCCTCGACCGGCCCTCCTTTGCTGAAATCCACCAAGCCTTT 1533
Qy   405  AspArgHisSerThrSerSerGluGlnLeuArgGluGlyGlyArgThrProThrLeu 424
          :::::  |||||                                                                  Qy   745  GlnSerIle 747
Db   421  GAGAAACACTCCGGTACCATGGCCGTGTCCGCAATGCGCTGAGTATCCG-----  474                          ::::::::

Qy   425  GluIleLeuLysSerHisIleSerGlyIlePheArgProLysPheSer----------  440
```

Db   1534 GAAACAATG 1542

RESULT 7
US-09-949-016-3759
; Sequence 3759, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;   TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;   FILE REFERENCE: CL001307
;   CURRENT APPLICATION NUMBER: US/09/949,016
;   CURRENT FILING DATE: 2000-04-14
;   PRIOR APPLICATION NUMBER: 60/241,755
;   PRIOR FILING DATE: 2000-10-20
;   PRIOR APPLICATION NUMBER: 60/237,768
;   PRIOR FILING DATE: 2000-10-03
;   PRIOR APPLICATION NUMBER: 60/231,498
;   PRIOR FILING DATE: 2000-09-08
;   NUMBER OF SEQ ID NOS: 207012
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 3759
;   LENGTH: 5763
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-3759

Alignment Scores:
Pred. No.:   Length: 5763
Score: 3.61e-50   Matches: 158
                      622.00   Conservative: 79
Percent Similarity: 48.67%   Mismatches: 136
Best Local Similarity: 32.44%   Indels: 114
Query Match: 16.04%   Gaps: 17
DB: 4

US-10-660-763-2 (1-752) x US-09-949-016-3759 (1-5763)

Qy   360 LeuGlnGluAlaLeu--------------------------GlnGlyLeuGlnVal 369
              ::::|| || |||||||||||
Db   454 CTGGAAGAAGAGCCCTTCAGCGGCCAGTAGCATCTGACTTTGAGCCTCAGGGTCTGAGTGAA 513

Qy   370 AlaLeuCysSerGlnAlaLysLeuGlnAlaGlnGlnGluLeuLeuGlnThrLysLeuGlu 389
              ||||||| :::::|:||||| ||||||
Db   514 GCC----------GCTCGTTGGAACTCCAAGGAGAAAACCTTCTC- 546

Qy   390 HisLeuGluGlyGluProGlyProProValLeuLeuGlnGln------ 403
              |||||| || ||| :::
Db   547 --GCTGGACCCAGTGAAAATGACCCCAACCTTTCGTTGCACTGTATGATTTGTGGCC 603

Qy   404 ------AspAsp----------------------------------Arg 406
              ||||||| |
Db   604 AGTGGAGATAACACTCTAAGCATAACTAAAGGTGAAAAGTTCCGGGTCTTAGGCTATAAT 663

Qy   407 HisSerThrSerSerGluGlnGluArgGluGlyLysArg--------- 420
              ||| ::: |||||||||
Db   664 CACAATGGGGAATGGTGTGAAGCCAAACCAAAAATGCCAAGGCTGGGTCCCAAGCAAC 723

Qy   421 -----ThrPro----ThrLeuGlu------------------------ 425
              :::|||||| :::||||||
Db   724 TACATCACGCCAGTGAAACAGTCTCTGGAGAAACACTCCTGGTACCCATGGGCCTGTCCCGC 783

Qy   426 IleLeuLysSerHisIleSerGlyIlePheArgProLysPheSer 440
              ::||| ||||||| ::: |||
Db   784 AATGCCGCTGAGTATCTGCTGAGCAGCGGGATCAATGCAGCTTCTTGGTGCGTGAGAGT 843

Qy   440 -- 440

Db   844 GAGAGCAGTCCTGGCCAGAGGTCCATCTCGCTGAGATACGAAGGGAGGGTGTACCATTAC 903

Qy   441 --------------AsnLeuTyrArgLeuGluGluGlyGluGlyPhe ProSer 452
              :::||| ||||| ||||||
Db   904 AGGATCAACACTGCTTCTGATGCAAGCTCTACGTCTCCTCCGAGAGCCGCTTCAACACC 963

RESULT 8
US-08-604-989A-10
; Sequence 10, Application US/08604989A
; Patent No. 5834208
; GENERAL INFORMATION:
;   APPLICANT: Sakano, S.
;   TITLE OF INVENTION: No. 5834208e1 Tyrosine Kinase
;   NUMBER OF SEQUENCES: 11
;   CORRESPONDENCE ADDRESS:

Qy   453 IleProLeuLeuIleAspHis----------------------LeuLeuSerThr---Gln 464
              :::|:::: ||| |||:::||||
Db   964 CTGGCCCAGTTGGTTCATCATCATTCAACGTGGCCGACGGGCTCACCACCGCTCCAT 1023

Qy   465 GlnProLeuThrLysLysSerGlyValValLeuHisArgAlaAlaValProLys---AspLys 483
              ::::|::: || :::||| :::
Db   1024 TATCCAGCCCAAAGCGCAACAAGCCACCTGTCTATGGTGTGTCCCCAACTACGACAAG 1083

Qy   484 TrpValLeuAsnHisGluAspLeuvalLeuGlyLeuGlnIleGlyArgGlyAsnPheGly 503
              || :::   :::::|||
Db   1084 TGGGAGATGGAACGACACGGACATCACCATGAGCACAAGCTGGGCGGGGCCAGTACGGG 1143

Qy   504 GluValPheSerGlyArgLeuArgLeuAlaAlaAspAsnThrLeuValAlaValLysSerCysSerArg 523
              ||||| ||| :::   :::
Db   1144 GAGGTGTACGAGGGCGTGTGGAAGAAATACAGCTGGACGGTGCCGTGAAGACCTTGAAG 1203

Qy   524 Glu---ThrLeuProProAspLeuLysAlaLysPheLeuGlnLeuAlaArgIleLeuLys 542
              ||| :::|||||||||
Db   1204 GAGGACACCATGAGAGTGGAA---------GAGTTCTTGAAAGAAGCTGCAGTCATGAAA 1254

Qy   543 GlnTyrSerHisProAsnIleValArgLeulleGlyValCysThrGlnLysGlnProIle 562
              ::: ||||||||| :::::: |||
Db   1255 GAGATCAAACACCCTAACCTGGTGCAGCTCCTGGGGGTCTGACACCCGGGAGCCCCGTTC 1314

Qy   563 TyrIleValMetGluValGlnGlyGlyAspPheLeuThrPheLeuArgThrGluGly 582
              ||||| ||| :::
Db   1315 TATATCATCACTGAGTTCATGACCTACGGGAACCTCCTGGACTACCTGAGG---GAGTGC 1371

Qy   583 AlaArgLeuArgValLys-----ThrLeuLeuGlnMetValGlyAlaAlaAlaAlaGly 600
              ::: ||||| ::::::
Db   1372 AACCCGCCAGGAGGTGAACGCGCTGGTGCTGTCCCACTAGATCTCGTCAGCC 1431

Qy   601 MetGluTyrLeuGluSerLysCysCysIleHisArgAspLeuAlaAlaArgAsnCysLeu 620
              |||||||| :::||| ::: :::|||
Db   1432 ATGGAGTACCTGGAGAGAAAACTCATCACAGAGATCTTGCTGCCCGAAAACTGCCTG 1491

Qy   621 ValThrGluGlyAsnValLeuLysIleSerAspPheGlyMetSerArgGluGluArgGluAlaAlaAsp 640
              ||| :::   :::::: |||
Db   1492 GTAGGGGAGGAGAACCACTTGGTGAAGGTAGCTGATTTTGGCCTCAGGTTGATGACAGGG 1551

Qy   641 GlyValTyrAlaAlaSerGlyTyrLeuArgGlnValProValLysTrpProValProGlu 660
              || :::
Db   1552 GACACCTACACAGCCCCATGCTGGACCCAAG---TTCCCCATCAAATGACTGCACCCGAG 1608

Qy   661 AlaLeuAsnTyrGlyArgTyrSerSerGluSerAspValTrpSerPheGlyIleLeuLeu 680
              ::::|| :::||||||
Db   1609 AGCCTGGCCTACAACAAGTTCCATCAAGTCCGACGTCTCGGCATTTGGAGTATTGCTT 1668

Qy   681 TrpGluThrPheSerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnGlnThrArg 700
              :::   :::|||
Db   1669 TGGGAAATTGCTACCTATGGCATGTCCCCTTACCCGGAATTGACCTGTCCCAGGTGTAT 1728

Qy   701 GluPheValGluLysGlyGlyArgLeuProCysProGluLeuCysProAspAlaValPhe 720
              ::::||| :::
Db   1729 GAGCTGCTAGAGAAGGAACTACCGCATGGAGGCTGCCCAGAGGAGGTCACTGAAGAGTCTAT 1788

Qy   721 ArgLeuMetGluGlnCysTrpAlaTyrGluProGlyGlnArgProSerPheThrIle 740
              :::|| :::
Db   1789 GAACTCATGCGAGCATGTGGCAGTGGAATCCCTTGACCGGCCCTCCTTTGCTGAAATC 1848

Qy   741 TyrGlnGluLeuGlnSerIle 747
              ::::|||
Db   1849 CACCAAGCCTTTGAAACAATG 1869

```
        ADDRESSEE:  Pennie & Edmonds LLP
        STREET:  1155 Avenue of the Americas
        CITY:  New York
        STATE:  New York
        COUNTRY:  USA
        ZIP:  10036-2711
  COMPUTER READABLE FORM:
        MEDIUM TYPE:  Diskette
        COMPUTER:  IBM Compatible
        OPERATING SYSTEM:  DOS
        SOFTWARE:  FastSEQ Version 2.0
  CURRENT APPLICATION DATA:
        APPLICATION NUMBER:  US/08/604,989A
        FILING DATE:  February 23, 1996
        CLASSIFICATION:  435
  ATTORNEY/AGENT INFORMATION:
        NAME:  Charles E. Miller
        REGISTRATION NUMBER:  24,576
        REFERENCE/DOCKET NUMBER:  1920-026
  TELECOMMUNICATION INFORMATION:
        TELEPHONE:  (212) 790-9090
        TELEFAX:  (212) 869-8864/9741
        TELEX:  66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
  SEQUENCE CHARACTERISTICS:
        LENGTH:  1521 base pairs
        TYPE:  nucleic acid
        STRANDEDNESS:  double
        TOPOLOGY:  linear
  MOLECULE TYPE:  cDNA to mRNA
  ORIGINAL SOURCE:
        ORGANISM:  human
        STRAIN:  UT-7
```

US-08-604-989A-10

```
Alignment Scores:
Pred. No.:              1.17e-49      Length:        1521
Score:                  607.50        Matches:        173
Percent Similarity:     49.21%        Conservative:    75
Best Local Similarity:  34.33%        Mismatches:     174
Query Match:            15.66%        Indels:          82
DB:                     2             Gaps:            17
```

US-10-660-763-2 (1-752) x US-08-604-989A-10 (1-1521)

```
Qy  272 ProAspValProProCysValThrPheAspGluSerLeuLeuGluGlu---GlyGluPro  290
                                                        |||   ::::::
Db   78 CCCCCCGTTCCTGCGAGCCTCGCACCCCCTCCCGTCAGCCAGGATGGCCAACGAGGCG  137

Qy  291 LeuGluProGlyGlyGluLeuGlnLeuGluAsnGluLeuThrValGluSerValGlnHisThrLeu  310
Db  138 CTGGGGCCCCGGGCACCCAGTGTATCACCAAATGGAGCACACCCCGCCCA---------  188

Qy  311 ThrSerValThrAspGluLeuAlaValAlaThr-GluMetValPheArgArgGlnGluMe  330
        |||:::                           |||||
Db  189 ---------------GCCAGGGAGCTGGCCTTCCGCAAGGGCGACGT  221

Qy  330 tValThrGlnLeuGlnLeuGluArgAsnGluLeuArgAsnThrHisProArgGluAr  350
Db  222 GGTCACCATCCTGGAGGCC--------TGCGAGAACAAGAGCTGGTACCGCGTCAA  269

Qy  350 gValGlnLeuGlyLeuArgGlnValLeuGlnLeuGluGlnAlaLeuGlnLeuGlyValAl  370
        ||||:::
Db  270 GCACCACCAGTGACAGAGGGGCGTCTGCAGCTGGGGCGCGGAGCGCGGGAGGC  329

Qy  370 aLeuCysSerGlnAlaLysLeuGln----------------------AlaGlnGl  381
        |||||                   :::
Db  330 CCTCTGCCCAGCACCCAGCTCCAGCTGGGCCGTGTTCCGGCCCGTGGTTCCTGGT  389

Qy  381 nGluLeuLeuGlnThrLysLeuGluHisLeuGlyProGlyProProValLeuLeu  401
        ||||||
Db  390 GGAGGCTGTCCAG---------CAGCTGCCGAGCCCCGAGGATGGGCATCTCGGTT  437
```

```
Qy  401 uLeuGlnAspAspArgHisSerThrSerSerGluGlnGlyArgGluGlyGlyArgTh  421
                                                              |||
Db  438 GCGGGAGTCCGGCGCCAC---------------------------CCCGGCGACTACGT  470

Qy  421 rProThrLeuGluIleLeuLysSerHisIleSerGlyIlePheArgProLysPheSerAs  441
Db  471 CCTGTGCGTGGCTGAGCTTTGGCCGCGACGTCATCAC--------------------  504

Qy  441 nLeuTyrArg--LeuGluGlyGluGlyPheProSerIle------ProLeuLeuGluAs  458
            ||||       :::       :::|||                |||||:||
Db  505 ----TACCGGTGCTGACAGCCACGAGGGCCACCTCACAATCGATCGAGGCCGTGTTCTTCTG  560

Qy  458 pHisLeuSerThrGlnLeuProLeuThrLysSerGlyValValLeuHisArgAl  478
        :::                ::                       |||:
Db  561 CAACCTCATGGACATGGTGGACATTACGACAAGGACAAGGGCGCCTATCTGCACCAAGCT  620

Qy  478 aVal---ProLysAspLys  483
Db  621 GGTGAGACCAAGCGGAAACACGGGACCAAGTCGGCCGAGGAGAGCTGGCCAGGGCGG  680

Qy  484 -TrpValLeuAsnHisGluAspArgLeuGlyGluGlnIleGlyArgGlyAsnPheGl  503
         :::||||||    :::      |||||||             |||
Db  681 CTGGTTACTGACCTGCAGCATTTGACATTGGAGCACAGATCCGAGACGGAGAGTTTGG  740

Qy  503 yGluValPheSerGlyArgLeuArgAlaAspAsnThrLeuAlaValLysSerCysAr  523
        |||                                       ::::
Db  741 AGCTGTCCTGCAGGGTGAGTACCTGGGCAAAG----GTGGCCGTGAAGAAT------  789

Qy  523 gGluThrLeuProProAspLeuLysAlaLys---PheLeuGlnGluAlaArgIleLeuLy  542
Db  790 ------ATCAAGTGTGATGTGACAGCCCAGGCCTTCCTGGACGACGGCCGTCATGAC  842

Qy  542 sGlnTyrSerHisProAsnIleValArgLeuIleGlyValCysThrGlnLysGlnProI1  562
        :::|||                    ::::||||:::
Db  843 GAAGATGCAACACGAGAACCTGGCGTGCCGTTCCTGGGCGTGATCCTGCAC---CAGGGGCT  899

Qy  562 eTyrIleValMetGluLeuValGlnGlyAspPheLeuThrPheLeuArgThrGluG1  582
        :||||:::       :::    :::::::
Db  900 GTACATTGTCATGGAGCACGTGAAGCAAGAAGCTTGTCACCGCGACCCGGGG  959

Qy  582 y---AlaArgLeuArgValLysThrLeuGlnLeuMetValGlyValAspAlaAlaAlaGlyMe  601
        ||||||
Db  960 TCGAGCCCTGTGAACACCGCTCAGCTCCTGCAGTTTCTCGCAGTGGCCAGGGGCAT  1019

Qy  601 tGluTyrLeuGluSerLysCysCysIleHisArgAspLeuAlaAlaArgAsnCysLeuVa  621
           :::|||
Db 1020 GGAGTACCTGGAGCAAGAAGCTTGTCACCGCGACCTGGCCGCCCCAACATCCTGGT  1079

Qy  621 lThrGluLysAsnValLeuLysIleSerAspPheGlyMetSerArgGluGluAlaAspGl  641
        :::::::
Db 1080 CTCAGAGACCTGGTGCCAAGGTCAGCGACTTTGGCCTGCCAAAGCCGAGCGGAAGGG  1139

Qy  641 yValTyrAlaAlaSerGlyGlyLeuArgProValProValLysTrpThrAlaProGluAl  661
        |||||
Db 1140 GCTAGACTCAAGC------CGGCTGCCGTCAGTGGCAGCGGCGCCCGGAGGC  1184

Qy  661 aLeuAsnTyrArgTyrSerGluSerAspValTrpSerPheGlyIleLeuLeuTr  681
          :::::::
Db 1185 TCTCAAACACGGGAAGTTCACCAGCAAGTCGGATGGTCGGAGTTTTGGGGTGCTGCTCTG  1244

Qy  681 pGluThrPheSerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnGlnThrArgI  701
           :::|||
Db 1245 GGAGGTCTTCTCATATGACGGGCTCCGTACCCTAAAATGTCACTGAAGAGGTGTCGGA  1304

Qy  701 uPheValGluLysGlyGlyArgLeuProCysProGluLeuCysProProAspAlaValPheAr  721
         :::||||||
Db 1305 GGCCGGTGGAGAGGGTACCGCCATGGAACCCCCGAGGGCTGTCCAGGCCCGTGCACGT  1364

Qy  721 gLeuMetGluGlnCysTrpAlaTyrAlaTyrGlnArgProSerPheSerThrIleTy  741
        ||||||
Db 1365 CCTCATGAGCAGCTGCTGGGAGCAGAGCCCCGCCACCCTTCCGCAAACTGGC  1424

Qy  741 rGlnGluLeu  744
```

```
Db   1425 CGAGAAGCTG 1434
              :::::|||

RESULT 9
US-09-741-154-1
; Sequence 1, Application US/09741154
; Patent No. 6437110
; GENERAL INFORMATION:
;   APPLICANT: BEASLEY, Ellen M. et al
;   TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;   TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;   TITLE OF INVENTION: THEREOF
;   FILE REFERENCE: CL001061
;   CURRENT APPLICATION NUMBER: US/09/741,154
;   CURRENT FILING DATE: 2000-12-21
;   NUMBER OF SEQ ID NOS: 4
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1713
;   TYPE: DNA
;   ORGANISM: Human
US-09-741-154-1

Alignment Scores:
Pred. No.:                        Length:           1713
Score:              1.41e-49      Matches:           156
Percent Similarity: 607.50        Conservative:       53
Best Local Similarity: 51.23%     Mismatches:        115
Query Match:        38.24%        Indels:             84
                    15.66%        Gaps:               15
DB:

US-10-660-763-2 (1-752) x US-09-741-154-1 (1-1713)

Qy  378 GlnAlaGlnGlnGluLeuGlnThrLysLeuGluHisLeuGlyProGly---------- 394
            :::  |||||||||||||||::|||
Db  288 CGTGGTCAGCAGCAGCTTTCTGTGGTTCCACGGAAGATCTCGGGCCGGAGGCTGTCCA 347

Qy  395 --------------------------------------------GluProPro------ 397
                                                     |||||
Db  348 GCAGCTGCAGCCTCCCCGAGGAGATGGGCTGTTCCTGGTCGGGAGTCCGCGCCACCCCGG 407

Qy  398 ------ProValLeuLeuGlnAspAspArgHisSerThrSerSerGluGln 414
            |||||||::::::|||||
Db  408 CGACTACGTCCTGTGCGTGAGCTTTGGCCGCGACGTCATCCACTACCGCGTGCTGCACCG 467

Qy  415 GluArgGluGlyGlyArgThrPro-ThrLeuGluIleLeuLysSerHisIleSerGlyIl 434
            |||||||||||::|||||:::::::
Db  468 CGA--------------CGGCCACCTCACAATCGAT---------------GAGGCCGT 497

Qy  434 ePheArgProLysPheAsnLeuTyrArgLeuGluGlyGluGlyPheProSerIlePr 454
            |||||||::    |||       ::
Db  498 GTTC--------TTCTGCAACCTCATGGAC------------------------- 519

Qy  454 oLeuLeuIleAspHisLeuLeuSerThrGlnProLeuThrLysSerGlyValVa 474
            ::|||::::::||
Db  520 ---ATGGTGGAGCAT---------------TACAGCAAGAAGCAAGGGCGCTAT 554

Qy  474 lLeuHisArgAlaVal---ProLysAspLys----- 483
            ::  |||   |||||
Db  555 CTGCACCAAGCTGTGAGCAAAGCGGAAACACGGACCAAGCTCGGCCAGGAGGAGGCT 614

Qy  484 ---------TrpValLeuAsnHisGluArgLeuValLeuGlyGluGlnIleLeuGlyAr 499
                     ::  |||||||||
Db  615 GGCCAGGGCGGGCGGCTGGTTCACTGACCATTGAGCACAGATCGGAGA 674

Qy  499 gGlyAsnPheGlyValPheSerGlyArgLeuArgAlaAspAsnThrLeuValAlaVa 519
            |||||||||
Db  675 GGGGAGAGTTTGGAGCTGTCCTCCAGGGTGAGTACCTGGGCCAAAAG-----GTGGCCGT 728

Qy  519 lLysSerCysArgGluThrLeuProProAspLeuLysAlaLys---PheLeuGlnGluAl 538
            ||||:::    ::|::
Db  729 GAAGAAT--------------ATCAAGTGTGATGTGACAGCCCCAGGCCTTCCTGACGAGAC 776
```

```
Qy  538 aArgIleLeuLysGlnTyrSerHisProAsnIleValArgLeuIleGlyValCysThrGl 558
            ::::::   ::|   |||||::::|||
Db  777 GGCCGTCATGACGAAGATGCAACACGAGAACCTGGTGCGTCTTCCTGGCCGTGATCCTGCA 836

Qy  558 nLysGlnProIleTyrIleValMetGluValGlnGlyGlyAspPheLeuThrPheLe 578
            ||||   |||   |||::|||   ::::   :::
Db  837 C---CAGGGGCCTGTACATTGTCATGGAGCACGTGACAAGGGCAACCTGGTGAACTTTCT 893

Qy  578 uArgThrGluGly---AlaArgLeuArgValLysThrLeuLeuGlnMetValGlyAspAl 597
            ||||||   |||      :::
Db  894 GCGGACCCGGGTCGAGCCCTGTGAACACCGCTCAGCTCCCCAGTTTCTGCCACGT 953

Qy  597 aAlaAlaGlyMetGluTyrLeuGluSerLysCysCysIleHisArgAspLeuAlaAlaAr 617
            |||||||||||||||||::|||   :::   :::|||||||||
Db  954 GGGCCGAGGGCATGGAGTACCTGGAGAGCAAGAGTGTTGTCACCGGACCTGGCGCCGCCCG 1013

Qy  617 gAsnCysLeuValThrGluLysGlyValLeuValLysIleSerAspPheGlyMetSerArgGl 637
            ||||||||||   |||||::|||:::|||
Db 1014 CAACATCCTGGTCTGACGGACCTGGTGGCCAAGTCAGCGACTTTGGCCTGGCCCGCCAAAGC 1073

Qy  637 uGluAlaAspGlyValTyrAlaAlaSerGlyGlyLeuArgGlnValProValLysTrpTh 657
            ||:::   :::::::                     :::::::
Db 1074 CGAGCGGAAGGGCGTAGACTCAAGC---------------------CGGCTGCCCGTCAAGTGGAC 1118

Qy  657 rAlaProGluAlaLeuAsnTyrGlyArgTyrSerSerGluSerAspValTrpSerPheGl 677
            ||||||||||   |||||||||
Db 1119 GGGCGCCCGAGGCTCTCAAACACGGGAAGTTCACCGGAAGTCGGATGTCTGGAGTTTTGG 1178

Qy  677 yIleLeuLeuTrpGluTrpThrPheSerLeuGlyAlaSerProTyrProAsnLeuSerAsnGl 697
            |||||||||   :::||||||::|||
Db 1179 GGTGCTGCTGTCCTGGGAGTGGTCTTCTCATATGGACGGGCGTACCCTAAAATGTCACTGAA 1238

Qy  697 nGlnThrArgGluPheValGlnPheValGlyGlyLeuProCysProLeuCysProAs 717
            ::::      :::   |||::||||::::|||
Db 1239 AGAGTGTCCGGAGGCCGTGGAGAGGGGTACCGCATGGAACCCCCGAGGGCTGTCCAGG 1298

Qy  717 pAlaValPheArgLeuMetGluGlnCysTrpAlaTyrGluProGlyGlnArgProSerPh 737
            |||   ||||||
Db 1299 CCCCGTGCACCTCCTCATGAGCAGCTGCTGGGAGGCAGCAGCCCCCGGCCCACCCTT 1358

Qy  737 eSerThrIleTyrGlnGlnLeu 744
            :::::::|||
Db 1359 CCGCAAACTGGCCGAGAAGCTG 1380

RESULT 10
US-08-604-989A-11
; Sequence 11, Application US/08604989A
; Patent No. 5834208
; GENERAL INFORMATION:
;   APPLICANT: Sakano, S.
;   TITLE OF INVENTION:  No. 5834208e1 Tyrosine Kinase
;   NUMBER OF SEQUENCES: 11
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Pennie & Edmonds LLP
;     STREET: 1155 Avenue of the Americas
;     CITY: New York
;     STATE: New York
;     COUNTRY: USA
;     ZIP: 10036-2711
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/604,989A
;     FILING DATE: February 23, 1996
;     CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Charles E. Miller
;     REGISTRATION NUMBER: 24,576
;   REFERENCE/DOCKET NUMBER: 1920-026
;   TELECOMUNICATION INFORMATION:
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```
;    TELEPHONE:   (212) 790-9090
;    TELEFAX:     (212) 869-8864/9741
;    TELEX:       66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
;    SEQUENCE CHARACTERISTICS:
;    LENGTH: 1942 base pairs
;    TYPE: nucleic acid
;    STRANDEDNESS: double
;    TOPOLOGY: linear
;    MOLECULE TYPE: cDNA to mRNA
;    ORIGINAL SOURCE:
;    ORGANISM: human
;    STRAIN: UT-7
US-08-604-989A-11

Alignment Scores:
Pred. No.:            2.71e-49        Length:         1942
Score:               605.50          Matches:         173
Percent Similarity:   49.01%         Conservative:     74
Best Local Similarity: 34.33%        Mismatches:      175
Query Match:          15.61%         Indels:           82
DB:                                  Gaps:             17
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US-10-660-763-2 (1-752) x US-08-604-989A-11 (1-1942)

```
Qy   272  ProAspValProProCysValThrPheAspGluSerLeuLeuGluGlu---GlyGluPro  290
          ||    |||||||||  ::                            :||||||
Db   285  CCCCGCGCTTCCTCCGAGCCTGGCACCCCCTCCCGTTCTCAGCCAGGATGCCAACGAGGCG  344

Qy   291  LeuGluProGlyGluLeuGlnLeuAsnGluLeuThrValGluSerValGlnHisThrLeu   310
          |||||||       ::::::::::
Db   345  CTGGGACCCCCGGGCACCCAGTGTATCACCAAATGGAGCACACACCCGCCCCA-------   395

Qy   311  ThrSerValThrAspGluLeuAlaValAlaThr-GluMetValPheArgArgGlnGluMe   330
                                           |||||||||:::  :::::
Db   396  -----------------------------------GCCAGGGGAGCTGGCCTTCCGCAAGGGCGACGT  428

Qy   330  tValThrGlnLeuGlnGlnLeuArgAsnGluLeuArgThrHisProArgGluAr        350
          :||||||  |||:::||
Db   429  GGTCACCATCCTGAGGCC---------TGCGGAACAAGAGCTGGTACCGCGTCAA       476

Qy   350  gValGlnLeuLeuGlyLysArgGlnValLeuGlnLeuGluAlaLeuGlnGlyLeuGlnValAl   370
          :||||::
Db   477  GCACCACCACGTGGACAGGAGGGGTGCTGGCCAGCTGGGGGCGTGCGGGAGGC         536

Qy   370  aLeuCysSerGlnAlaLysLeuGln------------------AlaGlnGl              381
          |||||||::
Db   537  CCTCTTCCGCAGACCCCAAGCTTCAGCCTCAGCCTGTGTTCCACGGGAAGATCTCGGGCCA   596

Qy   381  nGluLeuLeuGlnThrLysLeuGluHisLeuGlyProGlyGluProProValLeuGl        401
          ||::||
Db   597  -----------------CAGCTGCAGCCTCCCGGAGGATGGGCTGTTCCTGGT        644

Qy   401  uLeuGlnAspAspArgHisSerThrSerSerSerGluGlnLeuArgGlnLeuArgGlyGlyArgTh   421
          ||||:::
Db   645  GCGGGAGTCCCGGCCCAC--------------------------CCCGGCGACTACGT    677

Qy   421  rProThrLeuGluIleLeuLysSerHisIleSerGlyIlePheArgProLysPheSerAs   441
          ::||                  :::
Db   678  CCTGTCGCGTGAGCTTTGGCCCGACGTCATCCAC-----------------------    711

Qy   441  nLeuTyrArg---LeuGluGlyGluGlyProSerIle------ProLeuLeuIleAs   458
          :||||          |||:::          ::
Db   712  ---TACCGCGTGCTGCACCCGCACGGCCACCTCACAATGAGCATGGAGGCCGTGTTCTTCTG  767

Qy   458  pHisLeuLeuSerThrGlnThrGlnProLeuThrLysLysSerGlyValValLeuHisArgAl   478
          ::|||||           :::
Db   768  CAACCTCATGGACACATGGTGGAGCATTACAGCAAGGACAAGGCGCTATCTGCACCAAGCT   827

Qy   478  aVal---ProLysAspLys-----------------------------------------   483
          :||       |||  |||
Db   828  GGTGAGACAAGCGGAAACACGGGACCAAGTCGGCGGACCAGAGCTGGCCAGGGCGCGGG   887
```

```
Qy   484  -TrpValLeuAsnHisGluAspLeuValLeuGlyGluGlnIleGlyArgGlyAsnPheGl   503
           :::::|||||                                        ||||:
Db   888  CTGGTTACTGAACCTGCAGCATTGACCATTGGGAGCAGATCGGAGAGGAGAGAGTTTGG   947

Qy   503  yGluValPheSerGlyArgLeuArgAlaAspAsnThrLeuValAlaValLysSerCysAr   523
          |||                            :::|||||||||
Db   948  AGCTGTCCTGGAGGGTGAGTACCTGGGCAAAG-------GTTGGCCGTGAAGAAT-----  996

Qy   523  gGluThrLeuProProAspLeuLysAlaLys---PheLeuGlnGluAlaArgIleLeuLeuy  542
          :::     |||||                        :::::
Db   997  -----ATCAAGTGTGATGTGACAGCCCAGGCCTTCTGGACAGCGGCCGTCATGAC  1049

Qy   542  sGlnTyrSerHisProAsnIleValArgLeuIleGlyValCysThrGlnLysGlnProI   562
          :::       ||||                          :::||||||||
Db  1050  GAAGATGCAACACGAGAACCTGGTGCGTCCTCCGGGGTGATCCTGCAC---CAGGGGCT  1106

Qy   562  eTyrIleValMetGluLeuValGlnGlyGlyAspPheLeuThrPheLeuArgThrGluGl   582
          :||||                                 ::::
Db  1107  GTACATTGTCATGGAGCCACGTGAGCAAGGGCAACCTGGTGAACTTTCTGCGACCCGGGG  1166

Qy   582  y---AlaArgLeuArgValLysThrLeuGlnGluMetValGlyMetAlaAlaAlaGlyMe   601
          :      ||||                                  ||||||||||
Db  1167  TCGAGCCCTCGTGAACACCGCTTCCTGCAGTTTCTCTGCACGTGGCCGAGGGCAT  1226

Qy   601  tGluTyrLeuGluSerLysCysCysIleHisArgAspLeuAlaAlaArgAsnCysLeuVa   621
          :|||                             ::||||||
Db  1227  GGAGTACCTGGAGGAGCAAGAAGCTTGTCACCCGACCTGGCGCCGCCCCAACATCCTGT  1286

Qy   621  lThrGluLysAsnValLeuLeuLysIleSerAspPheGlyMetSerArgGluGluAlaAspG   641
          |||                                   ||||||||||||
Db  1287  CTCAGAGGACCTGGTGCGCCAAGGTCAGCGACTTTGGCCTGCCAAAGCCGAGCGGAAGG  1346

Qy   641  yValTyrAlaAlaSerGlyGlyLeuArgGlnValProValLysTrpThrAlaProGluAl   661
          ||||                                              |||||||
Db  1347  GCTAGACTCAAGC----------CGGCTGCCCCGTCAAGTGACCGAGGGGACGGACGGAGGC  1391

Qy   661  aLeuAsnTyrGlyArgTyrSerSerGluSerAspValTrpSerPheGlyIleLeuLeuTr   681
          :||::::                                ||||:::::
Db  1392  TCTCAAACACGGGAGTTCACCAGCAAGTCGGATGTCGGAGTTTGGGGTGCTCTCG  1451

Qy   681  pGluThrPheSerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnGlnThrArgGl   701
          |||                                            :::
Db  1452  GGAGGTCTTCTCATATGGACGGGCTCTACCCTAAAATGTCACTGAAAGAGGTGTCGA  1511

Qy   701  uPheValGluLysGlyGlyArgLeuProGluLeuCysProAspAlaValPheAr       721
          |||                                   :::
Db  1512  GGCCGTGGAGAGGGGTACCGCATGGAACCCCGAGGGCTGTCCAGGCCCGTGCACGT  1571

Qy   721  gLeuMetGluGlnGlnCysTrpAlaTyrAlaTyrGlyProGlyGlnArgProSerPheIleTy   741
          :::                                ::::::
Db  1572  CCTCATGCAGCAGTGCTGCTGGGAGGCAGAGCCCGCGCCCACCCTTCCGCAAACTGGC  1631

Qy   741  rGlnGluLeu  744
          ||||||||
Db  1632  CGAGAAGCTG  1641
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RESULT 11
US-08-426-509A-1
; Sequence 1, Application US/08426509A
; Patent No. 6326469
; GENERAL INFORMATION:
;    APPLICANT:  Ullrich,, Axel
;    APPLICANT:  Gishizsky,, Mikhail
;    APPLICANT:  Sures,, Irman G.
;    TITLE OF INVENTION:  NOVEL MEGAKARYOCYTIC PROTEIN
;    TITLE OF INVENTION:  TYROSINE KINASSS
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;    ADDRESSEE:  Pennie & Edmonds
;    STREET:  1155 Avenue of the Americas
;    CITY:  New York,
;    STATE:  New York
;    COUNTRY:  USA
```

```
ZIP: 10036-2711
COMPUTER READABLE FORM:
  MEDIUM TYPE: Diskette
  COMPUTER: IBM Compatible
  OPERATING SYSTEM: DOS
  SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/426,509A
  FILING DATE: 21-APR-1995
  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/232,545
  FILING DATE:
ATTORNEY/AGENT INFORMATION:
  NAME: Coruzzi, Laura A
  REGISTRATION NUMBER: 30,742
  REFERENCE/DOCKET NUMBER: 7683-0074-999
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 212-790-9090
  TELEFAX: 212-869-9741
  TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
  LENGTH: 2000 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: unknown
  TOPOLOGY: unknown
US-08-426-509A-1
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Alignment Scores:
Pred. No.:                      2000
Score:              2.84e-49    173
Percent Similarity: 605.50      74
Best Local Similarity: 49.01%   175
Query Match:        34.33%      82
DB:                 15.61%      17
                    3
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US-10-660-763-2 (1-752) x US-08-426-509A-1 (1-2000)

```
Qy  272  ProAspProProCysValThrPheAspGluSerLeuLeuGluGlu---GlyGluPro  290
             ::: |||||||||||||
Db  335  CCCCGGCTTCCTCGAGCCTGGCACCCCCTCCCGTCTCAGCCAGGATGCCAACGAGGGCG  394
             |||     ||| |: |

Qy  291  LeuGluProGlyGlyLeuGlnLeuLeuAsnGluLeuThrValGluSerValGlnHisThrLeu  310
             |||  |:||
Db  395  CTGGGCCCCCGGGCACCCAGTGTATCACCAAATGCGAGCACACCCGCCCCAA-------  445

Qy  311  ThrSerValThrAspGluLeuValAlaValAlaThr-GluMetValPheArgArgGlnGluMe  330
             |||||    :||||  |||||
Db  446  -------------------------GCCAGGGAGCTGGCCTTCCGCAAGGGCGACGT  478

Qy  330  tValThrGlnLeuGlnGluLeuArgAsnGluGluAsnThrHisProArgGluAr  350
             |||||| ||:|
Db  479  GGTCACCATCCTGGAGGCC---------------TGCGAGAACAAGAGCTGGTACCGCGTCAA  526

Qy  350  gValGlnLeuGluGlyLysArgGlnValLeuGluAlaLeuGlnLeuGlnValAl  370
             ||||| ::|
Db  527  GCACCACCAGTGACAGAGAGGGGCTGCCAGCTGGGCGGCGTGGGCGAGGC  586

Qy  370  aLeuCysSerGlnAlaLysLeuGln------------------------AlaGlnGl  381
             ||||  :: ||
Db  587  CCTCTCCGAGACCCCAAGCTCAGCTCCATGCCGTTCAAGGATCTCGGGCCA  646

Qy  381  nGluLeuLeuGlnThrLeuGluHisLeuGlyLysHisSerGlyIlePheArgProValLeuGlu  401
             ||:||| ::|||
Db  647  GGAGGCTGTCCAG---------CAGCTGCAGCTCCCGAGCATGGGCTGTTCCTGGT  694

Qy  401  uLeuGlnAspArgHisSerThrSerSerSerGluGlnArgGluGlnTyrGlyArgTh  421
             |||| ::
Db  695  GCGGGAGTCCGCGCCGCCAC----------CCCGGCGACTACGT  727

Qy  421  rProThrLeuIleLeuLysSerHisIleSerGlyIlePheArgProLysPheSerAs  441
             ::: |
```

```
Db  728  CCTGTCGCTGAGCTTTGGCCGGACGTCATCCAC----------------  761

Qy  441  nLeuTyrArg---LeuGluGlyGlyPheProSerIle---ProLeuLeuIleAs  458
             :::|||    ||||:
Db  762  ----TACCGCGTGCTGCACCGGACGGCCACCTCACAATCATGAGCGCGTGTTCTTCTG  817

Qy  458  pHisLeuLeuSerThrArgGlnProLeuThrLysLysSerGlyValValLeuHisArgAl  478
             :::|| :: :::|||
Db  818  CAACCTCATGACACATGTGAGCAATTACAGCAAGGACAAGGGCGCTATCTGCACCAAGCT  877

Qy  478  aVal---ProLysAspLys-------  483
             |||
Db  878  GGTGAGACCAAAGCGGAAACACGGAACACGGACCAAGTCGGCGGAGGAGCTGGCCAGGGCGGG  937

Qy  484  -TrpValLeuAsnHisGluAspLeuValLeuGlyGlnIleGlyValArgGlyAsnPheGl  503
             |||:||||| :::|||
Db  938  CTGGTTACTGACCCTGCGAGCCATTGACATTGGGAGCACAGATCGGAGAGGAGAGTTTGG  997

Qy  503  yGluValPheSerGlyArgLeuArgLeuAlaAspAsnThrLeuValAlaValLysSerCysAr  523
             ||| :::
Db  998  AGCTGTCCTGCAGGTGAGTACCTGGGCAAAAG-----GTGGCCGTGAAGAAT------  1046

Qy  523  gGluThrLeuProAspLeuLysAlaLys---PheLeuGluGlnGluAlaArgIleLeuLy  542
             |||  :::::
Db  1047 ------ATCAAGTGTGATGTGACAGCCCAGGCCTTCCTGGACGAGACGGCCGTCATGAC  1099

Qy  542  sGlnTyrSerHisProAsnIleValArgLeuIleGlyValCysThrGlnLysGlnProIl  562
             ::: |||||||
Db  1100 GAAGATGCAACACGAACACCTGGTTGCGTCTCCTGGGCGTGATCCTGCAC---CAGGGGCT  1156

Qy  562  eTyrIleValMetGluLeuValGlnGlyGlyAspPheLeuThrPheLeuArgThrGluGl  582
             |||||||||||
Db  1157 GTACATTGTCATGGAGCAGGTGCAGTGAGCAAGGGCAACCTGGTGAACTTTCTGCGGACACCCGGGG  1216

Qy  582  y---AlaArgLeuArgValLysValGlyAspAlaAlaAlaGlyMe  601
             |||||||
Db  1217 CTCAGAGAGGACCTGGTGCGCAAGGTCAGCGACTTTGGCCCAAAGCCGAGCCGAAGGG  1276

Qy  601  tGluTyrLeuGluSerLysLysCysIleHisArgAspLeuAlaAlaArgAsnCysLeuVa  621
             ::::||||||||||
Db  1277 GGAGTACCTGGAGACGCAAGAGAGCTTGTGCACCGGCGACCTGGCCGCGCAACATCCTGGT  1336

Qy  621  lThrGluLysAsnValLeuLysIleSerAspPheGlyMetSerArgGluGluAlaAspGl  641
             :::||||||||
Db  1337 CTCAGAGAAGAACGTGGTGCCAAGGTCAGCGACTTTGGCCTGCAGTTTGGGGTGCTGCTCTG  1396

Qy  641  yValTyrAlaAlaSerGlyGlyLeuProValLysTrpThrAlaProGluAl  661
             :::: ||
Db  1397 GCTAGACTCAAGC----------CGGCTGCCCGTCAAGTGGACGGCGCCGGAGGC  1441

Qy  661  aLeuAsnTyrGlyTyrSerGluSerAspValTrpSerPheGlyIleLeuLeuTr  681
             :::::::|||||
Db  1442 TCTCAAACACGGGAGCTTCACCAGCAAGTCGGATGTCTGGAGTTTTGGGGTGCTGCTCTG  1501

Qy  681  pGluThrPheSerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnGlnThrArgGl  701
             ::::|||
Db  1502 GGAGGGTCTTCTCATATGGACGGCGCTCCTAAAATGTCACTGAAAGAGGTGTCGGA  1561

Qy  701  uPheValGluLysGlnGlyArgLeuProCysProGlyLeuCysProAspAlaValPheAr  721
             :::::
Db  1562 GGCCGTGCGGAGAGGGTACCGGCATGGAACCCCGAGGGGTGCGTCCAGGCCCGTGCACGT  1621

Qy  721  gLeuMetGluGlnCysTrpAlaTyrGlnProGlyGlnArgProSerPheThrLeuTy  741
             :::::||||
Db  1622 CCTCATGAGCAGCTGCGCTGGGAGGCGAGAGCCCGCGCCACCCTTCCGCAAACTGGC  1681

Qy  741  rGlnGluLeu  744
             :::::|||
Db  1682 CGAGAAGCTG  1691
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RESULT 12
US-08-232-545-1
; Sequence 1, Application US/08232545
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; Patent No. 6506578
; GENERAL INFORMATION:
;   APPLICANT: Ullrich, Axel
;   APPLICANT: Gishizky, Mikhail
;   APPLICANT: Sures, Irman G.
;   TITLE OF INVENTION: No. 6506578el Megakaryocytic Protein Tyrosine
;   TITLE OF INVENTION: Kinases
;   NUMBER OF SEQUENCES: 21
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Pennie & Edmonds
;     STREET: 1155 Avenue of the Americas
;     CITY: New York
;     STATE: New York
;     COUNTRY: U.S.A.
;     ZIP: 10036
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/232,545
;     FILING DATE: 22-APR-1994
;     CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Coruzzi, Laura A.
;     REGISTRATION NUMBER: 30,742
;     REFERENCE/DOCKET NUMBER: 7683-050
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (212)790-9090
;     TELEFAX: (212)869-9741
;     TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 2000 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: unknown
;     TOPOLOGY: unknown
;   MOLECULE TYPE: DNA
US-08-232-545-1
```

Alignment Scores:
```
Pred. No.:                              Length:             2000
Score:             2.84e-49             Matches:             173
Percent Similarity:  605.50             Conservative:         74
Best Local Similarity:  49.01%          Mismatches:          175
Query Match:         34.33%             Indels:               82
Db:                  15.61%             Gaps:                 17
                     4
```

US-10-660-763-2 (1-752) x US-08-232-545-1 (1-2000)

```
Qy    272  ProAspValProProCysValThrPheAspGluSerLeuLeuGlu---GlyGluPro   290
                |||  :::      ||||||||           |             :::::
Db    335  CCCCCGGTTCCTTCCTGCGACCTGCCACCCCCTCCGGTCTCAGCCAGGATGCCAACGAGGCG   394

Qy    291  LeuGluProGlyGluLeuGlnLeuAsnLeuLeuThrValGluSerValGlnHisThrLeu   310
                ||||||           :::::||   ::::
Db    395  CTGGGCCCCGGCACCCCCAGTGTATCACCAAAATGCGAGCACACCCCGCCCCA---------  445

Qy    311  ThrSerValThrAspGluValAlaValAlaThr-GluMetValPheArgArgGlnGluMe   330
                           :::     :::::  ||||||         ::::::
Db    446  ----------------GCCAGGGAGGCTGGCCTTCCGCAAGGGCGACGT   478

Qy    330  tValThrLeuGlnLeuGlnLeuGlnGluLeuArgAsnGluGlnLysAsnThrHisProArgGluAr  350
                ||||||:::::                 :::
Db    479  GGTCACCATCCTGGAGGCC-------------TGCGAGAACAAGAGCTGGTACCGCGTCAA   526

Qy    350  gValGlnLeuLeuGlyLysArgGlnValLeuGlnLeuAlaLeuGlnValLeuGluValAl   370
                |||||:::    ||:||     :::
Db    527  GCACCACCAGTGACAGGAGGGGCTGCTGCAGCTGGGCGTGCGGGAGCGGGAGGC   586

Qy    370  aLeuCysSerGlnAlaAlaLeuGln----------------AlaGlnGl   381
                ||||   |||||||                          :::
Db                                                          1562
```

Db 587 CCTCTCCGAGACCCCAAGCTCAGCCTCATGCCGTGGTTCCACGGGAGAGATCTCGGGCCA   646
Qy 381 nGluLeuGlnThrLysLeuGluHisLeuGlyProGlyGluProProValLeule 401
             ||| :::|| |||
Db 647 GGAGGCTGTCCAG----------CAGCTGCAGCCTCCCGAGATGGCGTGTTCCTGGT 694

Qy 401 uLeuGlnAspAspArgHisSerThrSerSerGluGlnGluArgGluGlyGlyArgTh 421
             : :::|| |||
Db 695 GCGGGAGTTCCGGCGCCAC----------CCCGGGACTACGT 727

Qy 421 rProThrLeuGluIleLeuLysSerHisIleSerGlyIlePheArgProLysPheSerAs 441
             :::   :: |||
Db 728 CCTGTGCTGAGCTTGGCCGCGACGTCATCCAC--------- 761

Qy 441 nLeuTyrArg--LeuGluGlyGluGlyPheProSerIle-----ProLeuIleAs 458
                  ||| :::||| :::||
Db 762 ----TACCGCGTCTGCACCGCAGCCACCTCACAATCGATGAGGCCGTGTTCTTCTG 817

Qy 458 pHisLeuSerThrGlnProLeuThrLysLysSerGlyValValLeuHisArgAl 478
                :::|| ::   :::
Db 818 CAACCTCATGGACATGGTGGAGCATTACGACAAGGACAAGGGGCTATCTGCACCAAGCT 877

Qy 478 aVal---ProLysAspLys----- 483
             ||| :::
Db 878 GGTGAGACCAAAGCGAAACACGGAACCAAGTCGGCGGAGGAGCTGGCCAGGGCGGG 937

Qy 484 -TrpValLeuAsnHisGluAspLeuValLeuGlyLeuGlnIleLeuGlyLeuArgGlyAsnPheGl 503
              |||:|||| ||||||
Db 938 CTGGTTACTGACCTGCAGCATTTGACATTGGAGCACAGATCGGGAGGGAGGAGAGTTTGG 997

Qy 503 yGluValPheSerGlyArgLeuArgAlaAlaAspAsnThrLeuValAlaValLysSerCysAr 523
             ||| || :::
Db 998 AGCTGTCCTGCAGGTGAGTACTCGGGCAAAAG-----GTGCCCGTGAAGAAT------- 1046

Qy 523 gGlyThrLeuProProAspLeuLysAlaLys---PheLeuGlyGluAlaArgIleLeuLy 542
                    ||| :::|| :::
Db 1047 -------ATCAAGTGTGATGTGACAGCCCAGGCCTTCCTGGACGAGACGGCCGTCATGAC 1099

Qy 542 sGlnTyrSerHisProAsnIleValArgLeuIleGlyValCysThrGlnLysGlnProl 562
             ::: |||
Db 1100 GAAGATGCAACACGAGAACCTGTGCGTCTCCTGGGCGGTGATCCTGCAC---CAGGGGCT 1156

Qy 562 eTyrIleValMetGluLeuValGlnGlyGlyAspPheLeuThrPheLeuArgThrGluGl 582
             |||||||||||| :::   :::
Db 1157 GTACATTGTCATGGAGCAGGTGAGCAGGGCAACCTGGTGAACTTTCTGCGGACACCCGGGG 1216

Qy 582 y---AlaArgLeuAlaLysThrLeuGlnMetValGlyAspAlaAlaAlaAlaGlyMe 601
                ||| ||| :::
Db 1217 TCGGAGCCCTCGTGAACACCGCTCAGCTTCCTGCCAGTTTTCTGCACGTGGCCGAGGCAT 1276

Qy 601 tGluTyrLeuGluSerCysCysGlyIleHisArgAspLeuAlaAlaArgAsnCysLeuVa 621
             |||||||||||||||||| :::||
Db 1277 GGAGTACCTGGAGAGCTGCTGGGCACCGGACCTGGCCGCCGACCTGGCCCAACATCCTGT 1336

Qy 621 lThrGluLysAsnValLeuLysIleSerAspPheGlyMetSerArgGluGluAlaAspGl 641
             :::|| :::
Db 1337 CTCAGAGAAGAACGTGGTGCAGGTCGACGACTTGGCCTGGCCAAAGCCGAGCGGAGAGG 1396

Qy 641 yValTyrAlaAlaSerGlyAlaGlyLeuArgGlnValLeuProValLysTrpThrAlaProGluLeul 661
             ::: |||||||
Db 1397 GCTAGACTCAAGC-----------------CGGCTGCCCGTCAAGTGACACGGGCCCCGAGGC 1441

Qy 661 aLeuAsnTyrGlyArgTyrSerGluSerAspValTrpSerPheGlyIleLeuLeuTr 681
             :::|| :::
Db 1442 TCTCAAACACGGGAGTTCACCAGCAGTCGGATGTCTGGAGTTTGGGGTGCTGCTCTG 1501

Qy 681 pGluThrPheSerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnGlnThrArgGl 701
             ::: |||||
Db 1502 GGAGGTCTTCTCATATGGACCGGCCTCGTACCCTAAAATGTCACTCAGAAAGAGGTGTCGA 1561

Qy 701 uPheValGluLysGlyTyrArgLeuProCysProProAspAlaValPheArg 721
             ||||||| :::
Db 1562 GGCCGTGGAGAGAGGTACCGCATGGAACCCCCGAGGGCGTCTCCAGCCCGTGCACGT 1621

```
Qy    335  CCCCGCTTCCTCCGAGCCTGCACCCCCTCCGTTCAGCCAGATGCCAACGAGGCG  394
                                                               
Db    335  CCCCGCTTCCTCCGAGCCTGCACCCCCTCCGTTCAGCCAGATGCCAACGAGGCG  394

Qy    291  LeuGluProGlyGlyGluLeuGlnLeuGlnLeuAsnGluLeuThrValGluSerValGlnHisThrLeu  310
              |||                                                                
Db    291  LeuGluProGlyGlyGluLeuGlnLeuGlnLeuAsnGluLeuThrValGluSerValGlnHisThrLeu  310

Qy    395  CTGGGCCCCGGCACCCAGTGTATCACCAAATGGAGCACACCCGCCCA---------  445
           |||                                                    
Db    395  CTGGGCCCCGGCACCCAGTGTATCACCAAATGGAGCACACCCGCCCA---------  445

Qy    311  ThrSerValThrAspGluLeuAlaValAlaValAlaThr-GluMetValPheArgArgGlnGluMe  330
                                                       ||||| ||||||           
Db    446  ------------------------------GCCAGGGGAGCTGGCCTTCCGCAAGGGACACGT  478

Qy    330  tValThrGlnLeuGlnGlnLeuGlnLeuLeuArgAsnGluGluGluLeuAsnThrHisProArgGluAr  350
                                                           ::                  
Db    479  ------------------TGGGAACAAGAGACTGGTACCGCGTCAA-------  526

Qy    350  gValGlnLeuLeuArgGlnGlyLysArgGlnLeuGlnLeuAlaLeuGlnGlyLeuGlnValAl  370
             :|||||                                                        ::: |||
Db    527  GCACCACCAGTGCAGAGGGGCGTGCTGGCAGCTGGGCGCTGCGGGAGACGGAGGC  586

Qy    370  aLeuCysSerGlnAlaLysLeuGln-----------------AlaGlnGl  381
           |||| |||                                         |||||
Db    587  CCTCTCCGCAGACCCCAAGCTCAGCCTCCGTGGTTCCACGGGAGATCTCGGCCCA  646

Qy    381  nGluLeuLeuGlnThrLysLeuGluHisLeuGlyProGlyGluProProValLeuLe  401
              ::     ::                                               
Db    647  -----------CAGCTGCAGCCTCCCAGGATGGCTGTTCCTGGT  694

Qy    401  uLeuGlnAspAspArgHisSerThrSerSerSerGluGlnLeuArgGluGlyArgTh  421
                                                               :::          
Db    695  GCGGGAGTCCGCGACTACGT  727

Qy    421  rProThrLeuGluIleLeuLysSerHisIleSerGlyIlePheArgProLysProPheSerAs  441
                                                                          
Db    728  CCCTGCGGTGAGCTTGGCGCGACGTCATCCAC-----------------  761

Qy    441  ------------------ProLeuLeuIleAs  458
            nLeuTyrArg---LeuGluGlyGlyPheProSerIle-----------
Db    762  ----TACCCGTGCTGCACCGACGGCCACCTCACAATCGATGAGGCCGTGTTCTTCTG  817

Qy    458  pHisLeuSerThrGlnGlnProLeuThrLysLysSerGlyValValLeuHisArgAl  478
           ::|||||||::                                           :||||||
Db    818  CAACCTCATCGACATGGTCGAGCATTACAGACAAGGGCTATCTGCACCAAGCT  877

Qy    478  aVal---ProLysAspLys-----------------  483
           GGTGAGACCAAAGCGAAACACGGACCAAGTCGGCCAGGAGAGCTGGCCAGGGCGGG  937
Db    878  GGTGAGACCAAAGCGAAACACGGACCAAGTCGGCCAGGAGAGCTGGCCAGGGCGGG  937

Qy    484  -TrpValLeuAsnHisGluAspLeuValLeuGlyGluGlnIleGlyArgGlyAsnPheGl  503
              |||   ||||| |:|||                                          
Db    938  CTGGTTACTGAACCTGCAGCATTTGACATTTGGGAGCCACAGATCGGAGAGGGAGAGTTTGG  997

Qy    503  yGluValPheSerGlyArgLeuArgAlaAspAsnThrLeuValAlaValLysSerCysAr  523
                                                                  -------
Db    998  AGCTGTCTCCAGGGGTGAGTACCTGGGGCAAAAG-----GTGGCCGTGAAGAAT----  1046

Qy    523  gGluThrLeuProProAspLeuLysAlaLys---PheLeuGluGlnAlaArgIleLeuLeuLy  542
                                              |||                            
Db    1047  ----------ATCAAGTGTGATGTGACAGCCCAGGCCTTCCTGGACGACGGCCGTCATGAC  1099

Qy    542  sGlnTyrSerHisProAsnIleValArgLeuLeuGlyValCysThrGlnGlnProIl  562
                                                                       
Db    1100  GAAGATGCAAACACGAGACAACCTGGTGCGTCTCCTGGGCGTGATCCTGCAC---CAGGGGCT  1156

Qy    562  eTyrIleValMetGluLeuValGlnGlyGlyAspPheLeuArgPheLeuArgThrGluGl  582
              |||||                                                        ||||||
Db    1157  GTACATTGTCATGGAGCTGGTGCAGGGCGGGGGACCCCGGGG  1216

Qy    582  y---AlaArgLeuArgValLysThrLeuLeuGlnMetValGlyTyrAlaAspAlaAlaGlyMe  601
                                                                             
Db    1217  TCCAGCCCTCGTGAACACCGCTCCTGCAGTTTCTGCACGTGCCGAGGGCAT  1276

Qy    601  tGluTyrLeuGluSerLysCysCysIleHisArgAspLeuAlaLeuAlaArgAsnCysLeuVa  621
                                                                          
Db    1277  GGAGTACCTGGAGAGCAAGAAGTTTGTGCACCGGGACCTGGCCCTGGCTGCCCGCAACATCCTGGT  1336
```

```
Qy    721  gLeuMetGluGlnCysTrpAlaTyrGluProGlyGlnArgProSerPheSerThrIleTy  741
              ||||||                                                      :::
Db    1622  CCTCATGAGCAGCTGCTGGGAGGCAGAGCCCGCCGGCCACCCTTCCGCAAACTGGC  1681

Qy    741  rGlnGluLeu  744
               :::||||||
Db    1682  CGAGAAGCTG  1691
```

RESULT 13

PCT-US95-05008-1

. Sequence 1, Application PC/TUS9505008

GENERAL INFORMATION:

APPLICANT: Sugen. Inc.
APPLICANT: 515 Galveston Drive
APPLICANT: Redwood City, California 94063-4720
APPLICANT: United States of America
APPLICANT: Wissenschaften E.V.
APPLICANT: Hofgarten Str. 2
APPLICANT: Munchen 80539
APPLICANT: Germany

TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine
TITLE OF INVENTION: Kinases

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/05008
FILING DATE: 24-APR-1995
CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/232,545
FILING DATE: 22-APR-1994
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-074

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)790-9090
TELEFAX: (212)869-9741
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2000 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA

PCT-US95-05008-1

Alignment Scores:

Pred. No.:
Score: 2.84e-49
Percent Similarity: 605.50
Best Local Similarity: 49.01%
Query Match: 34.33%
DB: 15.61%

Length: 2000
Matches: 173
Conservative: 74
Mismatches: 175
Indels: 82
Gaps: 17

US-10-660-763-2 (1-752) x PCT-US95-05008-1 (1-2000)

PCT-US95-05008-1

```
Qy    272  ProAspValProProCysValThrPheAspGluSerLeuLeuGlu---GlyGluPro  290
              |||||                                    ||||    ::::::      |||
```

```
Alignment Scores:
Pred. No.:                        3.55e-49              Length:        1398
Score:                            602.00               Matches:        174
Percent Similarity:               47.93%               Conservative:    69
Best Local Similarity:            34.32%               Mismatches:     164
Query Match:                      15.52%               Indels:         101
DB:                               2                    Gaps:            18

US-10-660-763-2 (1-752) x US-08-604-989A-9 (1-1398)

Qy    267  GlnTyrGlySerAlaProAspValProProCysValThrPheAspGluSerLeuLeuGlu  286
                :: :    ||    |:|:  |          |         ::|| ||::  || |
Db      5  CAACGAGGCGCTGGGCCCGGGCACCCAG-TGTATCACC----------AAATGCGAG      51

Qy    287  GluGlyGlyProLeuGluProGlyLeuGlnLeuLeuAsnGluLeuThrValGluSerVal  306
              ||  |||:||  ||| |||||||||||:|
Db     52  CACACCCCGCCCC--AAGCCAGGGGAGCTG------------------------------  78

Qy    307  GlnHisThrLeuThrSerValThrAspGluLeuAlaValAlaAlaThrGluMetValPheArg  326
            ||                                                  |||||| ||
Db     79  -----------------------------------------------------GCCTTCCGC  87

Qy    327  ArgGlnGluMetValThrGlnLeuGlnLeuGlnLeuArgAsnGluLeuGluAlaLeuGlnGly  346
            :::  |::::||:|                                   :|||
Db     88  AAGGGCGACGTGGTCACCATCCTGGAGCCC--------------TGCGAACAAGAGCTGG  135

Qy    347  ProArgGluArgValGlnLeuLeuLeuCysSerGlnAlaLysLeuGln------------  366
            |||   :::  |||||||||                           :::||||
Db    136  TACCGCGGTCAAGCACCACCACCAGTGGACACAGGAGGGGCTGCTGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGGCAGCTGGG  195
```

```
Db    195  GAGCGGGAGCCCTTCCGCAGACCCAAGCTCAGCTCATGCCGTGTTCACGGGGAAG        255

Qy    379  ---AlaGlnGluGlnLeuLeuGlnThrLysLeuGluHisGlyLeuGlyProGlyProPro   397
                 |||:   :  :                            |||
Db    256  ATCTCGGCGCCAGGAGGCTGTCCAG-----------CAGCTGCAGCCTCCCGAGGATGGG    303

Qy    398  ProValLeuLeuGlnAspAspArgHisSerSerSerGluGlnGlnArgGlu          417
            |||:: ::  |:: :::                                     ---CCC   336
Db    304  CTGTTCCTGGTGCGGGAGGTCCCGCGCCAC                               336

Qy    418  GlyGlyArgThrProThrLeuGluLeuLysSerHisIleSerGlyIlePheArgPro    437
            |||       :::              :::                            :::   381
Db    337  GGCGACTACGTCCTGTCGTGCGAGCTTTGGCCCGACGTCATCCAC                381

Qy    438  LysPheSerAsnLeuTyrArg---LeuGluGlyGluGlnPheProSerIle---Pro   454
                   ::  :                                          :::   
Db    382  ----------TACCGCGGTCGTGCCACGCGACGGCCCACCCTCACAATCGATGAGCGC    426

Qy    455  LeuLeuIleAspHisLeuLeuSerThrGlnProLeuThrLysSerGlyValVal    474
            :::  ::  |||                                            :::   486
Db    427  GTGTTCTTCTGCAACCTCATGACACATGGTGGACATTACAGCAGGACAAGGGCGCTATC   486

Qy    475  LeuHisArgAlaVal--ProLysAspLys                          483
            |||       ::                                            ---   
Db    487  TGCACCAAGCTGGTGACGATCCAAAGCCGAAACACGGGACCAAGCTCGGCCGAGGAGCTG   546

Qy    484  --------------TrpValLeuAsnHisGluAspLeuValLeuGlnIleGlyArg    499
                            ::                                      ---Pro
Db    547  GCCAGGGCGCGGTTTACTGAACCTGCAGATTTGACATTGGAGCACAGATCGGAGAG   606

Qy    500  GlyAsnPheSerGlyGluValPheSerGlyArgLeuArgAlaAspAsnThrLeuValAlaVal   519
            |||                :::                                       :::
Db    607  GGAGAGTTTGGAGCTGTCCTGCAGGGTGAGTACCTGGGCAAAG------GTGGCCGTG   660

Qy    520  LysSerCysArgGluThrLeuProProAspLeuLysAlaLys---PheLeuGlnGluAla   538
            |||                                                 :::     
Db    661  AAGAAT------------ATCAAGTGTGATGGACGGCCTTCCTGACGAGACG   708

Qy    539  ArgIleLeuLysGlnTyrSerHisProAsnIleValArgLeuIleGlyValCysThrGln   558
            ||| :::                                                 :::
Db    709  GCCGTCATGAGACGAAGATGCAACACGAGAACCTGGTCGCTCTCCTGGGGTGATCCTGAC   768
```

(Lower portion of page — continuation of alignment)

```
Qy    621  IThrGluLysAsnValLeuLysIleSerAspPheGlyMetSerArgGluValAlaAspGl   641
            |::||:|        ||:::::::  ::    ::               ||  ||
Db   1337  CTCAGAGGACCTGGTGCCAAGGTCAGCGACTTTGGCCTGGCCAAAGCCGAGGCGGAAGGG   1396

Qy    641  yValTyrAlaAlaSerGlyLeuGlyLeuArgGlnValProValLysTrpThrAlaProGluAl   661
            |:::  ::::::                                              ||
Db   1397  GCTAGACTCAAGC--------------------CGGCTGCCCGTCAAGTGGACGGCGCCCGAGGC   1441

Qy    661  aLeuAsnTyrArgGlyArgTyrSerSerGluSerAspValTrpSerPheGlyIleLeuLeuTr   681
            |||     :::::::::      ||:|||||||        |:|||||||||||||||||
Db   1442  TCTCAAACACCGGAAGTCACCAGCCAAGTCCGATGTCGGAGTTTTGGGGTGCTGCTCTG   1501

Qy    681  pGluThrPheSerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnGlnThrArgGl   701
            |||  |  :::::                  :::    :::     ::
Db   1502  GGAGGTCTTCTCATATGGACGGCGCTCCGTACCCTAAAATGTCACTGAAAGAGGTGTCGGA   1561

Qy    701  uPheValGluLysGlyGlyArgLeuProGluCysProLeuGluLysProAspAlaValPheAr   721
            |||  ||                |||
Db   1562  GGCCGTGGGAGAAGGGTACCCGCCATGGAACCCCCGAGGGCGTGTCCCCGTGCACGT   1621

Qy    721  gLeuMetGluGlnCysTrpAlaTyrGluProGlyAspArgProSerPheSerThrIleTy   741
            |||  :::          |||
Db   1622  CCTCATGAGCAGCTGCTGGGAGGCAGACCCGCCCGGCCCACCCTTCCCAAACTGGC   1681

Qy    741  rGlnGluLeu   744
            |||
Db   1682  CGAGAAGCTG   1691
```

RESULT 14
US-08-604-989A-9

; Sequence 9, Application US/08604989A
; Patent No. 5834208
GENERAL INFORMATION:
    APPLICANT: Sakano, S.
    TITLE OF INVENTION: No. 5834208el Tyrosine Kinase
    NUMBER OF SEQUENCES: 11
    CORRESPONDENCE ADDRESS:
        ADDRESSEE: Pennie & Edmonds LLP
        STREET: 1155 Avenue of the Americas
        CITY: New York
        STATE: New York
        COUNTRY: USA
        ZIP: 10036-2711
    COMPUTER READABLE FORM:
        MEDIUM TYPE: Diskette
        COMPUTER: IBM Compatible
        OPERATING SYSTEM: DOS
        SOFTWARE: FastSEQ Version 2.0
    CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/08/604,989A
        FILING DATE: February 23, 1996
        CLASSIFICATION: 435
    ATTORNEY/AGENT INFORMATION:
        NAME: Charles E. Miller
        REGISTRATION NUMBER: 24,576
        REFERENCE/DOCKET NUMBER: 1920-026
    TELECOMMUNICATION INFORMATION:
        TELEPHONE: (212) 790-9090
        TELEFAX: (212) 869-8864/9741
        TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 9:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 1398 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: double
        TOPOLOGY: linear
    MOLECULE TYPE: cDNA to mRNA
    ORIGINAL SOURCE:
        ORGANISM: human
        STRAIN: UT-7
US-08-604-989A-9

US-10-660-763-2.rni

```
US-09-949-016-5357 (1-752) x US-09-949-016-5357 (1-2572)

Qy    327  ArgGlnGluMetValThrLeuLeuGlnGlnGluLeuArgAsnGluGlu----------  343
               |||     |||      |||   ||| |||||
Db    409  CGGCAGCGCTGGGTGCTGGCCCTTAAAGAAGAAACGAGGAATAATAACAGTTTGTGCCT  468

Qy    344  AsnThrHisProArgGluArgValGlnLeuLeuGlyLysArgGlnValLeuGlnGluAla  363
                                  -----AATTTCTGATGATGGGAAGTG-GAGGTGCTGTTCTCAGCT  521
Db    469  AAATATCATCCT-------

Qy    364  LeuGlnGlyLeuGlnLeuValAlaLeuCysSerGlnAlaLysLeuGlnAlaGlnLeuGlu-  382
               |||||   |||        ::    :::    ||
Db    522  GG-AGAAGCTTGCAACAGGCTGTGCCCAATGATCCAACCAAGAATGCTTCAAAGAAGC    580

Qy    383  --------LeuLeuGlnThrLysLeuGluHisLeuGly-------------------------  392
                                     |||  ||| :::|||
Db    581  CTCTTCCTCCTACTCCTGAAGACAACAGCCACCTTTGGCAACCTGAAGAAACTGTGG    640

Qy    393  --------ProGlyGluProProValLeuLeuLeuGlnLeuGlnAsp  404
                                        :::   ||||||
Db    641  TCATTGCCTTATATGACTACCAAACCAAT-GATCCTCAGGAACTCGCACTGCGCGCCAAC  699

Qy    405  AspArgHisSer---ThrSerSerGlu-------------------GlnGluArgGlu  417
               :::        ||||||                     |||:::|||
Db    700  GAAGAGTACTGCCTGCTGGACAGTTCTGAGATTCACTGGTGGAGTTTGG  759

Qy    418  Gly-------------------------------------------------Gly  419
               |||                                               |||
Db    760  GGGTGGTACAATAAGAGTATCAGCCGAGACAAAGTCGAAAAACTCTTTTGACACAGGC  819

Qy    420  ArgThrProThrLeuGluIleLeuLysSerHisIleSerGlyIlePhe-----------  435
               :::                   :::|||
Db    820  AAAGAAGGAGCCTTCATCGTAAGGGATTCCAGGACTGCCAGGAACATACACCGTGTCTGTT  879

Qy    435  -------------------------------------------------------  435
Db    880  TTCACCAAGGCTGTTGTAAGTGAGAACAATCCCTGTATAAAGCATTATCACATCAAGGAA  939

Qy    436  --------ArgProLysPheSerAsnLeuTyrArgLeuGluGlyGlyPheProSer  452
                                    :::||
Db    940  ACAAATGACAATCCTAAG---CGATACTATGTGGCTAGAAAGTATGTTTCGATTCC  993

Qy    453  IleProLeuLeuIleAspHisAspHisLeuLeuSerThrGlnGlnProLeuThrLysSerGly  472
               |||||||:::         ::::::
Db    994  ATCCCCTTCTTTCATCCAACTAT-------------------------------- 1014

Qy    473  ValValLeuHisArgAlaValProLysAspTrpLeuValLeuAsnHisGluAspLeuVal  492
               ::: |||                    ||||||
Db    1015 -CACCAACATAATGGAGGAGGGAAATGGGTGATCGAGCCCCCTCAGAGCTCACT  1065

Qy    493  LeuGlyGlnIleGlyArgGlyAsnPheGlyGluValPheSerGlyArg---LeuArg  511
               :::          |||||||              ||||||
Db    1066 TTTGTGCAAGAGATTGGCAGTGGGCAATTTGGGGTTGGTCATCTGGCTCAAC  1125

Qy    512  AlaAspAsnThrLeuValAlaValLysSerCysArgGluThrLeuProProAspLeuLys  531
               :::|||            ::::::                      ||||||
Db    1126 AAGGACAAG---------GTGGCTATCAAAACCATTCGGGAAGGGCTATGTCAGAA----- 1173

Qy    532  AlaLysPheLeuGlnGluAlaArgIleLeuLysGlnTyrSerHisProAsnIleValArg  551
               |||||||            :::             :::|||
Db    1174 GAGGACTTCATAGAGGAGGGCTGAAGTAATGAAGAACTCTCATCCCAAACTGGTGCAG  1233

Qy    552  LeuIleGlyValCysThrGlnLysGlnProIleTyrIleValMetGluLeuValGlnGly  571
               ||||||            :::             ||||||
Db    1234 CTGTATGGGGTGTGCCTGGAGCAGGCCCCATTCGCCTGTGGTTTCATGGAGCAC  1293

Qy    572  GlyAspPheLeuThrPheLeuArgThrGluGlyAlaArgLeuArgValLysLysThrLeuLeu  591
               |||||||            ::::::              ::::::||||||
Db    1294 GGCTGCCTGTCAGATTATCTACCCACCAGCGGGGACTTTTGCTGCAGAGACCCTGCTG  1353

Qy    592  GlnMetValGlyAspAlaAlaAlaGlyMetGluTyrLeuGluSerLysCysIleHis  611
               |||      |||||||||
Db    592
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Qy    559  LysGlnProIleTyrIleValMetGluLeuValGlnGlyGlyAspPheLeuThrPheLeu  578
               |||                    :::              ||||||
Db    769  ---CAGGGGCTGTACATTGTCATGGAGCACGTGAGCAAGGGCAACCTGGTGAACTTTCTG  825

Qy    579  ArgThrGluGly---AlaArgLeuArgValLysThrLeuValGlnMetValGlyAspAla  597
               |||          :::   ::               ||||||
Db    826  CGGACCGAGGGTCGAGCCCTCGTGAACACGCCGTCTACCGCGCCTGTTCTCTGCACGTG  885

Qy    598  AlaAlaGlyMetGluTyrLeuGlnSerLysCysIleHisArgAspLeuAlaAlaArg  617
               |||||||              :::||||||||||||||||
Db    886  GCCGAGGGCCATGGAGGAGTACCTGGAGGAGCAAGAGAGCTTGTGCACCGGACCTGGCCGCCGC  945

Qy    618  AsnCysLeuValThrGluLysAsnValLeuLysIleSerAspPheGlyMetSerArgGlu  637
               |||||||              ::::::||||||||||||
Db    946  AACATCTGGTCTCAGAGGACCTGGTGGCCAAGGTCAGCGACTTTGGCCTGGCCAAAGCC  1005

Qy    638  GluAlaAspProlValTyrAlaAlaSerGlyGlyLeuArgGlnValProValLysTrpThr  657
               ||| :::       ::::::              ||||||
Db    1006 GAGGCCGAAGGGCTAGACTCAAGC----------CGGTGCCCGTCAAGTGGACG  1050

Qy    658  AlaProGluAlaLeuAsnTyrGlyTyrSerSerGluSerAspValProSerPheGly  677
               ||| :::       ||||||              ::::::||||||
Db    1051 GCGCCCAAACACGGGAAGTTCACCAGCAAGTCGGATTGTCTGGAGTTTTGGG  1110

Qy    678  IleLeuLeuTrpGluThrPheSerLeuGlyAlaSerProTyrProAsnLeuSerAsnGln  697
               :::||||||              ::::::||||||
Db    1111 GTGTGCTTCTCTGGGAGTCTTCATATGGACGGGCTACCCTAAAATGTCACTGAAA  1170

Qy    698  GlnThrArgGluValPheGluValGlyLysGlyLeuProCysProGluLeuCysProGluAsp  717
               :::||||||              ::::::||||||
Db    1171 GAGTGTGCGGAGCCGTGTGGAGAAGGGGTACCCGCATGGAACCCCGAGGGGCTGTTCCAGGC  1230

Qy    718  AlaValPheArgLeuMetGluGlnCysTrpAlaTyrGlnProGlyGlnArgProSerPhe  737
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Db    1231 CCCGTGCACGTCCTCATGAGCAGCGCTGCTGGGAGGCAGCAGCCCGCCGCCACCCTTC  1290

Qy    738  SerThrIleTyrGlnGluLeu  744
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Db    1291 CGCAAACTGGCCGAGAGCTG  1311
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RESULT 15
US-09-949-016-5357

; Sequence 5357, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5357
; LENGTH: 2572
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5357

Alignment Scores:
Pred. No.:   2572
Score: 2.05e-48   Matches: 165
                   598.50   Conservative: 68
Percent Similarity: 46.98%   Mismatches: 163
Percent Local Similarity: 33.27% Indels: 103
Best Local Similarity: 15.43%   Gaps: 14
Query Match: 4
DB:

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Db    1354  GGCATGTGTCTGGATGTGTGTGAGGGCATGGCCTACCTGGAAGAGAGGCATGTGTCATCCAC  1413

Qy     612  ArgAspLeuAlaAlaArgAsnCysLeuValThrGluLysAsnValLeuLysIleSerAsp  631
                  |||||||||||||||||||   :::||||:||||:||::||||
Db    1414  AGAGACTTGGCTGCCAGAAATTGTTTGGTGGGAGAAAACCAAGTCATCAAGGTGTCTGAC  1473

Qy     632  PheGlyMetSerArgGluGluAlaAspGlyValTyrAlaAlaSerGlyValGlyLeuArgGln  651
                  |||||:|||:||              :::||||||     :::
Db    1474  TTTGGGATGACAAGGTCGTTCTGGATGATCAGTACACCAGTTCCACAGGCACCAAA---  1530

Qy     652  ValProValLysTrpThrAlaProGluAlaLeuAsnTyrGlyArgTyrSerSerGluSer  671
                     :::||||||||||||           :::::   ||||||||:||::||
Db    1531  TTCCCGGTGAAGTGGGCATCCCCAGAGGTTTTCTCTTTCAGTGCGCTATAGCAGCAAGTCC  1590

Qy     672  AspValTrpSerPheGlyIleLeuLeuTrpGluThrPheGluSerLeuGlyAlaSerProTyr  691
                  |||||:|||:||:::||||     ||||||     ||||||
Db    1591  GATGTGTGGTCATTCGGTGTGCTGATGTGGGAAGTTTTCAGTGAAGGCAAAATCCCGTAT  1650

Qy     692  ProAsnLeuSerAsnGlnGlnThrArgGluPheValGluLysGlyGlyArgLeuProCys  711
                  |||                   :::|||||||||||||||||||||||
Db    1651  GAAAACCGAAGCAACTCAGAGGTGGTGGAAGACATCAGTACCGGATTTCGGTTGTACAAG  1710

Qy     712  ProGluLeuCysProAspAspAlaValPheArgLeuMetGluGlnCysTrpAlaTyrGluPro  731
                  |||   |||                |||:::::::::::||
Db    1711  CCCCGGCTGGCCTCCACACACGTCTACCAGATTATGAATCACTGCTGGAAAGAGAGACCA  1770

Qy     732  GlyGlnArgProSerPheSerThrIleTyrGlnGluLeuGlnSerIle  747
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Db    1771  GAAGATCGGCCAGCCTTCTCCAGACTGCCTGCCTCAACTGGCTGAAATT  1818
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Search completed: August 10, 2005, 10:21:54
Job time : 520 secs

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                    GenCore version 5.1.6
          Copyright (c) 1993 - 2005  Compugen Ltd.

OM protein - protein search, using sw model

Run on:     August  4, 2005, 13:47:46 ; Search time 159 Seconds
                               (without alignments)
                            1846.410 Million cell updates/sec

Title:       US-10-660-763-2
Perfect score: 3879
Sequence:    1 MGFSSELCSPQGHGVLQQMQ.........QRPSFSTIYQELQSIRKRHR 752

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:    1752860 seqs, 39039?842 residues

Total number of hits satisfying chosen parameters:     1752860

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     Published_Applications_AA:*
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    12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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    19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep:*
    20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
    21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
    22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	3879	100.0	752	13	US-10-003-295-2	Sequence 2, Appli
2	3879	100.0	752	15	US-10-660-763-2	Sequence 2, Appli
3	3834	98.8	822	13	US-10-003-295-4	Sequence 4, Appli
4	3834	98.8	822	15	US-10-660-763-4	Sequence 4, Appli
5	3620	93.3	820	17	US-10-732-923-13687	Sequence 13687, A
6	3620	93.3	820	17	US-10-732-923-13688	Sequence 13688, A
7	2635	67.9	824	17	US-10-732-923-13665	Sequence 13665, A
8	2571	66.3	898	17	US-10-732-923-13481	Sequence 13481, A
9	2570	66.3	873	17	US-10-732-923-13482	Sequence 13482, A
10	2561	66.0	873	17	US-10-732-923-13480	Sequence 13480, A
11	2561	66.0	1182	17	US-10-732-923-13479	Sequence 13479, A
12	2479	63.9	2479	17	US-10-732-923-13452	Sequence 13452, A
13	2479	63.9	2479	17	US-10-732-923-13461	Sequence 13461, A
14	1980	51.0	1980	17	US-10-732-923-13454	Sequence 13454, A
15	1942.5	50.1	477	17	US-10-732-923-13451	Sequence 13451, A
16	1853	47.8	774	9	US-09-886-319A-64	Sequence 64, Appl
17	1853	47.8	822	14	US-10-376-566-64	Sequence 64, Appl
18	1850	47.7	822	17	US-10-732-923-13685	Sequence 13685, A
19	1829.5	47.2	823	9	US-09-886-319A-63	Sequence 63, Appl
20	1829.5	47.2	823	14	US-10-376-566-63	Sequence 63, Appl
21	1534	39.5	823	18	US-10-941-635-69	Sequence 69, Appl
22	1528	39.4	292	16	US-10-664-421-69	Sequence 69, Appl
23	1450	37.4	533	17	US-10-732-923-13473	Sequence 13473, A
24	1450	37.4	634	17	US-10-732-923-13471	Sequence 13471, A
25	1444	37.2	275	16	US-10-763-418-38	Sequence 38, Appl
26	1332.5	34.4	879	17	US-10-732-923-13561	Sequence 13561, A
27	1135	29.3	893	17	US-10-732-923-13523	Sequence 13523, A
28	928.5	23.9	378	15	US-10-732-923-13509	Sequence 13509, A
29	911	23.5	251	15	US-10-464-805-30	Sequence 30, Appl
30	899	23.2	251	8	US-08-987-689A-30	Sequence 30, Appl
31	899	23.2	251	14	US-10-292-524-30	Sequence 30, Appl
32	669.5	17.3	257	10	US-09-823-187-46	Sequence 46, Appl
33	668.5	17.2	257	10	US-09-863-776-42	Sequence 42, Appl
34	661	17.0	258	11	US-09-964-956-75	Sequence 75, Appl
35	661	17.0	258	15	US-10-042-865-100	Sequence 100, App
36	661	17.0	258	15	US-10-072-012-801	Sequence 801, App
37	661	17.0	258	15	US-10-072-012-858	Sequence 858, App
38	657	16.9	256	10	US-09-976-782-40	Sequence 40, Appl
39	657	16.9	257	10	US-09-976-782-29	Sequence 29, Appl
40	657	16.9	657	15	US-10-087-684-100	Sequence 100, App
41	657	16.9	257	15	US-10-218-779-100	Sequence 100, App
42	656	16.9	254	15	US-10-052-648A-43	Sequence 43, Appl
43	655	16.9	2029	15	US-10-746-545-33	Sequence 33, Appl
44	642	16.6	250	15	US-10-074-978A-153	Sequence 153, App
45	642	16.6	280	9	US-09-515-806-15	Sequence 15, Appl

ALIGNMENTS

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Query Match      100.0%;  Score 3879; DB 13; Length 752;
Best Local Similarity   100.0%;  Pred. No. 3.5e-223;
Matches  752;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 MGFSSELCSPQGHGVLQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHMSLQDSGGQS 60
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Db    1 MGFSSELCSPQGHGVLQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHMSLQDSGGQS 60

Qy   61 RAISPDSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLLSLLIREROQLRKTYSEQW 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RAISPDSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLLSLLIREROQLRKTYSEQW 120

Qy  121 QQLQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEASKDKDRDKAKDKVRSLWKLF 180
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Db 121 QQLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEASKDKDRDKAKDKYVRSLWKLF 180
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Qy 121 QQLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEASKDKDRDKAKDKYVRSLWKLF 180

Db 181 AHHNRYVLGVRAAQLHHQHHQLLLPGLLRSLQDLHEEMACILKEILQEYLEISSLVQDE 240
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Qy 181 AHHNRYVLGVRAAQLHHQHHQLLLPGLLRSLQDLHEEMACILKEILQEYLEISSLVQDE 240

Db 241 VVAIHREMAAAAARIQPEAEYQGFLRQYGSAPDVPPCVTFDESLLEEGEPLEPGELQLNE 300
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Qy 241 VVAIHREMAAAAARIQPEAEYQGFLRQYGSAPDVPPCVTFDESLLEEGEPLEPGELQLNE 300

Db 301 LTVESVQHTLTSVTDELAVATEMVFRRQEMVTQLQQELRNEEENTHPRERVQLLGKRQVL 360
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         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy 301 LTVESVQHTLTSVTDELAVATEMVFRRQEMVTQLQQELRNEEENTHPRERVQLLGKRQVL 360

Db 361 QEALQGLQVALCSQAKLQAQQELLQTKLEHLGPGEPPVLLLQDDRHSTSSSEQEREGGR 420
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         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy 361 QEALQGLQVALCSQAKLQAQQELLQTKLEHLGPGEPPVLLLQDDRHSTSSSEQEREGGR 420

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Qy 421 TPTLEILKSHISGIFRPKFSNLYRLEGEGFPSIPLLIDHLLSTQQPLTKKSGVVLHRAVP 480

Db 481 KDKWVLNHEDLVLGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETLPPDLKAKFLQEARI 540
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Db 661 ALNYGRYSSESDVWSFGILLWETFSLGASPYPNLSNQQTREFVEKGGRLPCPELCPDAVF 720
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Db 721 RLMEQCWAYEPGQRPSFSTIYQELQSIRKRHR 752
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Qy 721 RLMEQCWAYEPGQRPSFSTIYQELQSIRKRHR 752

Query Match   100.0%; Score 3879; DB 15; Length 752;
Best Local Similarity   100.0%; Pred. No. 3.5e-223;
Matches 752; Conservative   0; Mismatches 0; Indels 0; Gaps   0;

Qy   1 MGFSSELCSPQGHGVLQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHMSLQDSGGQS 60
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Db 61 RAISPDSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKTYSEQW 120
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Db 241 VVAIHREMAAAAARIQPEAEYQGFLRQYGSAPDVPPCVTFDESLLEEGEPLEPGELQLNE 300

Qy 301 LTVESVQHTLTSVTDELAVATEMVFRRQEMVTQLQQELRNEEENTHPRERVQLLGKRQVL 360
Db 301 LTVESVQHTLTSVTDELAVATEMVFRRQEMVTQLQQELRNEEENTHPRERVQLLGKRQVL 360

Qy 361 QEALQGLQVALCSQAKLQAQQELLQTKLEHLGPGEPPVLLLQDDRHSTSSSEQEREGGR 420
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Qy 421 TPTLEILKSHISGIFRPKFSNLYRLEGEGFPSIPLLIDHLLSTQQPLTKKSGVVLHRAVP 480
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Qy 481 KDKWVLNHEDLVLGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETLPPDLKAKFLQEARI 540
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Qy 541 LKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLTFLRTEGARLRVKTLLQMVGDAAAG 600
Db 541 LKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLTFLRTEGARLRVKTLLQMVGDAAAG 600

Qy 601 MEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREEADGVYAASGGLRQVPVKWTAPE 660
Db 601 MEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREEADGVYAASGGLRQVPVKWTAPE 660

Qy 661 ALNYGRYSSESDVWSFGILLWETFSLGASPYPNLSNQQTREFVEKGGRLPCPELCPDAVF 720
Db 661 ALNYGRYSSESDVWSFGILLWETFSLGASPYPNLSNQQTREFVEKGGRLPCPELCPDAVF 720

Qy 721 RLMEQCWAYEPGQRPSFSTIYQELQSIRKRHR 752
Db 721 RLMEQCWAYEPGQRPSFSTIYQELQSIRKRHR 752

Query Match   98.8%; Score 3834; DB 13; Length 822;
Best Local Similarity   91.5%; Pred. No. 1.9e-220;
Matches 752; Conservative   0; Mismatches 0; Indels 70; Gaps   1;

Qy   1 MGFSSELCSPQGHGVLQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHMSLQDSGGQS 60

Left column

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  RAISPDSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKTYSEQW 120

Qy   121  QQLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEASKDKDRDKAKDKYVRSLWKLF 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  QQLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEASKDKDRDKAKDKYVRSLWKLF 180

Qy   181  AHHNRYVLGVRAAQLHQHHHQLLLPGLLRSLQDLHEEMACILKEILQEYLEISSLVQDE  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  AHHNRYVLGVRAAQLHQHHHQLLLPGLLRSLQDLHEEMACILKEILQEYLEISSLVQDE  240

Qy   241  VVAIHREMAAAAARIQPEAEYQGFLRQYGSAPDVPPCVTFDESLLEEGEPLEPGELQLNE 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  VVAIHREMAAAAARIQPEAEYQGFLRQYGSAPDVPPCVTFDESLLEEGEPLEPGELQLNE 300

Qy   301  LTVESVQHTLTSVTDELAVATEMVFRRQEMVTQLQQELRNEEENTHPRERVQLLGKRQVL 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  LTVESVQHTLTSVTDELAVATEMVFRRQEMVTQLQQELRNEEENTHPRERVQLLGKRQVL 360

Qy   361  QEALQGLQVALCSQAKLQAQQELLQTKLEHLGPGEPPPVLLQDDRHSTSSSEQEREGGR  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  QEALQGLQVALCSQAKLQAQQELLQTKLEHLGPGEPPPVLLQDDRHSTSSSEQEREGGR  420

Qy   421  TPTLEILKSHISGIFRPKFS----------------------------------------440
          ||||||||||||||||||||
Db   421  TPTLEILKSHISGIFRPKFSLPPPLQLIPEVQKPLHEQLWYHGAIPRAEVAELLVHSGDF 480

Qy   441  ------------------NLYRLEGEGFPSIPLLIDHLLSTQQPLTKK             470
                            ||||||||||||||||||||||||
Db   481  LVRESQGKQEYVLSVLWDGLPRHFIIQSLDNLYRLEGEGFPSIPLLIDHLLSTQQPLTKK 540

Qy   471  SGVVLHRAVPKDKWVLNHEDLVLGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETLPPDL 530
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  SGVVLHRAVPKDKWVLNHEDLVLGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETLPPDL 600

Qy   531  KAKFLQEARILKQYSHPNIVRLLGVCTQKQPIYIVMELVQGGDFLTFLRTEGARLRVKTL 590
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  KAKFLQEARILKQYSHPNIVRLLGVCTQKQPIYIVMELVQGGDFLTFLRTEGARLRVKTL 660

Qy   591  LQMVGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREEADGVYAASGGLR 650
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  LQMVGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREEADGVYAASGGLR 720

Qy   651  QVPVKWTAPEALNYGRYSSESDVWSFGILLWETFSLGASPYPNLSNQQTREFVEKGGRLP 710
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  QVPVKWTAPEALNYGRYSSESDVWSFGILLWETFSLGASPYPNLSNQQTREFVEKGGRLP 780

Qy   711  CPELCPDAVFRLMEQCWAYEPGQRPSFSTIYQELQSIRKRHR 752
          ||||||||||||||||||||||||||||||||||||||||||
Db   781  CPELCPDAVFRLMEQCWAYEPGQRPSFSTIYQELQSIRKRHR 822
```

Right column

```
US-10-660-763-4

Query Match       98.8%;
Best Local Similarity    91.5%;    Pred. No. 1.9e-220;
Matches  752;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   1;
                                                                   Score 3834; DB 15; Length 822;

Qy     1  MGFSSELCSPQGHGVLQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHMSLQDSGGQS  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  MGFSSELCSPQGHGVLQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHMSLQDSGGQS  60

Qy    61  RAISPDSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKTYSEQW 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  RAISPDSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKTYSEQW 120

Qy   121  QQLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEASKDKDRDKAKDKYVRSLWKLF 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  QQLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEASKDKDRDKAKDKYVRSLWKLF 180

Qy   181  AHHNRYVLGVRAAQLHQHHHQLLLPGLLRSLQDLHEEMACILKEILQEYLEISSLVQDE  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  AHHNRYVLGVRAAQLHQHHHQLLLPGLLRSLQDLHEEMACILKEILQEYLEISSLVQDE  240

Qy   241  VVAIHREMAAAAARIQPEAEYQGFLRQYGSAPDVPPCVTFDESLLEEGEPLEPGELQLNE 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  VVAIHREMAAAAARIQPEAEYQGFLRQYGSAPDVPPCVTFDESLLEEGEPLEPGELQLNE 300

Qy   301  LTVESVQHTLTSVTDELAVATEMVFRRQEMVTQLQQELRNEEENTHPRERVQLLGKRQVL 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  LTVESVQHTLTSVTDELAVATEMVFRRQEMVTQLQQELRNEEENTHPRERVQLLGKRQVL 360

Qy   361  QEALQGLQVALCSQAKLQAQQELLQTKLEHLGPGEPPPVLLQDDRHSTSSSEQEREGGR  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  QEALQGLQVALCSQAKLQAQQELLQTKLEHLGPGEPPPVLLQDDRHSTSSSEQEREGGR  420

Qy   421  TPTLEILKSHISGIFRPKFS----------------------------------------440
          ||||||||||||||||||||
Db   421  TPTLEILKSHISGIFRPKFSLPPPLQLIPEVQKPLHEQLWYHGAIPRAEVAELLVHSGDF 480

Qy   441  ------------------NLYRLEGEGFPSIPLLIDHLLSTQQPLTKK             470
                            ||||||||||||||||||||||||
Db   481  LVRESQGKQEYVLSVLWDGLPRHFIIQSLDNLYRLEGEGFPSIPLLIDHLLSTQQPLTKK 540

Qy   471  SGVVLHRAVPKDKWVLNHEDLVLGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETLPPDL 530
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  SGVVLHRAVPKDKWVLNHEDLVLGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETLPPDL 600

Qy   531  KAKFLQEARILKQYSHPNIVRLLGVCTQKQPIYIVMELVQGGDFLTFLRTEGARLRVKTL 590
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  KAKFLQEARILKQYSHPNIVRLLGVCTQKQPIYIVMELVQGGDFLTFLRTEGARLRVKTL 660

Qy   591  LQMVGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREEADGVYAASGGLR 650
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  LQMVGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREEADGVYAASGGLR 720

Qy   651  QVPVKWTAPEALNYGRYSSESDVWSFGILLWETFSLGASPYPNLSNQQTREFVEKGGRLP 710
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  QVPVKWTAPEALNYGRYSSESDVWSFGILLWETFSLGASPYPNLSNQQTREFVEKGGRLP 780

Qy   711  CPELCPDAVFRLMEQCWAYEPGQRPSFSTIYQELQSIRKRHR 752
          ||||||||||||||||||||||||||||||||||||||||||
Db   781  CPELCPDAVFRLMEQCWAYEPGQRPSFSTIYQELQSIRKRHR 822
```

```
Query Match           93.3%;   Score 3620;   DB 17;   Length 820;
Best Local Similarity 85.8%;   Pred. No. 1.1e-207;
Matches 705;  Conservative 21;  Mismatches 24;  Indels 72;  Gaps 2;

Qy    1  MGFSSELCSPQGHGVLQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHMSLQDSGGQS   60
            |||||||||||||| :||||||||||||||||||||||||||||||||||||||
Db    1  MGFSSELCSPQGHGAVQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHMSLQDGGG--   58

Qy   61  RAISPDSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKTYSEQW  120
Db   59  RGTGPYSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLGLLIRERQQLRKTYSEQW  118

Qy  121  QQLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEASKDKDRDKAKDKYVRSLWKLF  180
Db  119  QQLQQELTKTHNQDIEKLKSQYRALARDSAQARRKYQEASKDKDRDKAKDKYVRSLWKLF  178

Qy  181  AHHNRYVLGVRAAQLHHQHHQLLPGLLRSLQDLHEEMACILKEILQEYLEISSLVQDE    240
Db  179  AHHNRYVLGVRAAQLHHHHHQLMLPGLLQSLQDLHQEMACILKEILQEYLEISSLVQDE    238

Qy  241  VVAIHREMAAAAARIQPEAEYQGFLRQYGSAPDVPPCVTFDESLLEEGEPLEPGELQLNE  300
Db  239  VVAIHLEMAAAVARIQPEAEYQGFLRQYGSTPDVPPCVTFDESLLEEGEPLEPGELQLNE  298

Qy  301  LTVESVQHTLTSVTDELAVATEMVFRRQEMVTQLQQELRNEEENTHPRERVQLLGKRQVL  360
Db  299  LTVESVQHTLTSVTDELTVATQTVLSRQEAVAQLQRELQNEEQNTHPRERVQLLAKKQVL  358

Qy  361  QEALQGLQVALCSQAKLQAQOELLQTKLEHGPGEPPPVVLLQDDRHSTSSSEQEREGGR   420
Db  359  QEALQALQVALCSQAKLQAKLQAQRELLQAKLEQLGPGEPGPGPPVVLLQDDRHSTSSSEQEREGGR  418

Qy  421  TPTLEILKSHISGIFRPKFS                                         440
Db  419  TPTLEILKSHISGIFRPKFSLPPPLQLVPEVQKPLHEQLWYHGALPRAEVAELLTHSGDF  478

Qy  441  ----------------------------NLYRLEGEGFPSIPLLIDHLLSTQQPLTKK   470
Db  479  LVRESOGKQEYVLSVLWDGQPRHFIIESADNLYRLEGDGFASIPLLVDHLLRSQQPLTKK  538

Qy  471  SGVVLHRAVPKDKWVLNHEDLVLGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETLPPDL  530
Db  539  SGIVLNRAVPKDKWVLNHEDLVLGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETLPPDI  598

Qy  531  KAKFLQEARILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLTFLRTEGARLRVKTL  590
Db  599  KAKFLQEAKILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLTFLRTEGARLRMKTL  658

Qy  591  LQMVGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREEADGVYAASGGLR  650
Db  659  LQMVGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREEADGIYAASGGLR  718

Qy  651  QVPVKWTAPEALNYGRYSSESDVWSFGILLWETFSLGASPYPNLSNQQTREFVEKGGRLP  710
Db  719  QVPVKWTAPEALNYGRYSSESDVWSFGILLWETFSLGASPYPNLSNQQTREFVEKGGRLP  778

Qy  711  CPELCPDAVFRLMEQCWAYEPGQRPSFSTIYQELQSIRKRHR                   752
```

```
Query Match           93.3%;   Score 3620;   DB 17;   Length 820;
Best Local Similarity 85.8%;   Pred. No. 1.1e-207;
Matches 705;  Conservative 21;  Mismatches 24;  Indels 72;  Gaps 2;

Qy    1  MGFSSELCSPQGHGVLQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHMSLQDSGGQS   60
            |||||||||||||| :||||||||||||||||||||||||||||||||||||||
Db    1  MGFSSELCSPQGHGAVQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHMSLQDGGG--   58

Qy   61  RAISPDSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKTYSEQW  120
Db   59  RGTGPYSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLGLLIRERQQLRKTYSEQW  118

Qy  121  QQLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEASKDKDRDKAKDKYVRSLWKLF  180
Db  119  QQLQQELTKTHNQDIEKLKSQYRALARDSAQARRKYQEASKDKDRDKAKDKYVRSLWKLF  178

Qy  181  AHHNRYVLGVRAAQLHHQHHQLLPGLLRSLQDLHEEMACILKEILQEYLEISSLVQDE    240
Db  179  AHHNRYVLGVRAAQLHHHHHQLMLPGLLQSLQDLHQEMACILKEILQEYLEISSLVQDE    238

Qy  241  VVAIHREMAAAAARIQPEAEYQGFLRQYGSAPDVPPCVTFDESLLEEGEPLEPGELQLNE  300
Db  239  VVAIHLEMAAAVARIQPEAEYQGFLRQYGSTPDVPPCVTFDESLLEEGEPLEPGELQLNE  298

Qy  301  LTVESVQHTLTSVTDELAVATEMVFRRQEMVTQLQQELRNEEENTHPRERVQLLGKRQVL  360
Db  299  LTVESVQHTLTSVTDELTVATQTVLSRQEAVAQLQRELQNEEQNTHPRERVQLLAKKQVL  358

Qy  361  QEALQGLQVALCSQAKLQAQOELLQTKLEHGPGEPPPVVLLQDDRHSTSSSEQEREGGR   420
Db  359  QEALQALQVALCSQAKLQAKLQAQRELLQAKLEQLGPGEPGPGPPVVLLQDDRHSTSSSEQEREGGR  418

Qy  421  TPTLEILKSHISGIFRPKFS                                         440
Db  419  TPTLEILKSHISGIFRPKFSLPPPLQLVPEVQKPLHEQLWYHGALPRAEVAELLTHSGDF  478

Qy  441  ----------------------------NLYRLEGEGFPSIPLLIDHLLSTQQPLTKK   470
Db  479  LVRESOGKQEYVLSVLWDGQPRHFIIESADNLYRLEGDGFASIPLLVDHLLRSQQPLTKK  538

Qy  471  SGVVLHRAVPKDKWVLNHEDLVLGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETLPPDL  530
Db  539  SGIVLNRAVPKDKWVLNHEDLVLGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETLPPDI  598

Qy  531  KAKFLQEARILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLTFLRTEGARLRVKTL  590
Db  599  KAKFLQEAKILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLTFLRTEGARLRMKTL  658

Qy  591  LQMVGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREEADGVYAASGGLR  650
Db  659  LQMVGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREEADGIYAASGGLR  718

Qy  651  QVPVKWTAPEALNYGRYSSESDVWSFGILLWETFSLGASPYPNLSNQQTREFVEKGGRLP  710
Db  719  QVPVKWTAPEALNYGRYSSESDVWSFGILLWETFSLGASPYPNLSNQQTREFVEKGGRLP  778

Qy  711  CPELCPDAVFRLMEQCWAYEPGQRPSFSTIYQELQSIRKRHR                   752
Db  779  CPELCPDAVFRLMEQCWAYEPGQRPSFSAIYQELQSIRKRHR                   820
```

RESULT 6
US-10-732-923-13688
; Sequence 13688, Application US/10732923

```
Db   779  CPELCPDAVFRLMEQCWAYEPGQRPSFSAIYQELQSIRKRHR  820
          ||||||||||||||||||  ||||||||| ||||||||||||

RESULT 7
US-10-732-923-13665
; Sequence 13665, Application US/10732923
; Publication No. US2005010879lA1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
  SEQ ID NO 13665
; LENGTH: 824
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-732-923-13665

Query Match             67.9%;  Score 2635;  DB 17;  Length 824;
Best Local Similarity   62.7%;  Pred. No. 6.9e-149;
Matches   518;  Conservative   99;  Mismatches 133;  Indels  76;  Gaps  3;

Qy     1  MGFSSELCSPQGHGVLQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHM----SLQDS   56
          |||| ||| |||| || | ||||||||| |||||| ||||||||||| ||||    ||
Db     1  MGFGPELWCPKGHSELLRLQDSELRLLELMKKWMSQRAKSDREYAGMLHHMFSQLEKQEG   60

Qy    57  GGQSRAISPDSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKTY  116
          ||   | : | :| :|| : ||||| |||||:|||| |: ||| |||:|||:||||||::
Db    61  LGHLRATDHSSQIGESWWVLASQTETLSQTLRRHAEELAAGPLAKLSILIRDKQQLRKAF  120

Qy   117  SEQWQQLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEASKDKDRDKAKDKYVRSL  176
          ||||||| ||  :| || :||||:||| |:||| ||||||||||||| | |:||:|||||
Db   121  SEQWQQLSQEYARTTQQEMEKLKAQYRSLVRDSTQAKRKYQEASKDKEREKAKEKYVRSL  180

Qy   177  WKLFAHHNRYVLGVRAAQLHQHHHQLLPGLLRSLQDLHEEMACILKEILQEYLEISSL   236
          |||:| || ||| |||| || ::| : || | ||:: || | :|||||:||| :|||
Db   181  WKLYALHNQYVLAVRAAALHHHHHYQRALPLTHESLYSLQQEMVLVKEILGEYCISSL   240

Qy   237  VQDEVVAIHREMAAAARIQPEAEYQGFLRQYGSAPDVPPCVTFDESLLEEGEPLEPGEL   296
          |: || ||: || :|:: ||:| |  ||||  ::|| || |||||||||| | |||||
Db   241  VQBDVLAIHQEVAHAVEMIDPATEYSSFVQCHRYDSSEVPPAVTFDESLLEEAESLEPGEL  300

Qy   297  QLNELTVESVQHTLTSVTDELAVATEMVFRRQEMVTQLQQELRNEENTHPRERVQLLGK   356
          |||||| |||||:|||  :|  |  :: :|| |:| |||:|||: || | |:||:|||
Db   301  QLNELTIESVQHSLTSIEEELLASREAVSSKEQRVWELQVELRGEELALSPGERVHLLGK   360

Qy   357  RQVLQEALQGLQVALCSQAKLQAQQELLQTKLEHLGPGEPPPVLLQDDRHSTSSSEQER   416
          || | || : ||:||| |||||||::::  |||:|| ::|||| : :|:: :| : |||
Db   361  RQGLQEAQQQLQGLVCAQAKLQAQRDMLANKLAELGSEEPPPALPLQEDRQSVCSTDQER   420

Qy   417  EGGRTPTLEILKSHISGIFRPKFS----------                           440
          :| |  :| |:|:|||||| |:||
Db   421  SG--VTALETIKNHISGIFSPRFSLPPPVLIPEVQKPLCQQAWYHGAIPRSEVQELLKC   478

Qy   441  ----------------------NLYRLEGEGFPSIPLLIDHLLSTQQP              466
                                |||||||:| |:|||||||||| ||||
Db   479  SGDFLVRESQGKQEYVLSVLWDGQPRHFIIQAADNLYRLEGDGFPTIPLLIDHLLQSQQP  538

Qy   467  LTKKSGVVLHRAVPDKWVLNHEDLVLGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETL   526
          :|:|||:||:|||:|||||||||:||||:|||||||||||||||||||| |||||||||
Db   539  ITRKSGIVLTRAVLKDKWVLNHEDVLLGERIGRGNFGEVFSGRLRADNTPVAVKSCRETL  598

Qy   527  PPDLKAKFLQEARILKQYSHPNIVRLIGVCTQKQPIYIVMEIVQGGDFLTFLRTEGARLR  586
          || ||||||||||||||| ||||||||||||||||||||||:||||||| |||:||  |:
Db   599  PPELKAKFLQEARILKQYNHPNIVRLIGVCTQKQPIYIVMELVQGGDFLSFLRSEGPHLK  658

Qy   587  VKTLLQMVGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREEADGVYAAS  646
          :|  ::: |:||||||||||| ||||||||||||||||| ||||||||||: | || : :
Db   659  MKELIKMENAAAGMEYLESKHCIHRDLAARNCLVTEKNTLKISDFGMSRQBEDGVVAST   718

Qy   647  GGLRQVPVKWTAPEALNYGRYSSESDVWSFGILLWETFSLGASPYPNLSNQQTREFVEKG  706
          || ::| ||||||||||||||||||||||||||||| |||||:|| |||||||| : | |
Db   719  GGMKQIPVKWTAPEALNYGRYSSESDVWSFGILLWEAFSLGAVPYANLSNQQTRBAIEGG  778

Qy   707  GRLPCPELCPDAVFRLMEQCWAYEPGQRPSFSTIYQELQSIRKRHR  752
          ||| || ||| |||||| |||  :| |:|||: :||:|::||:|||
Db   779  VRLEPPEQCPEDVYRLMQRCWEYDPRRRPSFGAVHQDLIAIRRRHR  824

RESULT 8
US-10-732-923-13481
; Sequence 13481, Application US/10732923
; Publication No. US2005010879lA1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
  SEQ ID NO 13481
; LENGTH: 898
; TYPE: PRT
; ORGANISM: Fujinami sarcoma virus
US-10-732-923-13481

Query Match             66.3%;  Score 2571;  DB 17;  Length 898;
Best Local Similarity   61.4%;  Pred. No. 5e-145;
Matches   507;  Conservative  106;  Mismatches 137;  Indels  76;  Gaps  3;

Qy     1  MGFSSELCSPQGHGVLQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHM----SLQDS   56
          |||| ||| |||| || | ||||||||| |||||| ||||||||||| ||||    ||
Db    75  MGFGPELWCPKGHSELLRLQDSELRLLELMKKWMSQRAKSDREYAGMLHHMFSQLEKQEG  134

Qy    57  GGQSRAISPDSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKTY  116
          ||   | : | :| :|| : ||||| |||||:|||| |: ||| |||:|||:||||||::
Db   135  LGHLRATDHSSQIGESWWVLASQTETLSQTLRRHAEELAAGPLAKLSILIRDKQQLRKVF  194

Qy   117  SEQWQQLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEASKDKDRDKAKDKYVRSL  176
          ||||||| ||  :| || :||||:||| |:||| |||||||||||| | |:||:|||||
Db   195  SEQWQQLSQEYAWTTQQEVEKLKAQYRSLVRDSTQAKRKYQEASKDKEREKAKEKYVRSL  254

Qy   177  WKLFAHHNRYVLGVRAAQLHQHHHQLLPGLLRSLQDLHEEMACILKEILQEYLEISSL   236
          ||| | || ||| ||| || : | : || | ||:: || | :|||||:||| ::||
Db   255  SKLYALHNQYVLAVQAAALHRHHYQRALPTLHESLYSLQQEMVLVKEILGEYCSITSL   314

Qy   237  VQDEVVAIHREMAAAARIQPEAEYQGFLRQYGSAPDVPPCVTFDESLLEEGEPLEPGEL   296
          |: || ||: || :|:: ||:| |  ||||  ::|: || |||||||||| | |||||
Db   315  VQEDVLAIHQEVAHAVEMIDPATEYSSFVQCHRYDSEVPPAVTFDESLLEEAESLEPGEL  374

Qy   297  QLNELTVESVQHTLTSVTDELAVATEMVFRRQEMVTQLQQELRNEENTHPRERVQLLGK   356
          |||||| |||||:|||  :|  |  :: :|| |:| |||:|||: || | |:||:|||
Db   375  QLNELTIESVQHSLTSIEEELLASRKAVSSKEQRVWELQVELRGEELALSPGERVHLLGK  434

Qy   357  RQVLQEALQGLQVALCSQAKLQAQQELLQTKLEHLGPGEPPPVLLQDDRHSTSSSEQER   416
          || | || : ||:||| |||||||::::  |||:|| :|||| : :|:: :|: |||
Db   435  RQGLREAQQQLQGLVCAQAKLQAQRDMLTNKLAELGSDEPPPALPLQEDRQSACSTDQER  494

Qy   417  EGGRTPTLEILKSHISGIFRPKFS----------                           440
          :| |  :| |:|:|||||| |:||
Db   495  SG--VTALKTIKNHISGIFSPRFSLPPPVLIPEVQKPLCQQAWYHGAIPRSEVQELLKY   552

Qy   441  ----------------------NLYRLEGEGFPSIPLLIDHLLSTQQP              466
                                |||||||:| |:|||||||||| ||||
Db   553  SGDFLVRESQGKQEYVLSVLWDGQPRHFIIQAADNLYRLEDDGLPTIPLLIDHLLQSRP  612

Qy   467  LTKKSGVVLHRAVPDKWVLNHEDLVLGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETL   526
          :|:|||:||:|||:|||||||||:||||:|||||||||||||||||||| |||||||||
Db   613  ITRKSGIVLTRAVLKDKWVLNHEDVLLGERIGRGNFGEVFSGRLRADNTPVAVKSCRETL  672
```

```
Qy    527  PPDLKAKFLQEARILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLTFLRTEGARLR  586
                |||||||||||||||| ||:||||||||||||||||||||||||||||||| ||:||| ||
Db    673  PPELKAKFLQEARILKQCNHPNIVRLIGVCTQKQPIYIVMELVQGGDFLSFLRSKGPRLK  732

Qy    587  VKTLLQMVGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREEADGVYAAS  646
                ||:: :||  ||||||||||:||||||||||||||||| :||||||||||||| ||||
Db    733  MKKLIKMDNAAAGMEYLESKHCIHRDLAARNCLVTEKNTLKISDFGMSRQEEDGVYAST  792

Qy    647  GGLRQVPVKWTAPEALNYGRYSSESDVWSFGILLWETFSLGASPYPNLSNQQTREFVEKG  706
                |||| |||||||||||||||||||||||||||||||||||||||||||||:||||| :|:|
Db    793  GGMKQIPVKWTAPEALNYGWYSSESDVWSFGILLWEAFSLGAVPYANLSNQQTREAIEQG  852

Qy    707  GRLPCPELCPDAVFRLMEQCWAYEPGQRPSFSTIYQELQSIRKRHR  752
                ||||||||||||||||||||||||||:||:  |||||||:||||||
Db    853  VRLEPPEQCPEDVYRLMQRCWEYDPHRRPSFGAVHQDLIAIRKRHR  898
```

```
RESULT 9
US-10-732-923-13482
;   Sequence 13482, Application US/10732923
;   Publication No. US2005010879lA1
;   GENERAL INFORMATION:
;     APPLICANT: Edgerton, Michael D
;     TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
;     FILE REFERENCE: 38-15(52796)C
;     CURRENT APPLICATION NUMBER: US/10/732,923
;     CURRENT FILING DATE: 2003-12-10
;     PRIOR APPLICATION NUMBER: 10/310,154
;     PRIOR FILING DATE: 2002-12-04
;     NUMBER OF SEQ ID NOS: 24149
;   SEQ ID NO 13482
;     LENGTH: 873
;     TYPE: PRT
;     ORGANISM: Fujinami sarcoma virus
US-10-732-923-13482

  Query Match        66.3%;   Score 2570;  DB 17;   Length 873;
  Best Local Similarity  61.4%;  Pred. No. 5.6e-145;
  Matches  507;  Conservative 106;  Mismatches 137;  Indels  76;  Gaps    3;
```

```
Qy      1  MGFSSELCSPQGHGVLQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHM----SLQDS   56
                |||: |   :|| |: |||| |||||||||||||||||||||||||:|||      ::
Db     50  MGFGPELWCPKGHSELLRLQDSLRLLELMKKWMSQRAKSDREYAGMLHHMFSQLEKQEG  109

Qy     57  GGQSRAISPDSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKTY  116
                |||||||||||||||||||||||||||||: || || |||||| |:|||:|||||||||
Db    110  LGHLRATDHSSQIGESWWVLASQTETLSQTLRRHAEELAAGPLAKLSILIRDKQQLRKVF  169

Qy    117  SEQWQQLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEASKDKRDKAKDKYVRSL  176
                |||||||:|||| |||||||| ::||||||||||||||:|||||||||||||||||||
Db    170  SEQWQQLSQEYAWTTQQEVEKLKAQYRSLVRDSTQAKRKYQEASKDKEREKAKEKYVRSL  229

Qy    177  WKLFAHHNRYLGVRAAQLHHQHHHQLLPGLLRSLQDLHEEMACILKEILQEYLEISSL  236
                ||||:|| ||:|||| || |||:|||:||||:||:|||||||:|:||| ||:|||:|||
Db    230  SKLYALHNQYVLAVQAAALHHHHHYQRALPTLHESLYSLQQEMVLVKEILGEYCSITSL  289

Qy    237  VQDEVVAIHREMAAAAAARIQPEAEYQGFLRQYGSAPDVPPCVTFDESLLEEGEPLEPGEL  296
                |||||||:|| || |||||:|||||||:| ||||||||||||||||||||||:|||:||||
Db    290  VQEDVLAIHQEVAHAVEMIDPATEYSSFVQCHRYDSEVPPAVTFDESLLEEAENLEPGEL  349

Qy    297  QLNELTIESVQHTLTSVTDELAVATEMVFRRQEMVTQLQQELRNEEENTHPRERVQLLGK  356
                |||||||||||||||:|:|||||||:||| ||||| ||||||:||:|||||||||:|||||
Db    350  QLNELTIESVQHSLTSIEEELLASRKAVSSKEQRWELQVELRGEELALSPGERVHLLGK  409

Qy    357  RQVLQEALGLQVALCSQAKLQAQQELLQTKLEHLGPGEPPVLLIPEVQKPLCQQAWYHGAIPRSVEQELLKY  527
                 |||| ||| |||||||||||||||||||||||||||||||||||||||:||||||:|||||||||||||||
Db    470  SG--VTALKTKNHISGIFSPRFSLPPVPLIPEVQKPLCQQAWYHGAIPRSVEQELLKY

Qy    410  RQGLREAQQQLAQGLVCAQAKLQAQRDMLANKLAELGSEEPPALPLQEDRQSACSTDQER  469
                ||| ||
Db    417  EGGRIPTLEILKSHISGIFRPKFS--------------

Qy    470  SG--VTALKTKNHISGIFSPRFSLPPVPLIPEVQKPLCQQAWYHGAIPRSVEQELLKY  527
                ::|| |||::|| :||||
```

(Right column / RESULT 10)

```
Qy    441  --------------------------------------------NLYRLEGEGFPSIPLLIDHLSTQQP  466
                                                           || :||||| || || |||:
Db    528  SGDFLVRESQGKQEYVLSVLWDGQPRHFIIQAADNLYRLEDDGLPTIPLLIDHLLQSQRP  587

Qy    467  LTKKSGVVLHRAVPKDKWVLNHEDLVLIGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETL  526
                |||||||||||:||||||||||||||||||||:||||||||||| ||:||:||||||||||
Db    588  ITRKSGIVLTRAVLKDKWVLNHEDLVLLGERIGRGNFGEVFSGRLRADNTPVAVKSCRETL  647

Qy    527  PPDLKAKFLQEARILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLTFLRTEGARLR  586
                ||||||||||||||||| ||:|||||||||||||||||||||||||||:|||| |:|||||
Db    648  PPELKAKFLQEARILKQYCNHPNIVRLIGVCTQKQPIYIVMELVQGGDFLSFLRSKGPRLK  707

Qy    587  VKTLLQMVGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREEADGVYAAS  646
                :||: :||   |||||||||:||||||||||||||||| :||||||||||:| ||||||
Db    708  MKKLIKMDNAAAGMEYLESKHCIHRDLAARNCLVTEKNTLKISDFGMSRQEEDGVYAST  767

Qy    647  GGLRQVPVKWTAPEALNYGRYSSESDVWSFGILLWETFSLGASPYPNLSNQQTREFVEKG  706
                |||:| ||||||||||||| ||||||||||||||||:|||||:||:|||||||||::|:|
Db    768  GGMKQIPVKWTAPEALNYGWYSSESDVWSFGILLWEAFSLGAVPYANLSNQQTREAIEQG  827

Qy    707  GRLPCPELCPDAVFRLMEQCWAYEPGQRPSFSTIYQELQSIRKRHR  752
                 |||||||||:||:|||:|||||:|||||||| |:|||:|||||||
Db    828  VRLEPPEQCPEDVYRLMQRCWEYDPHRRPSFGAVHQDLIAIRKRHR  873
```

```
RESULT 10
US-10-732-923-13480
;   Sequence 13480, Application US/10732923
;   Publication No. US2005010879lA1
;   GENERAL INFORMATION:
;     APPLICANT: Edgerton, Michael D
;     TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
;     FILE REFERENCE: 38-15(52796)C
;     CURRENT APPLICATION NUMBER: US/10/732,923
;     CURRENT FILING DATE: 2003-12-10
;     PRIOR APPLICATION NUMBER: 10/310,154
;     PRIOR FILING DATE: 2002-12-04
;     NUMBER OF SEQ ID NOS: 24149
;   SEQ ID NO 13480
;     LENGTH: 873
;     TYPE: PRT
;     ORGANISM: Fujinami sarcoma virus
US-10-732-923-13480

  Query Match        66.0%;   Score 2561;  DB 17;   Length 873;
  Best Local Similarity  61.3%;  Pred. No. 1.9e-144;
  Matches  506;  Conservative 106;  Mismatches 138;  Indels  76;  Gaps    3;
```

```
Qy      1  MGFSSELCSPQGHGVLQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHM----SLQDS   56
                |||: |   :|| |: |||| |||||||||||||||||||||||||:|||      ::
Db     50  MGFGPELWCPKGHTELLRLQDSELRLLELMKKWMSQRAKSDREYAGMLHHMFSQLEKQEG  109

Qy     57  GGQSRAISPDSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKTY  116
                |||||||||||||||||||||||||||||: || || |||||| |:|||:|||||||||
Db    110  LGHLRATDHSSQIGESWWVLASQTETLSQTLRRHAEELAAGPLAKLSILIRDKQQLRKVF  169

Qy    117  SEQWQQLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEASKDKRDKAKDKYVRSL  176
                |||||||:|||| |||||||| ::||||||||||||||:|||||||||||||||||||
Db    170  SEQWQQLSQEYAWTTQQEVEKLKAQYRSLVRDSTQAKRKYQEASKDKEREKAKEKYVRSL  229

Qy    177  WKLFAHHNRYLGVRAAQLHHQHHHQLLPGLLRSLQDLHEEMACILKEILQEYLEISSL  236
                ||||:|| ||:|||| || |||:|||:||||:||:|||||||:|:||| ||:|||:|||
Db    230  SKLYALHNQYVLAVQAAALHHHHHYQRALPTLHESLYSLQQEMVLVKEILGEYCSITSL  289

Qy    237  VQDEVVAIHREMAAAAAARIQPEAEYQGFLRQYGSAPDVPPCVTFDESLLEEGEPLEPGEL  296
                |||||||:|| || |||||:|||||||:| ||||||||||||||||||||||:|||:||||
Db    290  VQEDVLAIHQKVAHAVEMIDPATEYSSFVQCHRYDSEVPPAVTFDESLLEEAENLEPGEL  349

Qy    297  QLNELTIESVQHTLTSVTDELAVATEMVFRRQEMVTQLQQELRNEEENTHPRERVQLLGK  356
                |||||||||||||||:|:|||||||:||| ||||| ||||||:||:|||||||||:|||||
Db    350  QLNELTIESVQHSLTSIEEELLASRKAVSSKEQRWELQVELRGEELALSPGERVHLLGK  409

Qy    357  RQVLQEALGLQVALCSQAKLQAQQELLQTKLEHLGPGEPPVLLQDDRHSTSSSEQER  416
                ||| ||||||||||||||||||:||
Db    357  RQVLQEALGLQVALCSQAKLQAQQELLQTKLEHLGPGEPPVLLQDDRHSTSSSEQER  416
```

```
Db       ||||||  ::|||||||||||:::|||   ||||:|||
     410 RQGLREAQQQLQGLVCAQAKLQAQRDMLANKLAELGSEEPPALPLQEDRQSARSTDQER 469

Qy   417 EGGRTPTLEILKSHISGIFRPKFS------- 440
         :|:||||||||||||||||:::|||
Db   470 SG--VTALKTIKNHISGIFSPRFSLPPPVPLIPEVQKPLCQQAWHGAIPRSEVQELLKY 527

Qy   441 ------------------------NLYRLEGEGFPSIPLLIDHLLSTQQP 466
                                    ||||:|||||||
Db   528 SGDFLVRESQGKQEYVLSVLWDGQPRHFIIQAADNLYRLEDDGLPTIPLLIDHLLQSQRP 586

Qy   467 LTKKSGVVLHRAVPKDKWVLNHEDLVLGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETL 526
         :|:|||||||||||||||||||||||||||||||:|||:
Db   588 ITRKSGIVLTRAVLKDKWVLNHEDVLLGERIGRGNFGEVFSGRLRADNTPVAVKSCRETL 647

Qy   527 PPDLKAKFLQEARILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLTFLRTEGARLR 586
         ||||:|||||||||||||||||||||||||||||||||:::||||||
Db   648 PPELKAKFLQEARILKQCNHPNIVRLIGVCTQKQPIYIVMELVQGGDFLSFLRSKGPRLK 707

Qy   587 VKTLLQMVGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREEADGVYAAS 646
         :|:|||||||||||||||||||||||||||||||||
Db   708 MKKLIKMENAAAGMEYLESKCHIHRDLAARNCLVTEKNTLKISDFGMSRQEEDGVYAST 767

Qy   647 GGLRQVPVKWTAPEALNYGRYSSESDVWSFGILLWETFSLGASPYPNLSNQQTREFVEKG 706
         |||::|:|||||||||||||||||||||||||| ||  ||:||
Db   768 GGMKQIPVKWTAPEALNYGWYSSESDVWSFGILLWEAFSLGAVPYANLSNQQTREAIEQG 827

Qy   707 GRLPCPELCPDAVFRLMEQCWAYEPGQRPSFSTIYQELQSIRKRHR 752
         :|||::|:|  ||:|||||
Db   828 VRLEPPEQCPEDVYRLMQRCWEYDPHRRPSFGAVHQDLIAIRKRHR 873
```

RESULT 11
US-10-732-923-13479
; Sequence 13479, Application US/10732923
; Publication No. US2005010879A1
; GENERAL INFORMATION:
;   APPLICANT: Edgerton, Michael D
;   TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
;   FILE REFERENCE: 38-15 (52796)C
;   CURRENT APPLICATION NUMBER: US/10/732,923
;   CURRENT FILING DATE: 2003-12-10
;   PRIOR APPLICATION NUMBER: 10/310,154
;   PRIOR FILING DATE: 2002-12-04
;   NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13479
; LENGTH: 1182
; TYPE: PRT
; ORGANISM: Fujinami sarcoma virus
US-10-732-923-13479

```
Query Match       66.0%;  Score 2561;  DB 17;  Length 1182;
Best Local Similarity  61.3%;  Pred. No. 2.7e-144;
Matches  506;  Conservative 106;  Mismatches 138;  Indels 76;  Gaps 3;

Qy    1 MGFSSELCSPQHGVLQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHM----SLQDS 56
        ||||||||||||||||||||||||||||||||||
Db  359 MGFGFGPELWCPKGHTELLRLQDSELRLLELMKKWMSQRAKSDREYAGMLHHMFSQLEKQEG 418

Qy   57 GGQSRAISPDSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKTY 116
        ||: :|| ||::||:|||||:|||||:||:||||:|||:|||||:||:||:::||||||:
Db  419 LGHLRATDHSSQIGESWVLASQTETLSQTLRRHAEELAAGPLAKLSILIRDKQQLRKVF 478

Qy  117 SEQWQQLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEASKDKDRDKAKDKYVRSL 176
        |||||||:||  :||:|||:|||:||||:||:|| ||||||||||||||||||||:|||
Db  479 SEQWQQLSQEYAWTTQQEVEKLKAQYRSLVRDSTQAKRKYQEASKDKEREKAKEKYVRSL 538

Qy  177 WKLFAHHNRYVLGVRAAQLHHQHHHQLLPGLLRSLQDLHEEMACILKEILQEYLEISSL 236
        :||:| ||:|||.|:||.|||:|||||:||||:|||:||| |  :||||| || ::||
Db  539 SKLYALHNQYVLAVQAAALHHHHHHYQRALPTLHESLYSLQQEMVLVLKEILGEYCSITSL 598

Qy  237 VQDEVVAIHREMAAAAARIQPEAEYQGFLRQYGSAPDVPPCVTFDESLLEGEPLEPGEL 296
        ||||::|||
Db  599 VQEDVLAIHQKVAHAVEMIDPATEYSSFPVQCHRYDSEVPPAVTFDESLLEEAENLEPGEL 658

Qy  297 QLNELTVESVQHTLTSVTDELAVATEMVFRRQEMVTQLQQELRNEEENTHPRERVQLLGK 356
        ||||||:||||||:|||  || | |::: :::|  : ||:||| ||||:| :|| ||||
Db  659 QLNELTIESVQHSLTSIEEELLASRKAVSSKEQRVWELQVELRGEELALSPGERVHLLGK 718

Qy  357 RQVLQEALQGLQVALCSQAKLQAQQELLQTKLEHLGPGEPPVLLQDDRHSTSSSEQER 416
        ||:|:||||||||||||||||||:::||.|||| ||| |||.|||:||::::::||:
Db  719 RQGLREAQQQLQGLVCAQAKLQAQRDMLANKLAELGSEEPPALPLQEDRQSARSTDQER 778

Qy  417 EGGRTPTLEILKSHISGIFRPKFS------- 440
        ||
Db  779 SG--VTALKTIKNHISGIFSPRFSLPPPVPLIPEVQKPLCQQAWHGAIPRSEVQELLKY 836

Qy  441 ------------------------NLYRLEGEGFPSIPLLIDHLLSTQQP 466
                                ||||:|||||||
Db  837 SGDFLVRESQGKQEYVLSVLWDGQPRHFIIQAADNLYRLEDDGLPTIPLLIDHLLQSQRP 896

Qy  467 LTKKSGVVLHRAVPKDKWVLNHEDLVLGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETL 526
        :|:|||||||||||||||||||||||||||||||:|||:
Db  897 ITRKSGIVLTRAVLKDKWVLNHEDVLLGERIGRGNFGEVFSGRLRADNTPVAVKSCRETL 956

Qy  527 PPDLKAKFLQEARILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLTFLRTEGARLR 586
        ||||:||||||||||||||||||||||||||||||||:::||||||
Db  957 PPELKAKFLQEARILKQCNHPNIVRLIGVCTQKQPIYIVMELVQGGDFLSFLRSKGPRLK 1016

Qy  587 VKTLLQMVGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREEADGVYAAS 646
        :|:|||||||||||||||||||||||||||||||||
Db 1017 MKKLIKMENAAAGMEYLESKCHIHRDLAARNCLVTEKNTLKISDFGMSRQEEDGVYAST 1076

Qy  647 GGLRQVPVKWTAPEALNYGRYSSESDVWSFGILLWETFSLGASPYPNLSNQQTREFVEKG 706
        |||::|:|||||||||||||||||||||||||| ||  ||:||
Db 1077 GGMKQIPVKWTAPEALNYGWYSSESDVWSFGILLWEAFSLGAVPYANLSNQQTREAIEQG 1136

Qy  707 GRLPCPELCPDAVFRLMEQCWAYEPGQRPSFSTIYQELQSIRKRHR 752
        :|||::|:|  ||:|||||
Db 1137 VRLEPPEQCPEDVYRLMQRCWEYDPHRRPSFGAVHQDLIAIRKRHR 1182
```

RESULT 12
US-10-732-923-13452
; Sequence 13452, Application US/10732923
; Publication No. US2005010879A1
; GENERAL INFORMATION:
;   APPLICANT: Edgerton, Michael D
;   TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
;   FILE REFERENCE: 38-15 (52796)C
;   CURRENT APPLICATION NUMBER: US/10/732,923
;   CURRENT FILING DATE: 2003-12-10
;   PRIOR APPLICATION NUMBER: 10/310,154
;   PRIOR FILING DATE: 2002-12-04
;   NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13452
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Gardner-Arnstein feline sarcoma virus
US-10-732-923-13452

```
Query Match       63.9%;  Score 2479;  DB 17;  Length 609;
Best Local Similarity  61.7%;  Pred. No. 1e-139;
Matches  507;  Conservative 11;  Mismatches 14;  Indels 290;  Gaps 3;

Qy    1 MGFSSELCSPQHGVLQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHMSLQDSGSGQS 60
        |||||||||||||  :|||||||||||||||||||||||||||||||||||||
Db    8 MGFSSELCSPQHGAEQOMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHMSLQDGGG-- 65

Qy   61 RAISPDSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKTYSEQW 120
        | :  :|||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db   66 RGTGPYSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLGLLIRERQQLRKTYSEQW 125

Qy  121 QQLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEASKDKDRDKAKDKYVRSLWKLF 180
        |||||||||||:||||||||||||||||||||:||||||||||||||||
Db  126 QQLQQELTKTHNQDIEKLKSQYRALARDSAQARRKYQEASKDKDRDKA----------- 173
```

```
Qy   61 RAISPDSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKTYSEQW 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  414 RGTGPYSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLGLLIRERQQLRKTYSEQW 473

Qy  121 QQLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEASKDKDRDKAKDKVYRSLWKLF 180
           ||||||||||||:||:||||||||||||||:||||||||||||||||||||----------
Db  474 QQLQQELTKTHNQDIEKLKSQYRALARDSAQARRKYQEASKDKDRDKA------------- 521

Qy  181 AHHNRYLVLGVRAAQLHHQHHQLLLPGLLRSLQDLHEEMACILKEILQEYLEISSLVQDE 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  522 ------------------------------------------------------------ 521

Qy  241 VVAIHREMAAAAARIQPEAEYQGFLRQYGSAPDVPPCVTFDESLLEEGEPLEPGELQLNE 300
           ------------------------------------------------------------
Db  522 ------------------------------------------------------------ 521

Qy  301 LTVESVQHTLTSVTDELAVATEMVFRRQEMVTQLQQELRNEEENTHPRERVQLLGKRQVL 360
           ------------------------------------------------------------
Db  522 ------------------------------------------------------------ 521

Qy  361 QEALQGLQVALCSQAKLQAQQELLQTKLEHLGPGEPPVLLQDDRHSTSSSEQEREGGR 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 KLEQLGPGEPPVLLQDDRHSTSSSEQEREGGR 555

Qy  421 TPTLEILKSHISGIFRPKFS--------------------------------------- 440
           ||||||||||||||||||||
Db  556 TPTLEILKSHISGIFRPKFSLPPPLQLVPEVQKPLHEQLWYHGALPRAEVAELLTHSGDF 615

Qy  441 --------------------------------NLYRLEGEGFPSIPLLIDHLLSTQQPLTKK 470
                                           ||||: ||||||||||  :|||||||||||
Db  616 LVRESQGKQEYVLSVLWDGQPRHFIIQSADNLYRPEGDGFASIPLLVDHLLRSQQPLTKK 675

Qy  471 SGVVLHRAVPKDKWVLNHEDLVLGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETLPPDL 530
           |||:|:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  676 SGIVLNRAVPKDKWVLNHEDLVLGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETLPPDI 735

Qy  531 KAKFLQEARILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLTFLRTEGARLRVKTL 590
           |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||:||
Db  736 KAKFLQEAKILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLTFLRTEGARLRMKTL 795

Qy  591 LQMVGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREEADGVYAASGGLR 650
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  796 LQMVGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREAADGIYAASGGLR 855

Qy  651 QVPVKWTAPEALNYGRYSSESDVWSFGILLWETFSLGASPYPNLSNQQTREFVEKGGRLP 710
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  856 QVPVKWTAPEALNYGRYSSESDVWSFGILLWETFSLGASPYPNLSNQQTREFVEKGGRLP 915

Qy  711 CPELCPDAVFRLMEQCWAYEPGQRPSFSTIYQELQSIRKRHR 752
           ||||||||||||||||||||||||||||||||||||||||||
Db  916 CPELCPDAVFRLMEQCWAYEPGQRPSFSAIYQELQSIRKRHR 957
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Query Match   51.0%;   Score 1980;   DB 17;   Length 477;

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Qy  181 AHHNRYLVLGVRAAQLHHQHHQLLLPGLLRSLQDLHEEMACILKEILQEYLEISSLVQDE 240
Db  174 ------------------------------------------------------------ 173

Qy  241 VVAIHREMAAAAARIQPEAEYQGFLRQYGSAPDVPPCVTFDESLLEEGEPLEPGELQLNE 300
Db  174 ------------------------------------------------------------ 173

Qy  301 LTVESVQHTLTSVTDELAVATEMVFRRRQEMVTQLQQELRNEEENTHPRERVQLLGKRQVL 360
Db  174 ------------------------------------------------------------ 173

Qy  361 QEALQGLQVALCSQAKLQAQQELLQTKLEHLGPGEPPVLLQDDRHSTSSSEQEREGGR 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  174 KLEQLGPGEPPVLLQDDRHSTSSSEQEREGGR 207

Qy  421 TPTLEILKSHISGIFRPKFS--------------------------------------- 440
           ||||||||||||||||||||
Db  208 TPTLEILKSHISGIFRPKFSLPPPLQLVPEVQKPLHEQLWYHGALPRAEVAELLTHSGDF 267

Qy  441 --------------------------------NLYRLEGEGFPSIPLLIDHLLSTQQPLTKK 470
           ||||||:||||||||  :|||||||||||
Db  268 LVRESQGKQEYVLSVLWDGQPRHFIIQSADNLYRPEGDGFASIPLLVDHLLRSQQPLTKK 327

Qy  471 SGVVLHRAVPKDKWVLNHEDLVLGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETLPPDL 530
           |||:|:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  328 SGIVLNRAVPKDKWVLNHEDLVLGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETLPPDI 387

Qy  531 KAKFLQEARILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLTFLRTEGARLRVKTL 590
           |||||||| |||||||||||||||||||||||||||||||||||||||||||||||:||
Db  388 KAKFLQEAKILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLTFLRTEGARLRMKTL 447

Qy  591 LQMVGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREEADGVYAASGGLR 650
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  448 LQMVGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREEADGIYAASGGLR 507

Qy  651 QVPVKWTAPEALNYGRYSSESDVWSFGILLWETFSLGASPYPNLSNQQTREFVEKGGRLP 710
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  508 QVPVKWTAPEALNYGRYSSESDVWSFGILLWETFSLGASPYPNLSNQQTREFVEKGGRLP 567

Qy  711 CPELCPDAVFRLMEQCWAYEPGQRPSFSTIYQELQSIRKRHR 752
           ||||||||||||||||||||||||||||||||||||||||||
Db  568 CPELCPDAVFRLMEQCWAYEPGQRPSFSAIYQELQSIRKRHR 609
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Query Match   63.9%;   Score 2479;   DB 17;   Length 957;
Best Local Similarity   61.7%;   Pred. No. 1.7e-139;
Matches 507;   Conservative 11;   Mismatches 14;   Indels 290;   Gaps 3;

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Qy    1 MGFSSELCSPQGHGVLQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHMSLQDSGGQS 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  356 MGFSSELCSPQGHGAEQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHMSLQDGGG-- 413
```

```
Db  300 REQVQLLAKKQVLQEALQALQVALCSQAKLQAQRELLQAKLEQLGPGEPPVVLLQDDRH 359
                                                              -NLYR 444
Qy

Qy  408 STSSSEQEREGGRTPTLEILKSHISGIFRPKFS------                         444
            ||||:|||||||||||||||||||||||||||||
Db  360 STSSSEQEREGGRTPTLEILKSHISGIFRPKFSLPPPLQLVPEVQKPLHEQLWYHGALPR 419

Qy  445 LE----------------------------GEGFPSIPLLI 457
            |:                          :|||:|||||:
Db  420 AEVAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXASIPLLV 479

Qy  458 DHLLSTQQPLTKKSGVVLHRAVPKDKWVLNHEDLVLGEQIGRGNFGEVFSGRLRADNTLV 517
            ||||:|||||||||:||:||||||||||||||||||||||||||||||||||||||||
Db  480 DHLLRSQQPLTKKSGIVLNRAVPKDKWVLNHEDLVLGEQIGRGNFGEVFSGRLRADNTLV 539

Qy  518 AVKSCRETLPPDLKAKFLQEARILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLTF 577
            |||||||||||:|||||||||:|||||||||||||||||||||||||||||||||||||
Db  540 AVKSCRETLPPDIKAKFLQEAKILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLTF 599

Qy  578 LRTEGARLRVKTLLQMVGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSRE 637
            |||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db  600 LRTEGARLRMKTLLQMVGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSRE 659

Qy  638 EADGVYAASGGLRQVPVKWTAPEALNYGRYSSESDVWSFGILLWETFSLGASPYPNLSNQ 697
            |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db  660 EADGVYAASGGLRLVPVKWTAPEALNYGRYSSESDVWSFGILLWETFSLGASPYPNLSNQ 719

Qy  698 QTREFVEKGGRLPCPELCPDAVFRLMEQCWAYEPGQRPSFSTIYQELQSIRKRHR 752
            ||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db  720 QTREFVEKGGRLPCPELCPDAVFRLMEQCWAYEPGQRPSFSAFYQELQSIRKRHR 774
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Search completed: August   4, 2005, 14:01:23
Job time : 164 secs

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Best Local Similarity 80.9%; Pred. No. 4.6e-110;
Matches  386; Conservative  11; Mismatches  10; Indels  70; Gaps  1;

Qy  346 HPRERVQLLGKRQVLQEALQGLQVALCSQAKLQAQELLQTKLEHLGPGEPPVVLLQDD 405
            |||::|:|||:|||||||||:||||||||||||||||:|||:|||:||||||||||||
Db    1 HPREQVQLLAKKQVLQEALQALQVALCSQAKLQAQRELLQAKLEQLGPGEPPVVLLQDD 60

Qy  406 RHSTSSEQEREGGRTPTLEILKSHISGIFRPKFS------------ 440
            |||||:|||||||||||||||||||||||||||||
Db   61 RHSTSSSEQEREGGRTPTLEILKSHISGIFRPKFSLPPPLQLVPEVQKPLHEQLWYHGAL 120

Qy  441 ------------------NLYRLEGEGFPSIPL 455
                               |||| |:|:|||||
Db  121 PRAEVAELLTHSGDFLVRESQGKQEYVLSVLWDGQPRHFIIQSADNLYRPEGDGFASIPL 180

Qy  456 LIDHLLSTQQPLTKKSGVVLHRAVPKDKWVLNHEDLVLGEQIGRGNFGEVFSGRLRADNT 515
            |:|||||:|||||||||:||:||||||||||||||||||||||||||||||||||||||
Db  181 LVDHLLRSQQPLTKKSGIVLNRAVPKDKWVLNHEDLVLGEQIGRGNFGEVFSGRLRADNT 240

Qy  516 LVAVKSCRETLPPDLKAKFLQEARILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFL 575
            ||||||||||||||:|||||||||:||||||||||||||||||||||||||||||||||
Db  241 LVAVKSCRETLPPDIKAKFLQEAKILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFL 300

Qy  576 TFLRTEGARLRVKTLLQMVGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMS 635
            |||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db  301 TFLRTEGARLRMKTLLQMVGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMS 360

Qy  636 REEADGVYAASGGLRQVPVKWTAPEALNYGRYSSESDVWSFGILLWETFSLGASPYPNLS 695
            |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||
Db  361 REEALDGVYAASGGLRLVPVKWTAPEALNYGRYSSESDVWSFGILLWETFSLGASPYPNLS 420

Qy  696 NQQTREFVEKGGRLPCPELCPDAVFRLMEQCWAYEPGQRPSFSFSTIYQELQSIRKRHR 752
            ||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db  421 NQQTREFVEKGGRLPCPELCPDAVFRLMEQCWAYEPGQRPSFSAFYQELQSIRKRHR 477
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RESULT 15
US-10-732-923-13451
; Sequence 13451, Application US/10732923
; Publication No. US2005010879lAl
; GENERAL INFORMATION:
;   APPLICANT: Edgerton, Michael D
;   TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
;   FILE REFERENCE: 38-15(52796)C
;   CURRENT APPLICATION NUMBER: US/10/732,923
;   CURRENT FILING DATE: 2003-12-10
;   PRIOR APPLICATION NUMBER: 10/310,154
;   PRIOR FILING DATE: 2002-12-04
;   NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13451
;   LENGTH: 774
;   TYPE: PRT
;   ORGANISM: Feline sarcoma virus
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(774)
;   OTHER INFORMATION: unsure at all Xaa locations
US-10-732-923-13451

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Query Match        50.1%;  Score 1942.5;  DB 17;  Length 774;
Best Local Similarity 68.9%;  Pred. No. 1.4e-107;
Matches  410; Conservative  18; Mismatches  72; Indels  95; Gaps  7;

Qy  246 REMAAAAARIQPEAEYQGFLRQYG--SAPDV-------PP------CVTFDESLLEEGE 289
            ||  ::: ||||::|:|||||:|||  :| ||       ||      :
Db  187 RENPAEESQALPLREGPNNRPQYWPFSASDLYNWKSHNPPFSQDPVALTNLIESILVTHQ 246

Qy  290 PLEPGELQLNE--LTVESVQHTLTSVTDELAVATEMVFRRQEMVTQLQQELRNEEENTHP 347
            |  | | |   : |:               :   :    |
Db  247 PTWDDCCQLLQALLTGEERQRVLLE-------ARKQVPGEDGRPTQLPNVIDETFPLTHP 299

Qy  348 RERVQLLGKRQVLQEALQGLQVALCSQAKLQAQQELLQTKLEHLGPGEPPVVLLQDDRH 407
            ||:||:|:|||||||||||||||||||||||||:||||||||||||||||||||||||||
```

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              GenCore version 5.1.6
       Copyright (c) 1993 - 2005  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:   August  9, 2005, 20:15:00 ; Search time 2010.27 seconds
                                       (without alignments)
                                       7274.725 Million cell updates/sec

Title:        US-10-660-763-1_COPY_72_2327
Perfect score: 2256
Sequence:     1 atgggctcctcctctggct.........gcatccgaaagcggcatcgg 2256

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched:     7297361 seqs, 3241162794 residues

Total number of hits satisfying chosen parameters:      14594722

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    Published Applications NA:*
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         2:  /cgn2_6/ptcodata/1/pubpna/PCT_NEW_PUB.seq:*
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        23:  /cgn2_6/ptcodata/1/pubpna/US11A_PUBCOMB.seq:*
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        26:  /cgn2_6/ptcodata/1/pubpna/US60_PUBCOMB.seq:*

                              SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the total score of the result being printed,
and is derived by analysis of the total score distribution.
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Result No.	Score	Query Match	Length	DB	DB ID	Description
1	2256	100.0	2674	13	US-10-003-295-1	Sequence 1, Appli
2	2256	100.0	2674	18	US-10-660-763-1	Sequence 1, Appli
3	2023.4	89.7	2889	16	US-10-240-965-256	Sequence 256, App
4	328.8	14.6	2950	21	US-10-887-553A-240	Sequence 240, App
5	326.8	14.5	449	10	US-09-918-995-1503	Sequence 1503, Ap
6	296.2	13.1	361	9	US-09-948-802-5	Sequence 5, Appli
7	296.2	13.1	361	15	US-10-121-925-5	Sequence 5, Appli

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 8   271.6  12.0   1779  18  US-10-280-576-19         Sequence 19, Appl
 9   227.2  10.1  15297  13  US-10-003-295-3          Sequence 3, Appli
10   227.2  10.1  15297  18  US-10-660-763-3          Sequence 3, Appli
11   201.2   8.9   3875  15  US-10-101-510-525        Sequence 525, App
12   198     8.8   2955   9  US-10-384-339C-1         Sequence 1, Appli
13   198     8.8   3370   9  US-09-967-768A-144       Sequence 144, App
14   198     8.8   3370  16  US-10-354-358-101        Sequence 101, App
15   198     8.8   3370  16  US-10-210-120-19         Sequence 19, Appl
16   198     8.8   3370  19  US-10-776-827-82         Sequence 82, Appl
17   198     8.8   3370  20  US-10-473-974-219        Sequence 219, App
18   198     8.8   3370  21  US-10-843-641A-6289      Sequence 6289, Ap
19   198     8.8   3370  22  US-10-909-035-19         Sequence 19, Appl
20   185.4   8.2   3042  19  US-10-384-339C-2         Sequence 2, Appli
21   185.4   8.2   3921  10  US-09-921-406C-29        Sequence 29, Appl
22   185.4   8.2   3921  15  US-10-007-926A-222       Sequence 222, App
23   185.4   8.2   3921  16  US-10-269-909-19         Sequence 19, Appl
24   185.4   8.2   3921  17  US-10-366-288-1          Sequence 1, Appli
25   185.4   8.2   3921  18  US-10-172-118-1036       Sequence 1036, Ap
26   185.4   8.2   3921  18  US-10-342-887-1036       Sequence 1036, Ap
27   185.4   8.2   3921  18  US-10-287-226-319        Sequence 319, App
28   185.4   8.2   3921  19  US-10-648-593-1          Sequence 223, App
29   185.4   8.2   3921  20  US-10-473-974-223        Sequence 223, App
30   185.4   8.2   3935  21  US-10-616-403-5          Sequence 5, Appli
31   185.4   8.2   3935  21  US-10-897-711-1          Sequence 4, Appli
32   176.2   7.8   1518  18  US-10-280-576-24         Sequence 24, Appl
33   174.6   7.7    816  19  US-10-377-268-3          Sequence 3, Appli
34   174.6   7.7   1050  19  US-10-377-268-4          Sequence 4, Appli
35   174.6   7.7   3030  16  US-10-325-430-8          Sequence 8, Appli
36   174.6   7.7   3416   8  US-08-987-699A-1         Sequence 1, Appli
37   174.6   7.7   3416  15  US-10-292-524-1          Sequence 1, Appli
38   174.6   7.7   3416  17  US-10-464-805-2          Sequence 2, Appli
39   174.6   7.7   3416  17  US-10-305-720-1483       Sequence 1483, Ap
40   174.6   7.7   3416  21  US-10-860-066-1          Sequence 1, Appli
41   174.6   7.7   3544  14  US-10-161-803-51         Sequence 51, Appl
42   174.6   7.7   4089  17  US-10-291-808-13         Sequence 13, Appl
43   174.6   7.7   4089  19  US-10-620-052A-7         Sequence 7, Appli
44   174.6   7.7   4151  14  US-10-161-803-52         Sequence 52, Appl
45   174.6   7.7   4151  16  US-10-325-430-7          Sequence 7, Appli
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                              ALIGNMENTS

RESULT 1
US-10-003-295-1
; Sequence 1, Application US/10003295
; Publication NO. US20020168741A1
; GENERAL INFORMATION:
;  APPLICANT: GAN, Weiniu et al.
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION: THEREOF
;  FILE REFERENCE: CL001183DIV
;  CURRENT APPLICATION NUMBER: US/10/003,295
;  CURRENT FILING DATE: 2001-12-06
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;  LENGTH: 2674
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-003-295-1

Query Match             100.0%;  Score 2256;  DB 13;  Length 2674;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 2256;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     1 ATGGGCTTCTCTTCTGAGCTGTGCAGCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    72 ATGGGCTTCTCTTCTGAGCTGTGCAGCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG 131

Qy    61 GAGGCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGCGGGTCAAGAGT 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db   132 GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGCGGGGTCAAGAGT 191
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   121 GACAGGGAGTATGGCAGGACTGCTTCACCACATGTCCCTGCGACAGCAGTGGGGGCCAGAGC 180

Db   192 GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCGACAGCAGTGGGGGCCAGAGC 251
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   181 CGGGCCATCAGCCCTGACAGCCCCATCAGTCAGTCCTGGGCTGAGATCACCAGCCAAACT 240

Db   252 CGGGCCATCAGCCCTGACAGCCCCATCAGTCAGTCCTGGGCTGAGATCACCAGCCAAACT 311
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   241 GAGGGCCTGAGCCGCTTGCTCGCGGCAGCACGCAGGATCTGAACTCAGGGCCCCTGAGC 300

Db   312 GAGGGCCTGAGCCGCTTGCTCGCGGCAGCACGCAGGATCTGAACTCAGGGCCCCTGAGC 371
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   301 AAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCTTCGCAAGACCACACGCGAGCAGTGG 360

Db   372 AAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCTTCGCAAGACCACACGCGAGCAGTGG 431
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   361 CAGCAGCTGCGACAGGGACTGCACAGGGACAGCCCCAAGCCCAGCAACCCACAGACTGAAGAGC 420

Db   432 CAGCAGCTGCGACAGGGACTGCACAGGGACAGCCCCAAGCCCAGCAACCCACAGACTGAAGAGC 491
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   421 CAGTACCGGACTGCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCAGC 480

Db   492 CAGTACCGGACTGCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCAGC 551
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   481 AAAGACAAGGACCGTGACAAGGCCAAGGACAAGTATGTGCGGCTGCGCCTGCGCGGCCTGTGGGGT 540

Db   552 AAAGACAAGGACCGTGACAAGGCCAAGGACAAGTATGTGCGGCTGCGCCTGCGCGGCCTGTGGGGT 611
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   541 GCTCACCACAACCGCTATGTGCTGCGGGGCTGCGCAGCTACACCAGCACCAC 600

Db   612 GCTCACCACAACCGCTATGTGCTGCGGGGCTGCGCAGCTACACCAGCACCAC 671
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   601 CACCAGCTTCCTGCTTCCTGCGTCTGCGGTCACTGCGAGGAGGAGATGGCT 660

Db   672 CACCAGCTTCCTGCTTCCTGCGTCTGCGGTCACTGCGAGGAGGAGATGGCT 731
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   661 TGCATCCTGAAGGAGATCCTCGAGAATACCTGGAGATTAGGAGCCGCTGGTGCAGGATGAG 720

Db   732 TGCATCCTGAAGGAGATCCTCGAGAATACCTGGAGATTAGGAGCCGCTGGTGCAGGATGAG 791
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   721 GTGGTTGGCCATTCACCGGAGAGATGGCTGCAGCGTCGCTGCGAGCCTGAGGCTGAG 780

Db   792 GTGGTTGGCCATTCACCGGAGAGATGGCTGCAGCGTCGCTGCGAGCCTGAGGCTGAG 851
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   781 TACCAAGGCTTCTCTGCGACAGTATGGGTCCGACCCTGACGTGTCACGTTC 840

Db   852 TACCAAGGCTTCTCTGCGACAGTATGGGTCCGACCCTGACGTGTCACGTTC 911
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   841 GATGAGTCACTGCTTGAGGAGATCCTGGAGGAGGGTGAACCCTGGGGAGCTGAACGAG 900

Db   912 GATGAGTCACTGCTTGAGGAGATCCTGGAGGAGGGTGAACCCTGGGGAGCTGAACGAG 971
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   901 CTGACTGTGGAGAGCGTGCAGCGGCAGAGATGGTTAGCAGCTGACACAGATGAGCTGGCTGTGGCC 960

Db   972 CTGACTGTGGAGAGCGTGCAGCGGCAGAGATGGTTAGCAGCTGACACAGATGAGCTGGCTGTGGCC 1031
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   961 ACCGGAGATGGTGTTCAGGCGGCAGCGGAGAGAGCTCCGGAAT 1020

Db  1032 ACCGGAGATGGTGTTCAGGCGGCAGCGGAGAGAGCTCCGGAAT 1091
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1021 GAAGAGGAGAACACCCACCCCGGGAGCGGGTGCAGCTGCTGCTCTGGGCAAGAGGCAAGTGCTG 1080

Db  1092 GAAGAGGAGAACACCCACCCCGGGAGCGGGTGCAGCTGCTGCTCTGGGCAAGAGGCAAGTGCTG 1151
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1081 CAAGAGGACACTGCAGGGCTGCGACCAAGCTGGAGCACCTGGGCCGGGCGCGCCCGGAGCCCGTG 1211

Db  1152 CAAGAGGACACTGCAGGGCTGCGACCAAGCTGGAGCACCTGGGCCGGGCGCGCCCGGAGCCCGTG 1271
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1141 CAGGAGTTGCTGCGAGACCAAGCTGGAGCACCTGGGCCCCGGGCGCGCCCGGAGCCCCGGTGTGCTG 1200

Db  1212 CAGGAGTTGCTGCGAGACCAAGCTGGAGCACCTGGGCCCCGGGCGCGCCCGGAGCCCCGGTGTGCTG 1271
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Qy  1201 CTCCTGCAGGATGACCGGCACTCCACGTCGTCCTCCGGAGCAGGAGTCGGAGCAGGAGGGGGAGG 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1272 CTCCTGCAGGATGACCGGCACTCCACGTCGTCCTCCGGAGCAGGAGTCGGAGCAGGAGGGGGAGG 1331

Qy  1261 ACACCCACGCTGGAGATCCTTAAGAGCCACATCAGGAATCTTCCGCCCCAAGTTCTCG 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1332 ACACCCACGCTGGAGATCCTTAAGAGCCACATCAGGAATCTTCCGCCCCAAGTTCTCG 1391

Qy  1321 AACCTGTACCGGACTGGAAGGGGAGGCTTTCACCAGCATTCCTTTGCTCATCGACCACCTA 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1392 AACCTGTACCGGACTGGAAGGGGAGGCTTTCACCAGCATTCCTTTGCTCATCGACCACCTA 1451

Qy  1381 CTGAGCACCCAGCAGCCCTCACCAAGAGAGTGGTGTTGTTCCTGCACAGGGCTGTGCCC 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1452 CTGAGCACCCAGCAGCCCTCACCAAGAGAGTGGTGTTGTTCCTGCACAGGGCTGTGCCC 1511

Qy  1441 AAGGACAAGTGGGTGTGTGAACCATGAGGACGCCTGCGAGCCGACAACACCCTGGTGGCGGTGAAG 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1512 AAGGACAAGTGGGTGTGTGAACCATGAGGACGCCTGCGAGCCGACAACACCCTGGTGGCGGTGAAG 1571

Qy  1501 AACTTTGGCGAAGTGTTCAGCCGGACGCCTGACCTGACCCTGACCTGCGGTCTCATTGGTGTCTGCACCCAGAAGGCGGAGGATC 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1572 AACTTTGGCGAAGTGTTCAGCCGGACGCCTGACCTGACCCTGACCTGCGGTCTCATTGGTGTCTGCACCCAGAAGGCGGAGGATC 1631

Qy  1561 TCTTGTGTCGAGAGCGTCCCACCTGACCCTGACCTGCCTCAGGGCCAAGTTTCTACAGGAAGCGAGGATC 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1632 TCTTGTGTCGAGAGCGTCCCACCTGACCCTGACCTGCCTCAGGGCCAAGTTTCTACAGGAAGCGAGGATC 1691

Qy  1621 CTGAAGCAGTACAGACCACCCCAACATCGTGCGTCATTGGTGTCTGCACCAGAAGCAG 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1692 CTGAAGCAGTACAGACCACCCCAACATCGTGCGTCATTGGTGTCTGCACCAGAAGCAG 1751

Qy  1681 CCCATCACATCCTGTCATGGAGCTTGTGCAGGGGGCGACTGCTGCGAGATGGTGCAGCTGCTGGC 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1752 CCCATCACATCCTGTCATGGAGCTTGTGCAGGGGGCGACTGCTGCGAGATGGTGCAGCTGCTGGC 1811

Qy  1741 GAGGGGGGGCCCGGCCCGTGCTGCGGGTGAGACTGCTGCGTCGAGATGGTGGGGATGCAGCTGCTGGC 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1812 GAGGGGGGGCCCGGCCCGTGCTGCGGGTGAGACTGCTGCGTCGAGATGGTGGGGATGCAGCTGCTGGC 1871

Qy  1801 ATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACCTGCTCGGGAACTGCCTG 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1872 ATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACCTGCTCGGGAACTGCCTG 1931

Qy  1861 GTGACAGAGAAGAATGTCCTGAAGATCAGTCAGCTTGGGATGTCCCGGAGGAAGCCGAT 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1932 GTGACAGAGAAGAATGTCCTGAAGATCAGTCAGCTTGGGATGTCCCGGAGGAAGCCGAT 1991

Qy  1921 GGGGTCTATGCAGCCTTCAGCAGTCCCGTGAAGTGGACCGCGCCACCTGAG 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1992 GGGGTCTATGCAGCCTTCAGCAGTCCCGTGAAGTGGACCGCGCCACCTGAG 2051

Qy  1981 GCCCTTAACTACGGCCGCTACTCCTCCGAAAGCGACGTGTGGAGCTTTGGCATCTTGCTC 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2052 GCCCTTAACTACGGCCGCTACTCCTCCGAAAGCGACGTGTGGAGCTTTGGCATCTTGCTC 2111

Qy  2041 TGGGAGACCTTCAGCCTTGTGGAGAAGGGGGGCCGTCTGCCCCCTATCAGCAATCAGCAGACACGG 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2112 TGGGAGACCTTCAGCCTTGTGGAGAAGGGGGGCCGTCTGCCCCCTATCAGCAATCAGCAGACACGG 2171

Qy  2101 GAGTTTGTGGAGAAGGGAGGCTATGAGCCTGGGCCTGGGCCTATGAGCCGCAGTGTCCTCAGCACCATC 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2172 GAGTTTGTGGAGAAGGGAGGCTATGAGCCTGGGCCTGGGCCTATGAGCCGCAGTGTCCTCAGCACCATC 2231

Qy  2161 AGGCTCATGGAGCGCTGCGAGAGCTGCAGAGCTGCGGCCCAGCTTCAGCACCATC 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2232 AGGCTCATGGAGCGCTGCGAGAGCTGCAGAGCTGCGGCCCAGCTTCAGCACCATC 2291

Qy  2221 TACCAGGAGCTGCAGAGCTGCGAGAGAGACCCGAAAGCGGCATCGG 2256

Db  2292 TACCAGGAGCTGCAGAGCTGCGAGAGAGACCCGAAAGCGGCATCGG 2327
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RESULT 2
US-10-660-763-1
; Sequence 1, Application US/10660763
; Publication No. US20040063130A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001183DIVI
; CURRENT APPLICATION NUMBER: US/10/660,763
; CURRENT FILING DATE: 2003-09-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2674
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-660-763-1

Query Match   100.0%;   Score 2256;   DB 18;   Length 2674;
Best Local Similarity 100.0%;   Pred. No. 0;
Matches 2256;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Qy     1  ATGGGCTTCTCTTCTGAGCTGTGCAGCCCCAGGGCCCACGGGGTCTGCAGCAAATGCAG   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    72  ATGGGCTTCTCTTCTGAGCTGTGCAGCCCCAGGGCCCACGGGGTCTGCAGCAAATGCAG  131

Qy    61  GAGGCCGAGCTTCGTCTACTGAGAGGGATGAGAAAGTGGATGGCCCAGCGGGTCAAGAGT  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   132  GAGGCCGAGCTTCGTCTACTGAGAGGGATGAGAAAGTGGATGGCCCAGCGGGTCAAGAGT  191

Qy   121  GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCGAGGACAGTGGGGGCCAGAGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   192  GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCGAGGACAGTGGGGGCCAGAGC 251

Qy   181  CGGGCCATCAGCCTGACAGCCCCATCAGTCAGTCCTCGGCTCCTGGGCTGAGATCACCAGCCAAACT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   252  CGGGCCATCAGCCTGACAGCCCCATCAGTCAGTCCTCGGCTCCTGGGCTGAGATCACCAGCCAAACT 311

Qy   241  GAGGGCCTGAGCGCGTTGCTGCGGCGCACGGCAGCAGGATCTGAACTCAGGGCCCCTGAGC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   312  GAGGGCCTGAGCGCGTTGCTGCGGCGCACGGCAGCAGGATCTGAACTCAGGGCCCCTGAGC 371

Qy   301  AAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCTTCGCAAGGACTTACACCGAGCAGTGG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   372  AAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCTTCGCAAGGACTTACACCGAGCAGTGG 431

Qy   361  CAGCAGCTGCGAGCGCGCTTGCTGGGCGCAGCAGGACACCCCACCAGCAGGACTTGAGAGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   432  CAGCAGCTGCGAGCGCGCTTGCTGGGCGCAGCAGGACACCCCACCAGCAGGACTTGAGAGC 491

Qy   421  CAGTACCGAGCTCTGGACGGACAGTGCCCAAGCCAAGGACCTACCAGGAGGCCAGC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   492  CAGTACCGAGCTCTGGACGGACAGTGCCCAAGCCAAGGACCTACCAGGAGGCCAGC 551

Qy   481  AAAGACAAGGACCGTGACAAGGCCAAGGACAGTATGTGCGCCAGCCTGTGGAAGCTCTTT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   552  AAAGACAAGGACCGTGACAAGGCCAAGGACAGTATGTGCGCCAGCCTGTGGAAGCTCTTT 611

Qy   541  GCTCACCACAACCGCTATGTCGGGGCTGCGGGCTGCGCAGCTACACCACCAC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   612  GCTCACCACAACCGCTATGTCGGGGCTGCGGGCTGCGCAGCTACACCACCAC 671

Qy   601  CACCAGTCCTGCTGCCCGGTCACTCGACGGACCTGACGAGGACCTGACGAGGACGATGGCT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   672  CACCAGTCCTGCTGCCCGGTCACTCGACGGACCTGACGAGGACCTGACGAGGACGATGGCT 731

Qy   661  TGCATCCTGAAGGAGATCCTCCAGGAATACCTGGAGATTAGCAGCCTGGTCAGCAGGATGAG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   732  TGCATCCTGAAGGAGATCCTCCAGGAATACCTGGAGATTAGCAGCCTGGTCAGCAGGATGAG 791
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Qy   721  GTGGTGGCCATCACCGGGGAGATGGCTGCAGCTGCTGCCCGCATCCAGCCTGAGGCTGAG  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   792  GTGGTGGCCATCACCGGGGAGATGGCTGCAGCTGCTGCCCGCATCCAGCCTGAGGCTGAG  851

Qy   781  TACCAAGGCTTCCTGCTGGCAGACAGTGGGTCCGACGTCCCACCTGTGTCACGTTC      840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   852  TACCAAGGCTTCCTGCTGGCAGACAGTGGGTCCGACGTCCCACCTGTGTCACGTTC      911

Qy   841  GATGAGTCACTGCTTGAGGAGGTGAACCGCTGGAGCCTGGGAGCTCAGCTGAACAG      900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   912  GATGAGTCACTGCTTGAGGAGGTGAACCGCTGGAGCCTGGGAGCTCCAGCTGAACAG     971

Qy   901  CTGACTGTGGAGAGCGTGCAGCACGCTGACCTCAGTGACAGTGCTGGCTGTGTGCC      960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   972  CTGACTGTGGAGAGCGTGCAGCACGCTGACCTCAGTGACAGTGCTGGCTGTGTGCC     1031

Qy   961  ACCGAGATGGTGTTCAGGCGCGCAGGAGGAGATGGTTACCGGCGCCAACGAGAGTCCGGAAT 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1032  ACCGAGATGGTGTTCAGGCGCGCAGGAGGAGATGGTTACCGGCGCCAACGAGAGTCCGGAAT 1091

Qy  1021  GAAGAGGAGAACACCCACCCCCGGGAGCGGGCGGGTGCAGTGCGGGTCAAGAGGCAAGTGCTG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1092  GAAGAGGAGAACACCCACCCCCGGGAGCGGGCGGGTGCAGTGCGGGTGCAGCAAGTGCTG 1151

Qy  1081  CAAGAAGCACTGCAGGGCCTGCAGTAGCGCTGTGTGAGCAGCCAGGCCAAGCTGCAGGCCCAG 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1152  CAAGAAGCACTGCAGGGCCTGCAGTAGCGCTGTGTGAGCAGCCAGGCCAAGCTGCAGGCCCCAG 1211

Qy  1141  CAGGAGTTGCTGCGACCAAGCTGGACCACCTGGGCGCTGAGCACCGTGTCTGCTGTG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1212  CAGGAGTTGCTGCGACCAAGCTGGACCACCTGGGCGCTGAGCACCGTGTCTGCTGTG 1271

Qy  1201  CTCCTGAGGATGAACCGCCACTCCACGTGTCCTCCACGTGTCCTGGAGCAGAGTGGGCCAGAGC 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1272  CTCCTGAGGATGAACCGCCACTCCACGTGTCCTCCACGTGTCCTGGAGCAGAGTGGGGAAGG 1331

Qy  1261  ACACCCACGCTGGAGATCCTTAAGAGCCACCAATCTCAGGAATCTTCCGCCCCAAGTTCTCG 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1332  ACACCCACGCTGGAGATCCTTAAGAGCCACCACATCTCAGGAATCTTCCGCCCCAAGTTCTCG 1391

Qy  1321  AACCTGTACCGACTGGAAGGCTTCTCCTTGTGCTCATCGACCACCTA 1380
          |||||||||||||||||||||||||||||||||||||||||||||||
Db  1392  AACCTGTACCGACTGGAAGGCTTTCCTTGTGCTCATCGACCACCTA 1451

Qy  1381  CTGAGCACCCAGCACCCCTCCACAGAAGAGTGGTGTGTTGTCCTGCGACAGGGCTGTGCCC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1452  CTGAGCACCCAGCACCCCTCCACAGAAGAGTGGTGTGTTGTCCTGCGACAGGGCTGTGCCC 1511

Qy  1441  AAGGACAAGTGGGTGCTGAACCATGAGGACGACCTGGTGTTGGGTGAGACGAGATTGGACGGGGG 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1512  AAGGACAAGTGGGTGCTGAACCATGAGGACGACCTGGTGTTGGGTGAGACGAGATTGGACGGGGG 1571

Qy  1501  AACTTTGGCGAAGTGTTCAGGGGACCGCCTGGCGAGCCAGCCCTGGTCGGCGGTGAAG 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1572  AACTTTGGCGAAGTGTTCAGGGGACCGCCTGGCGAGCCAGCCCTGGTCGGCGGTGAAG 1631

Qy  1561  TCTTGTCTGGAGAGACGCTCCCACCTGCCTCAAGGCCAGCCTGTGGAAGCTCTTT 1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1632  TCTTGTCTGGAGAGACGCTCCCACCTGCCTCAAGGCCAGCCTGTGGAAGCTCTTT 1691

Qy  1621  CTGAAGCAGTACAGCAGCCACAACATCGTGGCGTCTCATTGGTGTCTGCCACCAGAAGCAG 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1692  CTGAAGCAGTACAGCAGCCACAACATCGTGGCGTCTCATTGGTGTCTGCCACCAGAAGCAG 1751

Qy  1681  CCCATCTACATCGTCATGGAGAGCTTGTGCAGGGGGGGACTTCCTGGCGACTTCCTCCCACG 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1752  CCCATCTACATCGTCATGGAGAGCTTGTGCAGGGGGGGACTTCCTGGCGACTTCCTCCCACG 1811

Qy  1741  GAGGGGCCCCGCTCGTCTGCAGATGGTGGGGGATGCCAGCTGGCTGGC 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  1812  GAGGGGCCCCGCTCGTCTGCAGATGGTGGGGGATGCCAGCTGGCTGGC 1871

Qy  1801  ATGGAGTACCTGGGAGCAGTGCTGCTCATCCACCGGGACCTGCTGCTCGGAACTGCCTG   1860
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Db   1872 ATGGAGTACCTGGAGAGCAGCAAGTGCTGCATCCACCGGGACCTGGCTCGCTCCGAGAGGACCGCCTG 1931
           ||||||||||||||||
Qy   1861 GTGACAGAGAGAATGTCCTGAAGATCAGTCAGTGACTTTGGGATGTCCCGAGATGAAGCCGAT 1920
           |||||||||||||||||||||||||||||||||||
Db   1932 GTGACAGAGAGAATGTCCTGAAGATCAGTCAGTGACTTTGGGATGTCCCGAGATGAAGCCGAT 1991

Qy   1921 GGGGTCTATCCAGCCTCAGGGGGCCTCAGACAAGTCCCGTGAAGTGACCGCACCTGAG 1980
           |||||||||||||||||||||||||||||||
Db   1992 GGGGTCTATCCAGCCTCAGGGGGCCTCAGACAAGTCCCGTGAAGTGGACCCACCTGAG 2051

Qy   1981 GCCCTTAACTACGGCCGCTACTCCTTCCGAAAGCGACGTGTGGAGCTTTGGCATCTTGCTC 2040
           |||||||||||||||||||||||||||
Db   2052 GCCCTTAACTACGGCCGCTACTCCTTCCGAAAGCGACGTGTGGAGCTTTGGCATCTTGCTC 2111

Qy   2041 TGGGAGACCTTCAGCCTGGGGCCTTCCCCTATCCCACCTCAGCAATCAGCAGACACGG 2100
           |||||||||||||||||||||||||||||
Db   2112 TGGGAGACCTTCAGCCTGGGGCCTTCCCCTATCCCACCTCAGCAATCAGCAGACACGG 2171

Qy   2101 GAGTTTGTGGGAAGGGGGCCGTCTGCCCTGCCCTGCGTGTCTGATGCCGTGTTC 2160
           ||||||||||||||||||||||||||||
Db   2172 GAGTTTGTGGGAAGGGGGCCGTCTGCCCTGCCCTGCGTGTCTGATGCCGTGTTC 2231

Qy   2161 AGGCTCATGGAGCAGTGCTGGGCCTATGAGCCTGGGCAGCGCGCCCAGCTTCAGCACCATC 2220
           |||||||||||||||||||||||||||||||||
Db   2232 AGGCTCATGGAGCAGTGCTGGGCCTATGAGCCTGGGCAGCGCGCCCAGCTTCAGCACCATC 2291

Qy   2221 TACCAGGAGTCTGCAGAGCATCCGAAAGCGGCATCGG 2256
           ||||||||||||||||||||
Db   2292 TACCAGGAGTCTGCAGAGCATCCGAAAGCGGCATCGG 2327

Query Match   89.7%; Score 2023.4; DB 16; Length 2889;
Best Local Similarity 91.4%; Pred. No. 0; Indels 211; Gaps 2;
Matches 2255; Conservative   0; Mismatches   1; Mismatches   0;

Qy   1 ATGGGCTTCTCTTCTGAGCTGCAGCCCCCAGGCCACGGGGTCCTGCAGCAAATGCAG 60
           |||||||||||||||||||||||||||||||
Db   188 ATGGGCTTCTCTTCTGAGCTGTGCAGCTGCAGCCCCCAGGCCACGGGGTCCTGCAGCAAATGCAG 247

Qy   61 GAGGCCGAGTTCGTCTACTGAGGGCATGAGAAAGTGGATGGCCCCAGGGGTCAAGAGT 120
           |||||||||||||||||||||||||||||||
Db   248 GAGGCCGAGTTCGTCTACTGAGGGCATGAGAAAGTGGATGGCCCCAGGGGTCAAGAGT 307

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Qy   1200  GCTCCTGCAGGATGACCGCCACTCCACGTGTCCTCCTGGAGCAGGAGGCGAGAGGGGGAAG  1259
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1388  GCTCCTGCAGGATGACCGCCACTCCACGTGTCCTCCTGGAGCAGGAGGCGAGAGGGGGAAG  1447

Qy   1260  GACACCACCAGCTGGAGATCCTTAAGAGCCACATCTCAGGAATCTTCCGCCCCAAGTTCTC  1319
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1448  GACACCACCAGCTGGAGATCCTTAAGAGCCACATCTCAGGAATCTTCCGCCCCAAGTTCTC  1507

Qy   1320  G------------------------------------------------------------  1320
           |
Db   1508  GCTCCCTCCACCGCTGCAGCTCATTCCGGAGGTGCAGAAGCCCCTGCATGAGCAGCAGTGTG  1567

Qy   1321  ------------------------------------------------------------  1320
Db   1568  GTACACGGGGCCATCCCGAGGGCAGAGGTGCTGCTGGTGCTGACTGGGGACTT  1627

Qy   1321  ------------------------------------------------------------  1320
           AACCTGTACCGACTGAAGGGAAGGCTT
Db   1628  CCTGGTGCGCGGAGAGCCAGGGCAAGCAGGAGTACGTTGCTGCTGTCGGTGTGGGATGGTCT  1687

Qy   1350  TCCTAGCATTCCTTTGCTCATCGACCACTACTGAGCAGCCCTCACCAAGAA  1409
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1688  GCCCCGCACTTCATCATCCAGTCCTTGGATAACCTGTACCGACTGAAGGGAAGGCTT  1747

Qy   1410  GAGTGCTGTGTTGTCCTGCACAGGGCTGTGCCCAAGGACAAGTGGGTGCTGAACCATGAGGA  1469
Db   1748  TCCTAGCATTCCTTTGCTCATCGACCACTACTGAGCAGCCCTCACCAAGAA  1807

Qy   1470  CCTGGTGTTGGGTGAGCAGATTGGACGGGGAACTTTGGCGAAGTGTTCAGCGGACGCCT  1529
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1808  GAGTGCTGTGTTGTCCTGCACAGGGCTGTGCCCAAGGACAAGTGGGTGCTGAACCATGAGGA  1867

Qy   1530  CCTGGTGTTGGGTGAGCAGATTGGACGGGGAACTTTGGCGAAGTGTTCAGCGGACGCCT  1589
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1868  CCTGGTGTTGGGTGAGCAGATTGGACGGGGAACTTTGGCGAAGTGTTCAGCGGACGCCT  1927

Db   1928  GCGAGCCGACAACACCCGGTGGCCGTGAAGTCTTGTGCGAGACGCTCCCACCTGACCT  1987

Qy   1590  CAAGGCCAAGTTCTACAGGAGTTGTTCACAGGAGGGAGGGGAAGGCTTCCTAGCATTCCTTTGCTCATCGACCACTCGT  1649
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1988  CAAGGCCAAGTTCTACAGGAGTTGTTCACAGGAGGGAGGGGAAGGCTTCCTAGCATTCCTTTGCTCATCGACCACCTA  2047

Qy   1650  GCGTCTCATTGGTGTCTGCACCCAGAAGCAGCCCATCGTCATGTCGTCTGTGCA  1709
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2048  GCGTCTCATTGGTGTCTGCACCCAGAAGCAGCCCATCGTCTCAACTTATAGATCATCAC  1977

Qy   1710  GGGGGGCGACTTCCTGACCTTCCTGCCGGAGGGGCCCTGCGCGGGTGAAGACTCT  1769
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2108  GGGGGGCGACTTCCTGACCTTCCTGCCGGAGGGGCCCTGCGCGGGTGAAGACTCT  2037

Qy   1770  GCTGCAGATGGTGGGGGATGCAGCTGCTGGCATGGGGATGCAGGTACCTGGGCAAGCAGTGCTGCAT  1829
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2168  GCTGCAGATGGTGGGGGATGCAGCTGCTGGCATGGGGATGCAGGTACCTGGGCAAGCAGTGCTGCAT  2097

Qy   1830  CCACCCGGGACCTGGCTGCTCCGGAGAGGAGAAGAGGATGCCTCGACAGGAGAATGTCCTGAAGATCAG  1889
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2228  CCACCCGGGACCTGGCTGCTCCGGAGAGGAGAAGAGGATGCCTCGACAGGAGAATGTCCTGAAGATCAG  1557

Qy   1890  TGACTTGGGATGTCCCGAGGAAGCCGATGGGGTCTATCGGGTCTATGGGTCCTTAACTACGGCCCGTACTCCTCCGA  1949
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2155  AAAACATGTAAAGAAGATCTTCCTCAGGAATTGAAAATAAAATTTTTTACAAGAAGCCAAA  2214

Qy   1950  ACAAGTCCCCGTGAAGTGGACCACCTGGAAGTGGACCACCTGGGTCTACTCCTCCGA  2009
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2288  ATCCTGAAGCAGTACAGCAATATGATCATCCCAATATTGCTCAAACTTACAGGAGTTTGCACACAAAGA  1677

Qy   2010  AAGCGACGTGTGGAGCTTGGAGCTTTGGCATCTTGCTCTCGGGAGACCTTCAGCCTGGGGGCCTCCCC  2069
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1678  CAGCCCATCTACATACTCTCATCGGAGCTTGTGCAGGGGGACTTCCTGACCTTCCTGCCGC  1737

Qy   2070  CTATCCCAACCTCAGCAATCAGCAATCAGCAGACATCGAGCTGTTGTGGAGGTGGAGGTTGGCTGCCT  2129
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2335  AGGAAGAAGGATGAACTAAAACTCAAACAGTTAGTGAAATTTCATTAGACGCTGCTGCT  2394
```

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Db   2468  CTATCCCAACCTCAGCAATCAGCAGACATCAGCAGACACGGGGGGGGGGGGCCGTCTGCC  2527
Qy   2130  CTGCCCAGAGCTGTGTCCTGATGCCGTGTTCAGGCTCATGAGCCAGTGCTGCGGCCTATGA  2189
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2528  CTGCCCAGAGCTGTGTCCTGATGCCGTGTTCAGGCTCATGAGCCAGTGCTGCGGCCTATGA  2587
Qy   2190  GCCTGGGCAGCGGCCCAGCTTCAGCAGTCGCAGCCATCTCAGGAGCTGCAGCACGTGCAGAGCATCCGAAAGCG  2249
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2588  GCCTGGGCAGCGGCCCAGCTTCAGCAGTCGCAGCCATCTCAGGAGCTGCAGCACGTGCAGAGCATCCGAAAGCG  2647
Qy   2250  GCATCGG  2256
           |||||||
Db   2648  GCATCGG  2654
```

RESULT 4

US-10-887-553A-240

; Sequence 240, Application US/10887553A
; Publication No. US2005008543GA1
; GENERAL INFORMATION:
; APPLICANT: Garza, Dan
; APPLICANT: Li, Hao
; TITLE OF INVENTION: Method to treat conditions associated
; TITLE OF INVENTION: with insulin signalling dysregulation
; FILE REFERENCE: 4-33262
; CURRENT APPLICATION NUMBER: US/10/887,553A
; CURRENT FILING DATE:　2004-07-08
; PRIOR APPLICATION NUMBER: 60/485,883
; PRIOR FILING DATE: 2003-08-07
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 240
;   LENGTH: 2950
;   TYPE: DNA
;   ORGANISM: human

US-10-887-553A-240

```
Query Match            14.6%;    Score 328.8;  DB 21;   Length 2950;
Best Local Similarity  62.0%;    Pred. No. 1.8e-72;
Matches   573;  Conservative    0;  Mismatches  342;  Indels   9;  Gaps   3;
```

```
Qy   1321  AACCTGTACCGACTGAAGGGAGGGGAAGGCTTCCTAGCATTCCTTTGCTCATCGACCACCTA  1380
           |||||||||||||||||||||||||||||||||||||||||||||| |||
Db   1918  AACATGTATCGATTCGAGGGGCACTGGGTTTCAAACATTCCTCAACTTATAGATCATCAC  1977
Qy   1381  CTGAGCACCCAGCAGCCCTCACCAAGAAGAGTGGTGTCGTCGCACAGGGCTGTGCCC  1440
           ||||||||||||||||||| |||||||||||||| ||
Db   1978  TATACAACAAAACAGTCATCACTACTAAGAAATCAGGTGAGTTCTGCGAATCCTATTCCT  2037
Qy   1441  AAGGACAAG---TGGGTGCTGAACCATGAGGACCTGGTGTTGGGTGAGCAGATTGGACGG  1497
           |||||||      ||||||||| |||| ||||||||||
Db   2038  AAGGACAAGAACAGAAATGAGATTCTCAGTCATGAAGATGTCATGATTGGGAGAATTACTACTGGGCAAG  2097
Qy   1498  GGGAACTTTGGCGAAGTGTTCAGCGGACGCCTGCGAGCCGACAACACCCGGTGGCCGCGTG  1557
           ||                                     ||
Db   2098  GGAAATTTTGGTGAAGTATATAAGG---GCACATTAAAGGATAAAAACTTCTGTGTGCTGTT  2154
Qy   1558  AAGTCTTGTGCGAGAGACGCTCCCACCTGACCTCAAGGCCAAGTTCTACAGGAGGAAGGAGG  1617
           |||||||||||||||||||||||||
Db   2155  AAGTCTTGTGCGAGAGACGCTCCCACCTGACCTCAAGGCCAAGTTCTACAGGAGGAAGGAGG  2214
Qy   1618  ATCCTGAAGCAGTACAGCAATATGATCATCCCAATATTGCTCAAACTTACAGGAGTTTGCCCGA  1677
           |||| |||||||||||||||||| || |||
Db   2215  ATTCTCAAGCAGTACAGCAATATGATCATCCCAATATTGTCAAGGGGGACTTCCTGACCTTCCTGCCGCGC  1737
Qy   1678  CAGCCCATCTACACTCTCATCGGAGCTTGTGGTGTTTCAGGAGGTGATCTGGTGTTCCTCACCTTTCTCTGAGA  1737
           |||||||||||||
Db   2275  CAGCCTGTCTACATCATTATTGAACTTGGTTTCAGGGTGAATGGGTGAAGATGGGATCGCATGT  2334
Qy   1738  ACGGAGGGGGGCCGGCCTGCGAGCTTGTGCTGCTGGGAGACTCTGCTGCTGAGAGAAGTGCTGCT  1797
           |||||| |  |||
Db   2335  AGGAAGAAGGATGAACTAAAACTCAAACAGTTAGTGAAATTTCATTAGACGCTGCTGCT  2394
```

Db   240 CATCCACCGGGACCTGGCTGTCTCCGGAACTGCTCCTCGGTGACAGAGAAGAATGTCCTGAAGAT 299

Qy   1887 CAGTGACTTTGGGATGTCCCGAGAGGAAGCGACGATGGGGTCTATGCAGCCTCAGGGGGCCT 1946
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   300 CAGTGACTTTGGGATGTCCCGAGAGGAAGCCGATGGGGTCTATGCAGCCTCAGGGGGCCT 359

Qy   1947 CAGACAAGTCCCGTGAAGTGGACCGCACCTGAGGCCTTAACTACGGCCGCTACTCCTC 2006
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   360 CAGACAAGTCCCGTGAAGTGGACCGCACCTGAGGCCCTTAACTACGGCCGCTACTCCTC 419

Qy   2007 CGAAAGCGACGTGTGGCATCTT 2036
           |||||||||||||||||||||||
Db   420 CGAAAGCGACGTGTGGAGCTTTGGCATCTT 449

RESULT 6
US-09-948-802-5
; Sequence 5, Application US/09948802
; Publication No. US20020172981A1
; GENERAL INFORMATION:
; APPLICANT: ROBISON, KEITH E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
; TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR
; FILE REFERENCE: MNI-090
; CURRENT APPLICATION NUMBER: US/09/948,802
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 09/387,212
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 361
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: All occurences of n indicate any nucleotide
US-09-948-802-5

Query Match   13.1%; Score 296.2; DB 9; Length 361;
Best Local Similarity   97.4%; Pred. No. 2e-64;
Matches   333; Conservative   0; Mismatches   4; Indels   5; Gaps   3;

Qy   1613 CGAGGATCCTGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCC 1672
           || ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   20 CNAGGATCCTGAAGCAGTACAGCCACCACCAACATCGTGCGTCTCATTGGTGTCTGCACCC 79

Qy   1673 AGAAGCAGCAGCCATCTACATCGTCATCGTGTGTCAGGGGGGACTTCCTGACCTTCC 1732
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   80 AGAAGCAGCAGCCATCTACATCGTCATCGTGTGTCAGGGGGGACTTCCTGACCTTCC 139

Qy   1733 TCCGCACGAGGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGTGGGGGATGCAG 1792
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   140 TCCGCACGAGGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGTGGGGGATGCAG 199

Qy   1793 CTGCTGGCATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACCTGGCTGCTCGGA 1852
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   200 CTGCTGGCATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACCTGGCTGCTCGGA 259

Qy   1853 ACTGCCTGGTGCACAGAAGAAGAATGTCCTGAAG-ATCAGTGACTTT-GGGATGTCCCGAGA 1910
           ||||||||||||||||||||||||||||||||| |||||||||||| ||||||||||||||
Db   260 ACTGCCTGGTGCACAGAAGAAGAATGTCCTGAAGAATCAGTGACTTTGGGATGTCCCGAGA 319

Qy   1911 GGAAGCC---GATGGGGTCTATGCAGCCTCAGGGGGCCTCAG 1949
           |||||| |||||||||||||||||||||||||||||||
Db   320 GGAAGCCCGATTGGGGGTCTATGCAGCCTCAGGGGGCCTCAG 361

RESULT 7
US-10-121-925-5
; Sequence 5, Application US/10121925
; Publication No. US20030104505A1
; GENERAL INFORMATION:
; APPLICANT: ROBISON, KEITH E.

Qy   1798 GGCATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACCTGGCTGCTCGGAACTGC 1857
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2395 GGTATGTTGTATCTCGAGAGTAAAAACTGTATACACAGGGACCTTGCTGCAAGAGAAACTGC 2454

Qy   1858 CTGGTGACAGAGAGAATGTCCTGAGATCAGTGACTTTGGGATGTCCCGAGAGGAAGCC 1917
           ||||| ||||| |||||||||| ||||||||||||||||||| |||||||||||||||
Db   2455 CTGGTAGGTGAAAATAATGTTCTGAAAATCAGTGACTTTGGAATGTCTCGTCAAGAGGAT 2514

Qy   1918 GATGGGGTCTATGCAGCCTCAGGGGCCTCAGACAAGTCCCGTGAAGTGGACCGCACCT 1977
           ||||| |||| ||| || ||||||||||||| ||| || |||||||| |||||||||
Db   2515 GGTGGAGTGTATTCATCTTC---TGGCTTAAAGCAGATTCCATTAAATGGACAGCACCG 2571

Qy   1978 GAGGCCCTTAACTACGGCCGCTACTCCTCCGAAAGCGACGTGTGGCATCTTG 2037
           |||| ||||| |||||||||||||||| |||||||||| ||| ||| |||||
Db   2572 GAAGCTCTTAATTATGGGAGATACAGTTCAGAGAGTGACGTGTGGCATCCTT 2631

Qy   2038 CTCTCGGAGACCTTCAGCGTGGGGCCTCTCAGCCCCTCCCCATCCCCATCCCCAACCTCAGCAATCAGCAGACA 2097
           ||||| || ||||||||| ||| ||| ||| ||| ||| || ||| ||||||||||||||| |||||
Db   2632 CTCTGGGAGACCTTCAGCTTGGGGGTTTGTCCGTACCCTGGAATGACAAATCAGCAAGCA 2691

Qy   2098 CGGGAGTTTGTGGAGAGGGGGCCGTCGCCTCGCCTCGCCCAGAGTCTGTCCTGATGCCGTG 2157
           | |||| ||| |||| || |||| |||||| ||||||||||| | || || |||
Db   2692 AGAGAGCAAGTAGAAAGAGGATACCGGATCAGCTGCCACTGTCCAGAGGATATT 2751

Qy   2158 TTCAGGCTCATGGACGAGCAGTGCTGGCCTATGAGCCTGGGCAGCCGCCCAGCTTCAGCACC 2217
           |||||||| ||||| ||||| | |||||| |||| | ||| |||| |||||| || |||
Db   2752 TCCAAAATCATGATGAAGTGTTGGGATTATAAACCTGAAAAATCGCCCTAAGTTCAGTGAA 2811

Qy   2218 ATCTACCAGGAGCTGCAGAGCCATC 2241
           ||| || || ||| |||||| ||||
Db   2812 CTTCAGAAAGAGCTCACTACTATCATC 2835

RESULT 5
US-09-918-995-1503
; Sequence 1503, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1503
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(449)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-1503

Query Match   14.5%; Score 326.8; DB 10; Length 449;
Best Local Similarity   99.4%; Pred. No. 4.3e-72;
Matches   328; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy   1707 GCAGGGGGGGCCGACTTCCTGACCTTCCTCCGCACGAGGGGGCCCGCCTGCGGGTGAAGAC 1766
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   120 GCGAGGGGGGCCGACTTCCTGACCTTCCTCCGCACGAGGGGGCCCGCCTGCGGGTGAAGAC 179

Qy   1767 TCTGCTGCAGATGTGGGGGATGCAGCTGCTGGCATGGAGTACCTGGAGAGCAAGTGCTG 1826
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   180 TCTGCTGCAGATGTGGGGGATGCAGCTGCTGGCATGGAGTACCTGGAGAGCAAGTGCTG 239

Qy   1827 CATCCACCGGGACCTGGCTGCTCGGAACTGCCTGGTGCACAGAGAAGAATGTCCTGAAGAT 1886
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

```
;   TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
;   TITLE OF INVENTION:  PHOSPHATASE HOMOLOGUES AND USES THEREFOR
;   FILE REFERENCE: MNI-090
;   CURRENT APPLICATION NUMBER: US/10/121,925
;   CURRENT FILING DATE:  2002-04-12
;   PRIOR APPLICATION NUMBER: US/09/948,802
;   PRIOR FILING DATE: 2001-09-07
;   PRIOR APPLICATION NUMBER: 09/387,212
;   PRIOR FILING DATE: 1999-08-31
;   NUMBER OF SEQ ID NOS: 18
;   SOFTWARE: Patentin Ver. 2.0
;
; SEQ ID NO 5
;   LENGTH: 361
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: All occurences of n indicate any nucleotide
US-10-121-925-5

Query Match             13.1%;    Score 296.2; DB 15; Length 361;
Best Local Similarity   97.4%;    Pred. No. 2e-64;
Matches  333;   Conservative    0;  Mismatches   4;  Indels   5;  Gaps   3;

Qy   1613 CGAGGATCCTGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCC 1672
          | ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db     20 CNAGGATCCTGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCC   79

Qy   1673 AGAAGCAGCCCATCTACATCGTCATGGAGCTTGTGCAGGGGGGCACTTCCTGACCTTCC 1732
          |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db     80 AGAAGCAGCCCATCTACATCGTCATGGAGCTTGTGCAGGGGGGCACTTCCTGACCTTCC  139

Qy   1733 TCCGCACGGAGGGGCCCGCCGGGGTGAGACTCGTCGCAGATGGTGGGGATGCAG 1792
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    140 TCCGCACGGAGGGGGCCGCCGGGGTGAGACTCGTCGCAGATGGTGGGGATGCAG  199

Qy   1793 CTGCTGCATGGAGTACCTGACAGAGAAGAAGTCGTCGCATCCACCGGGACCTGCTCGGA 1852
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    200 CTGCTGCATGGAGTACCTGACAGAGAAGAAGTCGTCGCATCCACCGGGACCTGCTCGGA  259

Qy   1853 ACTGCCTGGTGACAGAGAAGAATGTCCTGAAG-ATCAGTGACTTT-GGGATGTCCCGAGA 1910
          ||||||||||||||||||||||||||||||||| |||||||||| |||||||||||||||
Db    260 ACTGCCTGGTGACAGAGAAGAATGTCCTGAAGAATCAGTGACTTTGGGGATGTCCCGAGA  319

Qy   1911 GGAAGCC--GATGGGGTCTCATGCAGCCTCAGGGGGCCTCAG 1949
          |||||||  |||||||||||||||||||||||||||||||||
Db    320 GGAAGCCCGATTGGGGTCTCATGCAGCCTCAGGGGGCCTCAG  361
```

RESULT 8
US-10-280-576-19
; Sequence 19, Application US/10280576
; Publication No. US20040044405A1
; GENERAL INFORMATION:
;   APPLICANT: Wolff, Matthew R.
;   TITLE OF INVENTION: VASCULAR STENT OR GRAFT COATED OR IMPREGNATED WITH PROTEIN
;   FILE REFERENCE: 09820.189
;   CURRENT APPLICATION NUMBER: US/10/280,576
;   CURRENT FILING DATE: 2002-10-22
;   PRIOR APPLICATION NUMBER: 60/343,732
;   PRIOR FILING DATE: 2001-10-25
;   NUMBER OF SEQ ID NOS: 25
;   SOFTWARE: Patentin version 3.1
;
; SEQ ID NO 19
;   LENGTH: 1779
;   TYPE: DNA
;   ORGANISM: Drosophila melanogaster
US-10-280-576-19

Query Match   12.0%;   Score 271.6; DB 18; Length 1779;
Best Local Similarity   57.0%;   Pred. No. 4e-58;
Matches 518;   Conservative   0; Mismatches 384; Indels   6; Gaps   1;

```
Db    844 TTCCGGTTCGAGGGACCACCATTTGCCAGCATCCAGAGAGCTGATCATGCAGTATCAC  903
          | ||| | ||   || |||        ||  |    ||  ||| ||| ||| ||  |||
Qy   1387 ACCCAGCAGCCCCTCACCCAGAAGAGTGGTGTTGTCTGCCACAGGAGCTGTGCCCAAGGAC 1446
          |    ||   ||     ||| ||| ||    |||    |   ||| ||||||     |||
Db    904 TCGGAATTGCCAGTGACCGTGAATCGGAGCCATACTCCGCAGACCCGTTTGCCGGGAG  963

Qy   1447 AAGTGGTGCTGAACCATGAGACCTCGTGTTGGGGTGAGCAGCAGATTGGACGGGGGAACTTT 1506
          ||| ||| |||||| || || || ||   | ||  ||| ||||  || ||  |  ||  |||
Db    964 CGCTGGGAGCTGAGCAACGATGATGTGTACTTCTGGAGGATTGGTCGGGGGAAACTTT 1023

Qy   1507 GGCGAAGTGTTCAGCGACGCCTGCGAGCCGACAACACCCTGTGGCGGTGAAGTCTTGT 1566
          |||||| |||||||||    || ||| ||     ||||  | || ||||  ||| |||
Db   1024 GGGGATGTCTACAAGGCCAAATGGGATGTGGCTGTCAAAACCTGT 1083

Qy   1567 CGAGAGACGCTCCCACCTGACCTCAAGGCCAAGTTTCTACAGGAAGCGAGGATCCTGAAG 1626
          |||| ||  |||  ||| || ||| ||  | |  | || ||| |||| |||   || |||
Db   1084 CGAATGACCCCTGCCCGACGAACAGAGACGTAAATTCCTACACGAAGGGCCATCCTCAAG 1143

Qy   1627 CAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCCAGAAGCAGCCCATC 1686
          |||| |   ||||| || ||  || || | ||  ||| ||  |||||  || | ||||||
Db   1144 CAATACGATCATCCAAATATCGTAAAATTGATTGGCATTTGTGCGAAGCAGCCCATC 1203

Qy   1687 TACATCGTCATGGAGCTTGTGCAGGGGCGACTTCCTCCGCACGTGCTGGCATGGAG 1746
          || ||| |  ||| || |  || || || |  |   |   |    | || ||| |||
Db   1204 ATGATTGTCATGGAATTGGTCGTGGTTCGCTTTTAACTATTTACGCAAGAACTCC 1263

Qy   1747 GCCCGCCTGCGGGTGAAGACTCGTCTGCAGATGGTGGGGGGATGCAGCTGCTGCGGCATGGA 1806
          |  |||   || || |||     |   |||  | || | || || ||   || || || |
Db   1264 AATGGCCTCACCACTGCCAACAAAATGGCATGGCATGTGCGAGATGCGGGGGCAGGCATGGA 1323

Qy   1807 TACCTGGAGAGCAAGTCTGCATCCACCGGGACTGCCTGGTGACA 1866
          || |||||||||| ||||| | ||  |   ||  ||  ||| ||
Db   1324 TATCTGGAGTCCAAAAACTGCATTCATCGGCATCTCGGCGGCGTAATTGTCTCGTTGAC 1383

Qy   1867 GAGAAGAATGTCCTGAAGATCAGTAGCATCAGTGACTTTGGGATGTCCGATGGGGTC 1926
          |||||||||| |||||  || | |  | | |||| || || ||  | | | || ||
Db   1384 TTGGACCACAGTGTGAAGATCCTCGCGATTTCCGATTTCCGGCAGATCCGCGGAGAA 1437

Qy   1927 TATGCAGCCTCAGGGGCCCTGAAGTGACCCACCTGAGGCCCTT 1986
          || | || | ||   | ||  |||| || || |  || ||| |
Db   1438 TATATAGTTTCCGATGCATGAAACAAATACCTGTGAAGTGAAGTGAAGTGCAGCGTCCCCAGGCCTTG 1497

Qy   1987 AACTACGGCCGCTACTCCTCCGAAAGCGACGTGTGAAGCTTTGGCATCTTGCTCTGGGAG 2046
          || ||  || |||| | ||   || |||| ||| || |   ||  || || | | | |||
Db   1498 AATTTCGGCAAGTACACTTCGTTGTGCGATGTGCTGCGATGGCATACTGATGTGGGAG 1557

Qy   2047 ACCTTCAGCCTGGGGCCTCCCCCCATCCCAACCTCAGCAATCAGACACGGGAGTTT 2106
          |||| |  || |  | ||  ||  ||    ||  | ||   || ||| ||  |||
Db   1558 ATCTTCTTCCAAGGGCGGCACGACACCCTACTCCCGCAGAGCCGCAGAGAGCGC 1617

Qy   2107 GTGGGAAGGGGGGGCCGTCTGCCCTGCCCTGTGTCCTGATGCCGTTCAGCTC 2166
          ||  |  ||| | ||  | ||| | ||     | | || | |   ||| |||
Db   1618 ATCGATACGGGGATATCGTATGCCAACGCCAACGAGAGCAGCGGCCCAGCTTCAGCACCATCTACCACTG 1677

Qy   2167 ATGGAGCAGTGCTGGGGCTATGAGCCTGGGCAGGCGGCCCAGCTTCAGCACCATCTACCACCAG 2226
          ||| ||     || ||| | |   ||   ||| || || ||||| | |||  ||  || ||
Db   1678 ATGCTCCAGTGCTGGGCAGCCGGAATCCCGACCGCATTTCGATGAGATCTACAAT 1737

Qy   2227 GAGCTGCA 2234
          ||| ||||
Db   1738 GTGGTGA 1745
```

RESULT 9
US-10-003-295-3
; Sequence 3, Application US/10003295
; Publication No. US20020168741A1
; GENERAL INFORMATION:
;   APPLICANT: GAN, Weiniu et al.
;   TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;   TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;   TITLE OF INVENTION: THEREOF

; FILE REFERENCE: CL001183DIV
; CURRENT APPLICATION NUMBER: US/10/003,295
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15297
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-003-295-3

Query Match　　10.1%;　　Score 227.2; DB 13; Length 15297;
Best Local Similarity　71.1%;　Pred. No. 7.9e-47;
Matches 394;　Conservative　0; Mismatches　8; Indels 152; Gaps　1;

Qy　　1 ATGGGCTTCTCTTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG 60
2563 ATGGGCTTCTCTTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG 2622

Qy　 61 GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGGACAGTGGGGGC 120
Db 2623 GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGGACAGTGGGGGC 2682

Qy　121 GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTCCCAGAGC 180
Db 2683 GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGCCAGAGC 2742

Qy　181 CGGGGCCATCAGCCCTGACAGCCCCATCAGTC----------------------- 211
Db 2743 CGGGGCCATCAGCCCTGACAGCCCCATCAGTCAGGTCAGGTGGGTCTCTATGGGACTCTGGTGGGT 2802

Qy　212 --- 211
Db 2803 GCTGGCGTATCTGCCTTCTCCTTCTCCTCGGGGCCCTCTCGGGGCAGTGGCTGGAGAT 2862

Qy　212 --- 211
Db 2863 CTGGCAGGCCAATGCTGGGAGGCCATTGTGCCCCTCCCCCATCTGTGCTG 2922

Qy　212 --AGTCCTGGGCTGAGATCACCAGCCAAACTGAGGGGCCTGAGCCGCTTGCTGCGGCAGC 268
Db 2923 TATAGTCCTGGGCTGAGATCACCAGCCAAACTGAGGGGCCTGAGCCGCTTGCTGCGGCAGC 2982

Qy　269 ACGCAGAGAGGATCTGAACTCAGGGGCCCTGAGCAAGCTGCTGCTCATCCGGGAACGGC 328
Db 2983 ACGCAGAGAGGATCTGAACTCAGGGGCCCTGAGCAAGCTGCTGCTCATCCGGGAACGGC 3042

Qy　329 AGCAGCTTCGCAAGACCTACAGCAGCAGTGGCAGCAGCTCACCAAGA 388
Db 3043 AGCAGCTTCGCAAGACCTACAGCAGCAGTGGCAGCAGCTCACCAAGG 3102

Qy　389 CCCACAGCCAGGAC 402
Db 3103 TGAGCGGGCAGCAC 3116

RESULT 10
US-10-660-763-3
; Sequence 3, Application US/10660763
; Publication No. US2004006313OAl
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001183DIVII
; CURRENT APPLICATION NUMBER: US/10/660,763
; CURRENT FILING DATE: 2003-09-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15297
; TYPE: DNA

; ORGANISM: Homo sapiens
US-10-660-763-3

Query Match　　10.1%;　　Score 227.2; DB 18; Length 15297;
Best Local Similarity　71.1%;　Pred. No. 7.9e-47;
Matches 394;　Conservative　0; Mismatches　8; Indels 152; Gaps　1;

Qy　　1 ATGGGCTTCTCTTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG 60
Db 2563 ATGGGCTTCTCTTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG 2622

Qy　 61 GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGGACAGTGGGGGC 120
Db 2623 GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGGACAGTGGGGGC 2682

Qy　121 GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTCCCAGAGC 180
Db 2683 GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGCCAGAGC 2742

Qy　181 CGGGGCCATCAGCCCTGACAGCCCCATCAGTC----------------------- 211
Db 2743 CGGGGCCATCAGCCCTGACAGCCCCATCAGTCAGGTCAGGTGGGTCTCTATGGGACTCTGGTGGGT 2802

Qy　212 --- 211
Db 2803 GCTGGCGTATCTGCCTTCTCCTTCTCCTCGGGGCCCTCTCGGGGCAGTGGCTGGAGAT 2862

Qy　212 --- 211
Db 2863 CTGGCAGGCCAATGCTGGGAGGCCATTGTGCCCCTCCCCCATCTGTGCTG 2922

Qy　212 ---AGTCCTGGGCTGAGATCACCAGCCAAACTGAGGGGCCTGAGCCGCTTGCTGCGGCAGC 268
Db 2923 TATAGTCCTGGGCTGAGATCACCAGCCAAACTGAGGGGCCTGAGCCGCTTGCTGCGGCAGC 2982

Qy　269 ACGCAGAGAGGATCTGAACTCAGGGGCCCTGAGCAAGCTGCTGCTCATCCGGGAACGGC 328
Db 2983 ACGCAGAGAGGATCTGAACTCAGGGGCCCTGAGCAAGCTGCTGCTCATCCGGGAACGGC 3042

Qy　329 AGCAGCTTCGCAAGACCTACAGCAGCAGTGGCAGCAGCTCACCAAGA 388
Db 3043 AGCAGCTTCGCAAGACCTACAGCAGCAGTGGCAGCAGCTCACCAAGG 3102

Qy　389 CCCACAGCCAGGAC 402
Db 3103 TGAGCGGGCAGCAC 3116

RESULT 11
US-10-101-510-525
; Sequence 525, Application US/10101510
; Publication No. US20030144829SAl
; GENERAL INFORMATION:
; APPLICANT: WAN, JACKSON
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/10/101,510
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/276,947
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 525
; LENGTH: 3875
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-525

Query Match　　　8.9%;　　Score 201.2; DB 15; Length 3875;
Best Local Similarity　54.9%;　Pred. No. 2.2e-40;
Matches 423;　Conservative　0; Mismatches 338; Indels　9; Gaps　1;

; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2955
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; TITLE: Eph A1
; PATENT DOCUMENT NUMBER: NM00532
US-10-384-339C-1

Query Match   8.8%;   Score 198;   DB 19;   Length 2955;
Best Local Similarity 54.7%;   Pred. No. 1.4e-39;
Matches 421;   Conservative 0;   Mismatches 340;   Indels 9;   Gaps 1;

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Qy  1451 GGGTGCTGAACCATGAGGACCTGGTGTTGGGTGAGCAGATTGGACGGGGAACTTTGGCG 1510
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Db  1874 GGGAGCTTGATCAGCGTGGCTGATGGTGGACACTGTCATAGGAGAAGGAGAGTTTGGGG 1933

Qy  1511 AAGTGTTCAGCGGACGACGCCTGCGAGCC--------GACAACACCCTGTGCGGTGAAGT 1561
         |||||| || ||| ||| | |  ||| ||        | ||| | | ||||| | |  || 
Db  1934 AAGTGTATCGAGGGACCCTGAGGCTCCCCAGCCAGGACTGCAAGACTGTGGCCATTAAGA 1993

Qy  1562 CTTGTCGAGAGACGCTCCCACCTGACCTCAAGGCCAGTTTCTACAGGAAGGCAGGATCC 1621
         | | |  | ||| | | ||||   | | | | ||||||| |  | || | || | | || 
Db  1994 CCTTAAAAGACACATCCCCAGGTGGGCCAGTGTGGGGAACTTCCTTCGAGAGGCAACTATCA 2053

Qy  1622 TGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCCAGAAGCAGC 1681
         ||   |||| | |||||||  | | |  | | | || |||  || | ||| | ||| |||
Db  2054 TGGGCCAGTTTAGCCACCCGCATATTCTGAAGGCGTCGTCACAAAGCGAAAGC 2113

Qy  1682 CCATCTACATCGTCATGGAGCTTGTGCAGGGGGGGGACTTCCTGCTGGTGGGGGAGC 1741
         | ||| | || || | | |  | || | |  ||| |||||||| | || | |||||||
Db  2114 CGATCATGATCATCACAGAATTTATGGAGAATGCAGCCCTGGATGCCTTCCTGAGGGGAGC 2173

Qy  1742 AGGGGGCCCGCCTGCGGGTGAAGACTTGCTGCTGGGGATGGGGGATGCCAGCTGGTGCTGCA 1801
         ||| || |||| |||| | | || |  | | | | || ||| | | || | ||  | ||||
Db  2174 GGGAGGACCAGCTGGTCCCTGGGGACCTGGGCCATGCTGCAGGCGCATAGCATCTGGCA 2233

Qy  1802 TGGAGTACCTGGAGAGCAAGTGCTGCATCACCGGACTTGGGCCTGCTCG 1861
         || | ||||| | |  | || | | ||  |  || ||| | |||||| |
Db  2234 TGAACTACCTCAGTAATCACAATTATGTCCACCGGGACGTCTGGCCTGCTGCA 2293

Qy  1862 TGACAGAGAAGAATGTCCTGGAAGCGACGTGTCCCGAGAGGAAGCCGATG 1921
         ||   | | || | || | | |  ||  ||| |  | | | || || | |
Db  2294 TGAATCAAAACCTGTCTGCTGCAAGGTGTCTGACTTTGGGATTGTGATGACT 2353

Qy  1922 GGGTCTATGCAGCCTCAGGGGGGCCTCAGACAAGTCCCCGTGAAGTGGACCGCACCTGAGG 1981
         ||| ||||  ||| ||||| ||  |    || | | ||  || || |||  |  | || ||
Db  2354 TTGATGCCACATACGAAACCGGGAGGAAAGATCCCTATCCGTTGGGACTCGTGTATGG 2413

Qy  1982 CCCTAACTACGGCCGCTACTCCTCCGAAAGCCGACGTGTGGACATCTTGCTCT 2041
         || | ||| | || | | |  |||| |  |||   | | || |  |  | | |
Db  2414 CCATTGCCCCATCGGATCTTCACCACAGCCAGGATGTGTGGGATTGTGATGT 2473

Qy  2042 GGGAGACCTTCAGCCTGGGGGCCTCGGGG 2101
         ||||| |||| |||| ||| | | | |||
Db  2474 GGGAGGTGCTGAGCTTTGGGGACAAGCCTTATGGGGAGATGAGCAATCAGGAGGTTATGA 2533

Qy  2102 AGTTTGTGGAGAAGGGGGGCCCGTCTGCCCCG 2161
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Db  2534 AGAGCATTGAGGATGGGTACCCGGTTGCCCTCG 2593

Qy  2162 GGCTCATGGAGCAGTGCTGGGCCTGGGCCGGCCCAGCTTC 2211
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Db  2594 AGCTCATGAAGAACTGCTGGGCATATGACCCGCCGCCGGCCACACTTC 2643
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RESULT 12
US-10-384-339C-1
; Sequence 1, Application US/10384339C
; Publication No. US20040175703A1
; GENERAL INFORMATION:
; APPLICANT: Kreutzer, Roland
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF A TARGET GE
; FILE REFERENCE: 20200/2002
; CURRENT APPLICATION NUMBER: US/10/384,339C
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: PCT/EP02/00152
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: DE 10100586.5
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: DE 10155280.7
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: DE 10158411.3
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: DE 10160151.4
; PRIOR FILING DATE: 2001-12-07

RESULT 13
US-09-967-768A-144
; Sequence 144, Application US/09967768A
; Patent No. US20020150877A1
; GENERAL INFORMATION:

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;   APPLICANT: Augustus, Meena
;   TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
;   TITLE OF INVENTION:   Sets
;   FILE REFERENCE: 689290-72
;   CURRENT APPLICATION NUMBER: US/09/967,768A
;   CURRENT FILING DATE:  2001-09-28
;   PRIOR APPLICATION NUMBER: US/60/236,109
;   PRIOR FILING DATE: 2000-09-28
;   PRIOR APPLICATION NUMBER: US/60/236,034
;   PRIOR FILING DATE: 2000-09-28
;   PRIOR APPLICATION NUMBER: US/60/236,111
;   PRIOR FILING DATE: 2000-09-28
;   NUMBER OF SEQ ID NOS: 325
;   SOFTWARE: PatentIn version 3.0
;   SEQ ID NO 144
;   LENGTH: 3370
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-967-768A-144

Query Match       8.8%;    Score 198;  DB 9;  Length 3370;
Best Local Similarity   54.7%;    Pred. No. 1.4e-39;
Matches   421;  Conservative    0;  Mismatches  340;    Indels    9;  Gaps    1;

Qy     1451 GGGTGCTGAACCATGAGGACCTGGTTGGGTGAGCAGATTGGACGGGGAACTTTGGCG 1510
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Db     1967 GGGAGCTTGATCCAGCGTGGCTGATGGTGGACACTGTCATAGGAGAAGGAGAGTTTGGGG 2026

Qy     1511 AAGTGTTCAGCGGACGCGCTGCGGAGCC--------GACAACACCCTGGTGCGGTGAAGT 1561
                |||||| |||| |||                 ||| ||
Db     2027 AAGTGTATCGAGGGGACCCTCAGGCTCCCCAGCCAAGACTGTGCCATTAAGA 2086

Qy     1562 CTTGTCGAGAGACGCGCTCCCACCTGACCTCAAGGCCAAGTTTCTACAGGAGGGATCC 1621
                |||||||||||                     ||| |||
Db     2087 CCTTAAAAGACAAACATCCCAGGTGGCCAGTGGTGGGAACTTCCTTCGAGACGCAACTATCA 2146

Qy     1622 TGAAGCAGTACAGCCACCCAAACATCGTGCCTCATTGGTGTCTCGCACCCAGAAGCAGC 1681
                |||| |||||                       ||||  ||
Db     2147 TGGGCCAGTTTAGCCACCCCGCATATTCTGCATCTCGGAAGGCGTCGTCACAAAGGCAAAGC 2206

Qy     1682 CCATCTACATCGTCATGGAGCTTGTGCGAGGGGGGACTTCCTGACCTTCCTCCGCACCG 1741
                |||||                     |||| |||
Db     2207 CGATCATGATCATCACAGAATTTATGGAGAATGCAGCCCCTGGATGCCTTCCTGAGGGGAGC 2266

Qy     1742 AGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAAGACTCTGCTGCGACGATGGTGGGGG 1801
                ||||||                     ||| |||
Db     2267 GGGAGGACCCAGCTGGTCCCTGGCAGCTAGTGGCCATGCTGCAGGGCATAGCATCTGGCA 2326

Qy     1802 TGGAGTACCCTGGAGAGCAAGTGCTGCATCCACCGGGGACCTGGCTGTCGGAACTGCCTGG 1861
                |||||||                     ||| ||||
Db     2327 TGAACTACCTCAGTAATCACAATTATGTCCACCGGGGAACCTGGCTGCCAGAAACATCTTGG 2386

Qy     1862 TGACAGAGAAGAATGTCCTGAAGATCAGTGACTTTGGGATGTCCCGAGAGGAGCCGATG 1921
                ||||||                     ||| |||
Db     2387 TGAATCAAAACCTGCTGCTGCAAGGTGTCTGACTTTGGCCTGTGTCCGCCTCCTGGATGACT 2446

Qy     1922 GGGTCTATGCAGCCTCAGGGGGGCCGTCCCTGCCTGCCCGAGAGCTGTGTCCTGATGCCGTGTTCA 1981
                |||||||                     ||| ||||
Db     2447 TTGATGGCACATACGAAACCGAAACCCAGGGAGGAAAGATCCCTATCCGTTGGACCCCCTGAAG 2506

Qy     1982 CCCTTAACTACACGGCCGCTACTCCTCCGAAAGCGACGTGTGAGAGCTTTGGCATCTTGCTCT 2041
                ||||||
Db     2507 CCATTGCCCATCCGGATCTTCACCCACAGCCAGCGATGTGTGAGAGCTTTGTGGGATTGTGATGT 2566

Qy     2042 GGGAGACCTTCAGCCTGGGGGGCCTCCCCCCTATCCCAACCTCAGCAATCAGCAGACACGGG 2101
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Db     2567 GGGAGGTGCTGAGCTTTGGGACAAGCCTTATGGGAGATGAGCAATCAGGAGGTTATGA 2626

Qy     2102 AGTTTGTGGGAGAGAGGGGGCCGTCTGCCCTGCCCAGAGCTGTGTCCTGATGCCGTGTTCA 2161
                |||||||                 |||  GACACACCCTGGTGCGGTGAAGT 1561
Db     2627 AGAGCATTGAGGATGGGGTACCGTCGTGCCCTCCTGGACTGGGACCTGCAAGACTCTGTATG 2686

Qy     2162 GGCTCATGGAGCAGTGCTGGGCCTATGAGCCTGGGCAGCGGCGCCCAGCTTC 2211
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Right column:

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Db     2687 AGTCTCATGATGAAGAACTGCTGGGCATATGACGGCGGCCGGCCCCGGCCCGGCCACACTTC 2736

RESULT 14
US-10-354-358-101
;  Sequence 101, Application US/10354358
;  Publication No. US20030157082A1
;  GENERAL INFORMATION:
;   APPLICANT: Millennium Pharmaceuticals, Inc
;   APPLICANT: Hunter, John Joseph
;   APPLICANT: MacBeth, Kyle J.
;   APPLICANT: Tsai, Fong-Ying
;   APPLICANT: Lescon, Andrea
;   APPLICANT: Lightcap, Eric S.
;   APPLICANT: Williamson, Mark
;   APPLICANT: Rudolph-Owen, Laura A.
;   TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
;   TITLE OF INVENTION:   CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
;   TITLE OF INVENTION:   7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,
;   TITLE OF INVENTION:   3703, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,
;   TITLE OF INVENTION:   9252, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469,
;   TITLE OF INVENTION:   8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,
;   TITLE OF INVENTION:   16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
;   TITLE OF INVENTION:   2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES
;   FILE REFERENCE: MPIO2-02OP1RNOMNIM
;   CURRENT APPLICATION NUMBER: US/10/354,358
;   CURRENT FILING DATE:  2003-01-30
;   PRIOR APPLICATION NUMBER: US 60/353,600
;   PRIOR FILING DATE: 2002-01-31
;   PRIOR APPLICATION NUMBER: US 60/364,517
;   PRIOR FILING DATE: 2002-03-15
;   PRIOR APPLICATION NUMBER: US 60/371,075
;   PRIOR FILING DATE: 2002-04-09
;   PRIOR APPLICATION NUMBER: US 60/371,507
;   PRIOR FILING DATE: 2002-04-10
;   PRIOR APPLICATION NUMBER: US 60/372,984
;   PRIOR FILING DATE: 2002-04-16
;   PRIOR APPLICATION NUMBER: US 60/374,194
;   PRIOR FILING DATE: 2002-04-19
;   PRIOR APPLICATION NUMBER: US 60/382,995
;   PRIOR FILING DATE: 2002-05-24
;   PRIOR APPLICATION NUMBER: US 60/385,023
;   PRIOR FILING DATE: 2002-05-31
;   PRIOR APPLICATION NUMBER: US 60/388,853
;   PRIOR FILING DATE: 2002-06-14
;   PRIOR APPLICATION NUMBER: US 60/389,395
;   PRIOR FILING DATE: 2002-06-17
;   Remaining Prior Application data removed - See File Wrapper or PALM.
;   NUMBER OF SEQ ID NOS: 122
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 101
;   LENGTH: 3370
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (94)...(3048)
US-10-354-358-101

Query Match       8.8%;    Score 198;  DB 16;  Length 3370;
Best Local Similarity   54.7%;    Pred. No. 1.4e-39;
Matches   421;  Conservative    0;  Mismatches  340;    Indels    9;  Gaps    1;

Qy     1451 GGGTGCTGAACCATGAGGACCTGGTTGGGTGAGCAGATTGGACGGGGAACTTTGGCG 1510
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Db     1967 GGGAGCTTGATCCAGCGTGGCTGATGGTGGACACTGTCATAGGAGAAGGAGAGTTTGGGG 2026

Qy     1511 AAGTGTTCAGCGGACGCGC------------GACACACCCTGGTGCGGTGAAGT 1561
                |||||||
Db     2027 AAGTGTATCGAGGGGACCCTCAGGCTCCCCAGCCAAGACTGTGCCATTAAGA 2086

Qy     1562 CTTGTCGAGAGACGCGCTCCCACCTGACCTCAAGGCCAAGTTTCTACAGGAGGGATCC 2211
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Db  1967  GGGAGCTTGATCCAGCGTGGCGTGGCTGATGCTGGACACTGTCGATGTGGAAGGAGAAGGAGAGTTTGGGG  2026
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Qy  1511  AAGTGTTCAGCGGACGCCTGCGAGCC-------GACAACACCCGTGTGGGCGGGTGAGT  1561
          ||||||                              ||||| || || ||||
Db  2027  AAGTGTATCGGAGGACCCTCAGCGTCCAAGACTGTCGTCACAAGCGAAGC  2086

Qy  1562  CTTGTCGAGAGACGCGCTCCCACCTGACCTCAGGCCAAGTTCTACAGGAAGGCAGGATCC  1621
          |   ||  ||| | |||   | || ||| |||  || ||||  || || ||  || | ||
Db  2087  CCTTAAAGACACACATCCCCAGTGTGGCGCAGTCGTGTGGGAACTTCCTTCGAGAGGCAACTATCA  2146

Qy  1622  TGAAGCAGTACAGCCACCCAACATCGTGCGTCTCATTGGTGTCTGCACCCAGAAGCAGC  1681
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Db  2147  TGGGCCAGTTTAGCCACCCGCATATTCGAATCTGAAGGCGTCGTCACAAGCGAAAGC  2206

Qy  1682  CCATCTACATGTCATGGAGCTTGTGCAGGGGCCGCACTTCCTGACCTTCCTCCGCACGG  1741
          ||||||||  | ||  ||    ||  || |||| ||       || ||||| || ||
Db  2207  CGATCATGATCATCACAGAATTATGAGAATGCAGCCCTGACTTGCTGCCAGAAACATCTTGG  2266

Qy  1742  AGGGGCCCGCCTGCGGGTGAGAGCTCTGCTCGCAGATGGTGGGGATGGCAGCTGCTGGCA  1801
          | ||| |||||     ||||| | |||| || ||| ||  ||    |||||
Db  2267  GGGAGGACCAGCTGGTCCCTGGGCAGTAGTGGCCATGCTGCAGGGGCATAGCATCTGGCA  2326

Qy  1802  TGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGCTGCTGCTCGGAACTGCCTGG  1861
          |||| ||||||||  || |      ||    || || || |  || |||| ||
Db  2327  TGAACTACCTGCAGTTGTCTCAGCTTTGGCCATGGCCTAGTTGCCCAGGACACCATCTTGG  2386

Qy  1862  TGACAGAGAAGAATGTCCTGAAAGCGACGTGGGAGCTTGGCATCTTGCTCT  1921
          ||| |||||    |||| || |      |||| |||| |||||  || |||
Db  2387  TGAATCAAAACCTGTCGTGCAGGTGTCTGACTTTGCTGACTTTGGGGATTGTGATGACT  2446

Qy  1922  GGGTCTATGCAGCCTGGGGGCCTCAGCCCCCCATCCAACCTCAGCAATCAGCAGACACGGG  1981
          ||||| ||| |     ||||  || |      ||| ||    |||||||||||||||||||
Db  2447  TTGATGGCACATACGAAACCCAGGAGGAAAGATCCCTATCCGTTGGACAGCCCCTGAAG  2506

Qy  1982  CCCTTAACTACGGCCGCTACTCTCCGAAAGCGACGTGTGGAGCTTTGGCATCTTGCTCT  2041
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Qy  2042  GGGAGACCTTCAGCGTGGGGGGCCGCCTCCTGGGCCAGGCGGCCAGCTTC  2101
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Db  2627  AGAGCATTGAGGATGGGTACCGGTTGCCCCCTCCTGTGGACTGGCCGCCAGCTTC  2686

Qy  2162  GGCTCATGGAGCAGTGCTCGGCCTATGAGCCTGGGCAGCCGGCCGCCAGCTTC  2211
          |||||||| | |||| ||  |  |||||||| ||| || || ||||||||||||
Db  2687  AGCTCATGAAGAACTGCTCGGCGCATATGACCGCGTGCCCGCCGCCCACACTTC  2736
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Query Match    8.8%;  Score 198;  DB 16;  Length 3370;
Best Local Similarity   54.7%;  Pred No. 1.4e-39;
Matches  421;  Conservative   0;  Mismatches  340;  Indels   9;  Gaps   1;

Qy  1451  GGGTGCTGAACCATGAGGACCTGGTGTTGGGTGAGCAGATTGGACGGGGAACTTTGGCG  1510
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Job time : 2017.27 secs

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           GenCore version 5.1.6
Copyright (c) 1993 - 2005  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:     August  9, 2005, 16:42:25 ; Search time 498.791 Seconds
                                    (without alignments)
                                    7400.775 Million cell updates/sec

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Perfect score: 2256
Sequence:   1 atgggctctctcttctgagct..........gcatccgaaagcggcatcgg 2256

Scoring table:  IDENTITY NUC
            Gapop 10.0, Gapext 1.0

Searched:   1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters:       2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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       2:  /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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2	2256	100.0	2674	4	US-10-003-295-1	Sequence 1, Appli
3	296.2	13.1	361	3	US-09-387-212-5	Sequence 5, Appli
4	296.2	13.1	361	3	US-09-948-802-5	Sequence 5, Appli
5	227.2	10.1	15297	3	US-09-817-180-3	Sequence 3, Appli
6	227.2	10.1	15297	4	US-10-003-295-3	Sequence 3, Appli
7	213	9.4	19152	3	US-09-949-016-12110	Sequence 12110, A
8	213	9.4	19153	4	US-09-949-016-15795	Sequence 15795, A
9	198	8.8	3370	4	US-09-814-915A-82	Sequence 82, Appl
10	185.4	8.2	3921	4	US-09-949-016-628	Sequence 628, App
11	185.4	8.2	3921	4	US-09-949-016-2120	Sequence 2120, Ap
12	174.6	7.7	3386	4	US-09-949-016-5662	Sequence 5662, Ap
13	174.6	7.7	3416	2	US-08-357-642A-2	Sequence 2, Appli
14	174.6	7.7	3416	2	US-08-460-626-2	Sequence 2, Appli
15	174.6	7.7	4089	4	US-09-016-434-1483	Sequence 1483, Ap
16	170.4	7.6	1611	1	US-07-820-011A-3	Sequence 3, Appli
17	170.4	7.6	1611	4	US-09-300-958A-13	Sequence 13, Appl
18	170.4	7.6	1611	3	US-09-860-473-3	Sequence 3, Appli
19	170.4	7.6	1611	4	US-09-444-711A-1	Sequence 1, Appli
20	170.4	7.6	1611	4	US-09-444-711A-3	Sequence 3, Appli
21	170.4	7.6	1611	5	PCT-US93-00445-3	Sequence 3, Appli
22	169.4	7.6	2455	4	US-09-949-016-4411	Sequence 4411, Ap
23	169.4	7.5	3623	1	US-08-306-691B-35	Sequence 35, Appl
24	169.4	7.5	5434	4	US-09-949-016-927	Sequence 927, App
25	169.4	7.5	5763	4	US-09-949-016-3759	Sequence 3759, Ap
26	169	7.5	3018	4	US-09-949-016-1097	Sequence 1097, Ap
27	169	7.5	3018	4	US-09-949-016-4749	Sequence 4749, Ap
28	169	7.5	4871	4	US-09-799-451-448	Sequence 448, App
29	168.2	7.5	2574	3	US-09-142-529-2	Sequence 2, Appli
30	168.2	7.5	2574	4	US-10-045-428A-2	Sequence 2, Appli
31	165.8	7.3	738	2	US-08-604-989A-8	Sequence 8, Appli
32	165.8	7.3	1398	2	US-08-604-989A-9	Sequence 9, Appli
33	165.8	7.3	1521	2	US-08-604-988A-10	Sequence 10, Appl
34	165.8	7.3	1713	3	US-09-741-154-1	Sequence 1, Appl
35	165.8	7.3	1942	2	US-08-604-989A-11	Sequence 11, Appl
36	165.8	7.3	2000	2	US-08-426-509A-1	Sequence 1, Appli
37	165.8	7.3	2000	4	US-08-232-545-1	Sequence 1, Appli
38	165.8	7.3	2000	5	PCT-US95-05008-1	Sequence 1248, Ap
39	163.6	7.3	2449	4	US-09-949-016-1248	Sequence 1248, Ap
40	163.6	7.3	5993	3	US-09-383-630-1	Sequence 1, Appli
41	163.6	7.3	5993	3	US-09-383-630-2	Sequence 2, Appli
42	162.6	7.2	1467	3	US-09-579-182-2	Sequence 2, Appli
43	162.2	7.2	2440	1	US-08-160-861-2	Sequence 2, Appli
44	162.2	7.2	2442	3	US-08-542-363-3	Sequence 3, Appli
45	162.2	7.2	2442	3	US-09-100-089-3	Sequence 3, Appli

ALIGNMENTS

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RESULT 1
US-09-817-180-1
; Sequence 1, Application US/09817180
; Patent No. 6340584
; GENERAL INFORMATION:
;   APPLICANT: GAN, Weiniu et al.
;   TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;   TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;   TITLE OF INVENTION:  THEREOF
;   FILE REFERENCE: CL001183
;   CURRENT APPLICATION NUMBER: US/09/817,180
;   CURRENT FILING DATE: 2001-03-27
;   NUMBER OF SEQ ID NOS: 4
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 2674
;   TYPE: DNA
;   ORGANISM: Human
US-09-817-180-1

Query Match            100.0%;  Score 2256;  DB 3;  Length 2674;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches 2256;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy      1 ATGGGCTCTCTCTTCTGAGCTGTGCAGCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG 60
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Db     72 ATGGGCTCTCTCTTCTGAGCTGTGCAGCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG 131

Qy     61 GAGGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGCGGGTCAAGAGT 120
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Db    132 GAGGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGCGGGTCAAGAGT 191

Qy    121 GACAGGGAGTATGCAGGACTGCTTCACCCATGTCCCTGCAGCAGTGGGGTGGGGCCAGAGC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    192 GACAGGGAGTATGCAGGACTGCTTCACCCATGTCCCTGCAGCAGTGGGGTGGGGCCAGAGC 251

Qy    181 CGGGCCATCAGCCTGACCAGCCCATCAGTCAGTCACGCCAGAGATCTGAACTCAGGGCCCTGAGC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    252 CGGGCCATCAGCCTGACCAGCCCATCAGTCAGTCACGCCAGAGATCTGAACTCAGGGCCCTGAGC 311

Qy    241 GAGGGCTGAGCCGCTTGCTGCGGCAGCACGGCAGCAGCTTCGGCAACGACCTACAGCAGTGG 300
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Db    312 GAGGGCTGAGCCGCTTGCTGCGGCAGCACGGCAGCAGCTTCGGCAACGACCTACAGCAGTGG 371

Qy    301 AAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCTTCGCAAGACCTACAGCAGCAGTGG 360
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Db    372 AAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCTTCGCAAGACCTACAGCAGCAGTGG 431

Qy    361 CAGCAGCTGCAGCAGGAGCTCACCAAGACCCAGACCCAGGACATTGAGAAGCTGAAGAGC 420
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Qy    432 CAGCAGCTGCGAGCAGGAGCTCACCAAGACCCAGCCAGGACATTGAGAGAGC 491
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Db    421 CAGTACCGAGCTCTGCACGGACAGTGCCCAAGCGCAAGTACCAGGAGGCCAGC 480

Qy    492 CAGTACCGAGCTCTGCACGGACACGGTGCCCAAGCGCAAGTACCAGGAGGCCAGC 551
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AAAGACAAGGACCGTGACAAGGCCAAGGAGAGACAAGTGTGCGGCTCCAGCCTGTGGAAGCTCTTT 540

Qy    552 AAAGACAAGGACCGTGACAAGGCCAAGGAGAGACAAGTATGTGCGGCTGCGAGCTACACCAGCACCAC 611

Db    541 GCTCCACCACAACCGTCACCGCTATGTGTCTGGGCGTGCCGGCTCACCACCAGCACCAC 600

Qy    612 GCTCCACCACAACCGTCACCGCTATGTGCGGGCGTGCCGGCTGCGAGCTACACCAGCACCAC 671

Db    601 CACCAGCTCCTGCTGCTGCCCGGCCTGCTGCGGCGTCACTGCAGGACCTGCACGAGGAGATGGCT 660

Qy    672 CACCAGCTCCTGCTGCTGCCCGGCCTGCTGCGGCGTCACTGCAGGACCTGCACGAGGAGATGGCT 731

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Qy    732 TGCATCCTGAAGGAGAATCCTGCAGGAATTACCTGGAGATTAGCAGCCTGGTGCAGGATGAG 791

Db    721 GTGGTGCCATTCACCGGGAGATGGCTGCAGCTGCTGCCCCGCATCCAGCCTGAGGCTGAG 780

Qy    792 GTGGTGCCATTCACCGGGAGATGGCTGCAGCTGCTGCCCCGCATCCAGCCTGAGGCTGAG 851

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Qy    852 TACCAAGGCTTCCTGCGACAGTATGGTCCGCACCTGTCCCACCCTGTGTCACGTTC 911

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Qy    912 GATGAGTCACTGCTTGTGGAGAGGGTGAACCGCGTGGGAGCTGGAGCTCCAGCTGAACGAG 971

Db    901 CTGACTGTGTGGAGAGCGTGCAGCACACACGCTGGCGCTGACAGATGAGCTGGCTGCGGCC 960

Qy    972 CTGACTGTGTGGAGAGCGTGCAGCACACACGCTGGCGCTGACAGATGAGCTGGCTGTGGCC 1031

Db    961 ACCGAGATGGTGTGTTCAGGCGGCGGAGATGGTTACGGCGCTGCAACAGGAGCTCGGAAT 1020

Qy   1032 ACCGAGATGGTGTGTTCAGGCGGCGGAGATGGTTACGGCGCTGCAACAGGAGCTCCGGAAT 1091

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Qy   1092 GAAGAGGAGAACACCACCCCGGAGCGGGGAGCGGGTGCAGTGCGAAGAGGCAAGTGCTG 1151

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Qy   1332 ACACCCAGCTGAGATCTTAAGAGCCACATCCGAGAATCTTCCGCCCCAAGTTCTCG 1391

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Qy   1392 AACCTGTACCGACTGGAAGGGAAGGGAGGCTTCCTAGCATTCCTTTGCTCATCGACCACCTA 1451

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Qy   1452 CTGAGCACCCAGCAGCCCTCACCAGAAGAGTGGTGTTGTGTCCTGCACAGGGCTGTGCCC 1511

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Qy   1512 AAGGACAAGTGGGTGCTGAACCATGAGGACCTGGTTGGGTGGTGCAGGACGGGGG 1571
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Db   1501 AACTTTGGCGAAGTGTTCAGCGGACGACGCTGCGAGCCGACAACACCCTGGTGCGGCGGTGAAG 1560

Qy   1572 AACTTTGGCGAAGTGTTCAGCGGACGACGCTGCGAGCCGACAACACCCTGGTGCGGCGGTGAAG 1631

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Qy   1632 TCTTGTCGAGAGACGCTCCACCTGACCTCAAGGCCAAGTTCTACAGGAAGCGAGGATC 1691

Db   1621 CTGAAGCAGTACAGCCACCCCAACATCGCGTCTCATTGGTGTCGACCAGAAGCAG 1680

Qy   1692 CTGAAGCAGTACAGCCACCCCAACATCGCGTCTCATTGGTGTCGACCAGAAGCAG 1751

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Qy   1752 CCCATCTACATCGTCATGGAGCTTGTGCAGGGGGGCGACTTCCTCCTCCGCACG 1811

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Qy   1812 GAGGGGGCCCGGCCTGCGGGTGAAGACTCGTGCTGCAGATGGTGGGGGATGGTGGGGGATGCAGCTGCTGGC 1871

Db   1801 ATGGAGTACCTGGAGAGCAAGTGCTCATCCACCGGCACCTGGCTGTCCGGAACTGCCTG 1860

Qy   1872 ATGGAGTACCTGGAGAGCAAGTGCTCATCCACCGGCACCTGGCTGTCCGGAACTGCCTG 1931

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Qy   1932 GTGACAGAGAGAAATGTCCTGAAGATCAGTGACTTTGGGGATGTGCCCGAGAGGAAGCCGAT 1991

Db   1921 GGGGTCTATGCAGCCTCAGGGGCCTCAGCAAGTGCCCCGTGAAGTGGACCACCTGAG 1980

Qy   1992 GGGGTCTATGCAGCCTCAGGGGCCTCAGCAAGTGCCCCGTGAAGTGGACCACCTGAG 2051

Db   1981 GCCCTTAACTACGGCCGCTACTCCTCCGAAAGCGACGTGTGGAGCTTTGGCATCTTGCTC 2040

Qy   2052 GCCCTTAACTACGGCCGCTACTCCTCCGAAAGCGACGTGTGGAGCTTTGGCATCTTGCTC 2111

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Qy   2112 TGGGAGACCTTCAGCCTGGGGCCCTCCCCTATCCCAACCTCAGCAATCAGCAGACACACGG 2171

Db   2101 GAGTTTGTGGAGAAGGGGGGGCGTGTCCCTGCCCCTGCCCCAGAGCTGTGTCCTGATGCCGTGTTC 2160

Qy   2172 GAGTTTGTGGAGAAGGGGGGGCGTGTCCCTGCCCCTGCCCCAGAGCTGTGTCCTGATGCCGTGTTC 2231

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Db   2221 TACCAGGAGCTGCAAGCATCCGAAAGCGGCATCGG 2256

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RESULT 2
US-10-003-295-1
; Sequence 1, Application US/10003295
; Patent No. 6686187
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001183DIV
; CURRENT APPLICATION NUMBER: US/10/003,295
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2674
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-003-295-1

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Query Match        100.0%;  Score 2256;  DB 4;  Length 2674;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 2256;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Db    72  ATGGGCTTCTCTTCTGAGCTGTGCAGCCCCAGGGCCACGGGTCCTGCAGCAAATGCAG  131

Qy    61  GAGGCCGAGCTTCGTCGTCACTGAGGGCATGAGAAAGTGGATGGCCCAGCGGGTCAAGAGT  120
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Db   132  GAGGCCCAGCTTCGTCGTCACTGAGGGCATGAGAAAGTGGATGGCCCAGCGGGTCAAGAGT  191

Qy   121  GACAGGGAGTATGCAGGACTGCTTCACCACCATGTCCCTGCAGGACAGTGGGGCCAGAGC  180
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Db   192  GACAGGGAGTATGCAGGACTGCTTCACCACCATGTCCCTGCAGGACAGTGGGGCCAGAGC  251

Qy   181  CGGGCCATCAGCACCCTGACAGCCCCATCAGTCCTGGGCTGAGATCACCAGCCAAAACT  240
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Db   252  CGGGCCATCAGCCCTGACAGCCCCATCAGTCCTGGGCTGAGATCACCAGCCAAAACT  311

Qy   241  GAGGGGCCTGAGCCGCTTGCTGCGGCAGCGACGCAGGAGGATCTGAACTCAGGGCCCTGAGC  300
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Db   312  GAGGGGCCTGAGCCGCTTGCTGCGGCAGCGACGCAGGAGGATCTGAACTCAGGGCCCTGAGC  371

Qy   301  AAGCTGAGCCTGCTGCTCATCCGGGAACGGACCAGCAGCTTCGCAAGAGCTTCACGGCAGTGG  360
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Db   372  AAGCTGAGCCTGCTGCTCATCCGGGAACGGACCAGCAGCTTCGCAAGAGCTTCACGGCAGTGG  431

Qy   361  CAGCAGCTGAGCAGCGGAGCTGCACCCACAGACCCCAAGAGGCCAAGCCAGAGGCCAGC  420
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Db   432  CAGCAGCTGAGCAGCGGAGCTGCACCCACAGACCCCAAGAGGCCAAGCCAGAGGCCAGC  491

Qy   421  CAGTACCGAGCTCTGCGACGGCAGTCGCAGGCGCCAAGGCCAAGCCAGGAGGCCAGC  480
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Db   492  CAGTACCGAGCTCTGCGACGGCAGTCGCAGGCGCCAAGGCCAAGCCAGGAGGCCAGC  551

Qy   481  AAAGACAAGGAGACCGTGACAAGGCCAAGGACAAGTATGTGCGCCAGCCTGTGGAAGCTCTTT  540
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Db   552  AAAGACAAGGAGACCGTGACAAGGCCAAGGACAAGTATGTGCGCCAGCCTGTGGAAGCTCTTT  611

Qy   541  GCTCACCACAACCGCTATGTGTCGGGCGTGCGGCTGCGCAGCTACACCACCAGCACCAC  600
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Db   612  GCTCACCACAACCGCTATGTGTCGGGCGTGCGGCTGCGCAGCTACACCACCAGCACCAC  671

Qy   601  CACCAGCTCCTGCTGCGGCCTGCGGCTCACTGCGCAGGACCTGCACGAGGAGGATGGCT  660
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Db   672  CACCAGCTCCTGCTGCGGCCTGCGGCTCACTGCGCAGGACCTGCACGAGGAGGATGGCT  731

Qy   661  TGCATCCTGAAGGAGATCCTGCAGGAATACCTGGAGATTAGCACCGTGGAGTCGTCAGGATGAG  720
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Db   732  TGCATCCTGAAGGAGATCCTGCAGGAATACCTGGAGATTAGCACCGTGGAGTCGTCAGGATGAG  791

Qy   721  GTGGTGCCATTCACCGGAGAGTGGGCTGCGCAGCTGCTGCCCGGATCCAGCCTGAGGCTGAG  780
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Db   792  GTGGTGCCATTCACCGGAGAGTGGGCTGCGCAGCTGCTGCCCGGATCCAGCCTGAGGCTGAG  851

Qy   781  TACCAAGGCTTCCTGGCACAGTATGGGTCGGCGGTCCCGCCACCTCCCGTGTCACGTTC  840
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Db   852  TACCAAGGCTTCCTGGCACAGTATGGGTCGGCGGTCCCGCCACCTCCCGTGTCACGTTC  911

Qy   841  GATGAGTCACTGCTTGAGGAGGGTGAACCGGTCCAGCTGAGCGGGAGTCCAGCTGAACGAG  900
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Db   912  GATGAGTCACTGCTTGAGGAGGGTGAACCGGTCCAGCTGAGCGGGAGTCCAGCTGAACGAG  971

Qy   901  CTGACTGTGGAGAGCGTGCAGCACGCTGCGCCAGCTGAGCCTGCTGTGGCC  960
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Db   972  CTGACTGTGGGAGAGCGTGCAGCACACCGCTGCGCCAGCTGAGCCTGCTGTGGCC  1031

Qy   961  ACCGAGATGGTGTTCAGGCGGCGCAGCACGCTGCAACGCTGCAACTTTACCGGCTCCGGAAT  1020
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Db  1032  ACCGAGATGGTGTTCAGGCGGCGCAGCACGCTGCAACGCTGCAACTTTACCGGCTCCGGAAT  1091
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Qy  1021  GAAGAGGAGAACACCCACCCCCCGGGAGCGGCGGGTCAGCTGCTGGGCAAGAGAGGCAAGTGCTG  1080
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Db  1092  GAAGAGGAGAACACCCACCCCCCGGGAGCGGCGGGTCAGCTGCTGGGCAAGAGAGGCAAGTGCTG  1151

Qy  1081  CAAGAAGCACTGCAGGGGCTGCAGGTAGCGCTGTGCAGCGAGGCTCAGCTGCGTGCAGGCCCAG  1140
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Db  1152  CAAGAAGCACTGCAGGGGCTGCAGGTAGCGCTGTGCAGCGAGGCTCAGCTGCGTGCAGGCCCAG  1211

Qy  1141  CAGGAGTTGCTGCAGACCAAGTGGAGCACCTTGGAGCACCTTGGGCGCCCCGCTGTGCTG  1200
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Db  1212  CAGGAGTTGCTGCAGACCAAGTGGAGCACCTTGGAGCACCTTGGGCGCCCCGCTGTGCTG  1271

Qy  1201  CTCCTGCAGGATGACCGGCCACTCCAGTCGTCCTCCGAGCAGCAGGAGCAGGGGGAGG  1260
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Db  1272  CTCCTGCAGGATGACCGGCCACTCCAGTCGTCCTCCGAGCAGCAGGAGCAGGGGGAGG  1331

Qy  1261  ACACCCACGCTGGAGATCCTTAAGAGCCACATCTCAGAGATCTTCCGCCCCAAGTTCTCG  1320
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Db  1332  ACACCCACGCTGGAGATCCTTAAGAGCCACATCTCAGAGATCTTCCGCCCCAAGTTCTCG  1391

Qy  1321  AACCTGTACCGACTGGAAGGGAAGGCTTCCTTGCTATCGACCACCTA  1380
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Qy  1381  CTGAGACCACCAGCAGCCCCTCACCAAGAAGAGTGGTGTTGTCCTGACAGGGCTGTGCCC  1440
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Db  1452  CTGAGACCACCAGCAGCCCCTCACCAAGAAGAGTGGTGTTGTCCTGACAGGGCTGTGCCC  1511

Qy  1441  AAGGACAAGTGGGTGCTGAACCATGAGACGACCGTGGTGTTGGTGGGTGAGCAGCGGGGG  1500
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Db  1512  AAGGACAAGTGGGTGCTGAACCATGAGACGACCGTGGTGTTGGTGGGTGAGCAGCGGGGG  1571

Qy  1501  AACTTTGGCGAAGTGTTCAGCGAGCGTCAGGGGGGCGACTTCCTCCGCACG  1560
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Db  1572  AACTTTGGCGAAGTGTTCAGCGAGCGTCAGGGGGGCGACTTCCTCCGCACG  1631

Qy  1561  TCTTGTCTGAGAGACGGTCCCACCTGACCTCAAGGCCAAGTTCTACAGGAAGCGAGGATC  1620
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Db  1632  TCTTGTCTGAGAGACGGTCCCACCTGACCTCAAGGCCAAGTTCTACAGGAAGCGAGGATC  1691

Qy  1621  CTGAAGCAGTACAGACCCACCCCAACATCGTGCGTCATTGGTGTCTGCACCAGAAGCAG  1680
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Db  1692  CTGAAGCAGTACAGACCCACCCCAACATCGTGCGTCATTGGTGTCTGCACCAGAAGCAG  1751

Qy  1681  CCCATCTACATCGTGTTGTGCAGGGGGCGACCTGCACGAGGAGGATGGCT  1740
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Db  1752  CCCATCTACATCGTGTTGTGCAGGGGGCGACCTGCACGAGGAGGATGGCT  1811

Qy  1741  GAGGGGGCCCCGCCGGGGTGAAGCTCTGCTGCAGATGGTGGGGGATGCAGCTGGC  1800
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Db  1812  GAGGGGGCCCCCGCCGGGGTGAAGCTCTGCTGCAGATGGTGGGGGATGCAGCTGGC  1871

Qy  1801  ATGGAGAGAAGAATGTCCTGAAGATCAGTGACTTTGGGATGTCTCGGAGGATGACTGCCTG  1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1872  ATGGAGAGAAGAATGTCCTGAAGATCAGTGACTTTGGGATGTCTCGGAGGATGACTGCCTG  1931

Qy  1861  GTGACAGAGAATGTCCTGAAGATCAGTGACTTTGGGAGTGCCCGAGGAAGCCACCGAT  1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1932  GTGACAGAGAAGAATGTCCTGAAGATCAGTGACTTTGGGAGTGCCCGAGGAAGCCACCGAT  1991

Qy  1921  GGGGTCTATGCAGCCTCAGGGGGCTCGGAGTCCCGTGAAGTGCCCGTGAAGTGACCGCACCTGAG  1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1992  GGGGTCTATGCAGCCTCAGGGGGCTCGGAGTCCCGTCAGAAGTGCCCGTGAAGTGACCGCACCTGAG  2051

Qy  1981  GCCCTTAACTACGGCCGCTACTCCTCCGGAAAGCGACGTGTGGCTTTGGCATCTTGCTC  2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2052  GCCCTTAACTACGGCCGCTACTCCTCCCGAAAGCGACGTGTGGCTTTGGCATCTTGCTC  2111

Qy  2041  TGGGAGACCTTCAGCCTGGGGCGCCTCCCCATCCCAACCTGCAATCAGCAGAACACG  2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2112  TGGGAGACCTTCAGCCTGGGGCGCCTCCCCATCCCAACCTGCAATCAGCAGAACACG  2171

Qy  2101  GAGTTTGTGGAGAAGGAGCTGTCCTCGGCCGAGCTGTGTCCTGATGCCGTGTTC
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Db    2172  ||||||||||||||||||||||||||||||||||||||||||||||||
            GAGTTTGTGGAGAAGAGGGGGCCGTCTGCCCTGCCCAGAGCTGTGTCCTGATGCCGTGTTC  2231
Qy    2161  AGGCTCATGAGAGCAGTGCTGGGCCTGGGCCTGGGCCAGCGGGGCCCAGCTTCAGCACCATC  2220
Db    2232  AGGCTCATGAGAGCAGTGCTGGGCCTGGGCCTGGGCCAGCGGGGCCCAGCTTCAGCACCATC  2291
Qy    2221  TACCAGGAGCTGCAGAGCATCCGAAAGCCGGCATCGG  2256
Db    2292  TACCAGGAGCTGCAGAGCATCCGAAAGCCGGCATCGG  2327
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RESULT 3
US-09-387-212-5
; Sequence 5, Application US/09387212A
; Patent No. 6309849
; GENERAL INFORMATION:
; APPLICANT: ROBISON, KEITH E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
; TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR
; FILE REFERENCE: MNI-090
; CURRENT APPLICATION NUMBER: US/09/387,212A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 5
; LENGTH: 361
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: All occurences of n indicate any nucleotide
US-09-387-212-5

Query Match   13.1%;   Score 296.2; DB 3;   Length 361;
Best Local Similarity   97.4%;   Pred. No. 6e-56;
Matches 333;   Conservative   0;   Mismatches   4;   Indels   5;   Gaps   3;

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Qy    1613  CGAGGATCCTGAAGCAGTACAGCCACCCCAACATCGTGCCTCCTCATTGGTGTGTCTGCACCC  1672
            |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    20    CNAGGATCCTGAAGCAGTACAGCCACCCCAACATCGTGCCTCCTCATTGGTGTCTGCACCC  79
Qy    1673  AGAAGCAGCCCATCTACATCTACATCGTCATGGAGCTTGTGCAGGGGGCGACTTCCTGACCTTCC  1732
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    80    AGAAGCAGCCCATCTACATCTACATCGTCATGGAGCTTGTGCAGGGGGCGACTTCCTGACCTTCC  139
Qy    1733  TCCGCACGGAGGGGGCCCGCCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGATGCAG  1792
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    140   TCCGCACGGAGGGGGCCCGCCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGATGCAG  199
Qy    1793  CTGCTGGCATGGAGTACCGGCAAGTGCTGCATCCACCGGGACCTGGCTGCTCGGA  1852
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db    200   CTGCTGGCATGGAGTACCGGCAAGTGCTGCATCCACCGGGACCTGGCTGCTCGGA  259
Qy    1853  ACTGCCTGGTGACAGAGAAGAATGTCCTGAAG-ATCAGTGACTTT-GGGATGTCCCGAGA  1910
            ||||||||||||||||||||||||||||||||| |||||||||| ||||||||||||||
Db    260   ACTGCCTGGTGACAGAGAAGAATGTCCTGAAGAATCAGTGACTTTGGGGATGTCCCGAGA  319
Qy    1911  GGAAGCC---GATGGGGTCTATGCAGCCTCAGGGGGGCCTCAG  1949
            ||||||   ||||||||||||||||||||||||||||
Db    320   GGAAGCCCGATTGGGGTCTATGCAGCCTCAGGGGGGCCTCAG  361
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RESULT 4
US-09-948-802-5
; Sequence 5, Application US/09948802
; Patent No. 6465232
; GENERAL INFORMATION:
; APPLICANT: ROBISON, KEITH E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
; TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR
; FILE REFERENCE: MNI-090
; CURRENT APPLICATION NUMBER: US/09/948,802
; CURRENT FILING DATE: 2001-09-07

Qy 121 GACAGGAGTATGCAGGACTGCTTCACCACATGTCCCTGAGGACAGTGGGGGCCAGAGC 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2683 GACAGGAGTATGCAGGACTGCTTCACCACATGTCCCTGAGGACAGTGGGGGCCAGAGC 2742

Qy 181 CGGGCCATCAGCCCTGACAGCCCATCAGTC----------- 211
         ||||||||||||||||||||||||||||||
Db 2743 CGGGCCATCAGCCCTGACAGCCCATCAGTCGGGTCTATGGGACTCTGGTGGGT 2802

Qy 212 ----------- 211
Db 2803 GCTGGGTATCTGCCTTCTCCTTCCTCTCGGGGGCCCTCTGGGGCAGTGGCTGGAGAT 2862

Qy 212 --AGTCCTGGGCTGAGATCACCAGCCAAACTGAGGGGCTGAGC 268
           ||||||||||||||||||||||||||||||||||||||||
Db 2863 CTGGCAGGCCAATGCTTGGGAGCCAATGTGCCCCCCTGCCTCCCATCTGTGCTG 2922

Qy 269 ACGCAGAGGATCTGAACTCAGGGCCCTGAGCAAGCTGAGCCTGCTCATCCGGAACGGC 328
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2983 ACGCAGAGGATCTGAACTCAGGGCCCCTGAGCAAGCTGAGCCTGCTCATCCGGGAACGGC 3042

Qy 329 AGCAGCTTCGCAAGACCTACAGGAGCTTCACCAAGA 388
         ||||||||||||||||||||||
Db 3043 AGCAGCTTCGCAAGACCTACAGGCGAGCAGCAGTGCGAGCAGCGAGCAGCTTCACCAAGG 3102

Qy 389 CCCACAGCCAGGAC 402
         ||| |||||||
Db 3103 TGAGCGGGCAGCAC 3116

RESULT 6
US-10-003-295-3
; Sequence 3, Application US/10003295
; Patent No. 6686187
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001183DIV
; CURRENT APPLICATION NUMBER: US/10/003,295
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15297
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-003-295-3

Query Match   10.1%; Score 227.2; DB 4; Length 15297;
Best Local Similarity   71.1%; Pred. No. 3.1e-40;
Matches 394; Conservative   0; Mismatches   0; Indels 8; Gaps 1;

Qy   1 ATGGGCTTCTCTTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2563 ATGGGCTTCTCTTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG 2622

Qy   61 GAGGCCGAGCTTCGTCTACTGAGGGGCATGAGAAAGTGGATGGCCCAGCGCGGTCAAGAGT 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2623 GAGGCCGAGCTTCGTCTACTGAGGGGCATGAGAAAGTGGATGGCCCAGCGCGGTCAAGAGT 2682

Qy 121 GACAGGAGTATGCAGGACTGCTTCACCACATGTCCCTGAGGACAGTGGGGGCCAGAGC 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2683 GACAGGAGTATGCAGGACTGCTTCACCACATGTCCCTGAGGACAGTGGGGGCCAGAGC 2742

Qy 181 CGGGCCATCAGCCCTGACAGCCCATCAGTC----------- 211
         ||||||||||||||||||||||||||||||
Db 2743 CGGGCCATCAGCCCTGACAGCCCATCAGTCGGGTCTATGGGACTCTGGTGGGT 2802

Qy 212 GCTGGGTATCTGCCTTCTCCTTCCTCTCGGGGGCCCTCTGGGGCAGTGGCTGGAGAT 2862

Qy 212 ----------- 211
Db 2863 CTGGCAGGCCAATGCTTGGGAGCCAATGTGCCCCCCTGCCTCCCATCTGTGCTG 2922

Qy 212 --AGTCCTGGGCTGAGATCACCAGCCAAACTGAGGGGCTGAGC 268
           ||||||||||||||||||||||||||||||||||||||||
Db 2923 TATAGTCCTGGGCTGAGATCACCAGCCAAACTGAGGGGCTGAGC 2982

Qy 269 ACGCAGAGGATCTGAACTCAGGGCCCTGAGCAAGCTGAGCCTGCTCATCCGGAACGGC 328
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2983 ACGCAGAGGATCTGAACTCAGGGCCCCTGAGCAAGCTGAGCCTGCTCATCCGGGAACGGC 3042

Qy 329 AGCAGCTTCGCAAGACCTACAGGAGCTTCACCAAGA 388
         ||||||||||||||||||||||
Db 3043 AGCAGCTTCGCAAGACCTACAGGCGAGCAGCAGTGCGAGCAGCGAGCAGCTTCACCAAGG 3102

Qy 389 CCCACAGCCAGGAC 402
         ||| ||||||
Db 3103 TGAGCGGGCAGCAC 3116

RESULT 7
US-09-949-016-12110
; Sequence 12110, Application US/0949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12110
; LENGTH: 19152
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12110

Query Match   9.4%; Score 213; DB 4; Length 19152;
Best Local Similarity 100.0%; Pred. No. 4.4e-37;
Matches 213; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ATGGGCTTCTCTTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 18741 ATGGGCTTCTCTTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG 18800

Qy   61 GAGGCCGAGCTTCGTCTACTGAGGGGCATGAGAAAGTGGATGGCCCAGCGCGGTCAAGAGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 18801 GAGGCCGAGCTTCGTCTACTGAGGGGCATGAGAAAGTGGATGGCCCAGCGCGGTCAAGAGT 18860

Qy   121 GACAGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACACTGCTTCACCACATG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 18861 GACAGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACACTGCTTCACCAGAGC 18920

Qy   181 CGGGCCATCAGCCCTGACAGCCCCATCAGTCAG 213
          |||||||||||||||||||||||||||||||||
Db 18921 CGGGCCATCAGCCCTGACAGCCCCATCAGTCAG 18953

RESULT 8
US-09-949-016-15795

```
Qy   1511  AAGTGTTCAGGGAGCGGCCTGCGAGCC--------GACAACACCCTGGTGCGGGTGAAGT  1561
                 ||||||                              |||||||  ||||  |||
Db   2027  AAGTGTATCGAGGGACCCTCAGGGTCCCAGCCAGGACTGCAAGACTGTGGCCATTAAGA  2086

Qy   1562  CTTGTCGAGACGCGTCCCACCTGACCTCAAGGCCAAGTTTCTACAGGAGGCGGAGGATCC  1621
                 ||||                                       |||||||||
Db   2087  CCTTAAAGACACATCCCCAGGTGGCCAGTGGCAACTTCCTTCGAGAGGCAACTATCA  2146

Qy   1622  TGAAGCAGTACAGCCACCCAACATCGTGGCTCTCATTGGTGTCTGCACCCAGAAGCAGC  1681
                 ||||                    ||                  |||
Db   2147  TGGGCCAGTTTAGCCACCCGCATATTCTGCAAGGCGTCGTCACAAAGGCAAAGC  2206

Qy   1682  CCATTCACATCGTCATGGAGCTTGTGCAGGGGGCGACTTCCTGACCTTCCTCCGCACGG  1741
                 ||||||   ||                   |||  |||||
Db   2207  CGATCATGATCATCACAGAATTTATGGAGAATGCAGCCCTGCAGTGGTGGGGGAGC  2266

Qy   1742  AGGGGGCCCCGCCTGCGGGTGAAGACTGCTGCAGAGTGGTGGGGGATGGCAGCTGCTGGCA  1801
                 ||||       |                        ||||||||
Db   2267  GGGAGGACCCAGCTGGTCCCTGGGCAGCTAGTTGGCCATGCTGCAGGGCATAGCATCTGGCA  2326

Qy   1802  TGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACACCTGGCTGCTCGGAACTGCCTGG  1861
                 |||  ||                   |||||||||||
Db   2327  TGAACTACCTCAGTAATCACAATTATGTCCACCGGGACACCTGGCTGCTCCAGAAACATCTTGG  2386

Qy   1862  TGACAGAGAAGAATGTCCTGAAGATCAGTCAGTTGGGATGTCCCGAGAGGAAGCCGATG  1921
                 ||   |||||                         |||
Db   2387  TGAATCAAAAACCTGTCGTCGCAAGGTGTCTGACTTTGGCTGGACCTCCTCGCTCCTGATGACT  2446

Qy   1922  GGGTCTCATGCAGCCTCAGGGGGGCCTGACAGTGGATGGCCCAGCCGGGGTCAAGAGT  1981
                 ||||                          ||||    |
Db   2447  TTGATGGCACATACGAAACCAGGGAGGGAAAGATCCCTATCCGTTGGACAGCTTGGCATCTTGCTCT  2506

Qy   1982  CCCTTAACTACGGCCGCTACTCCTCCGAAAGCGAGTGTGTGGACGGATGTGTGGATTGTGATGT  2041
                 ||||                                    |||
Db   2507  CCATTGCCCCATCCTCGGGGGGGGCCTCCCCATCCCAACCTGTTTATGGGGACAAGCCTTATGGGGACAAGTGTAGACACGGG  2566

Qy   2042  GGGAGACCTTCAGCCTTGGGGAGGGGGGCCGTGCTCGCCCTGCCCTGCCCAGAGCTGTGTCCTCAGAGTCGTGTCCTGATGCCGTGTTCA  2101
                 |||||                                                      |||
Db   2567  GGGAGGTGCTGAGCTTTGGGGACAAGCCTTATGGGGAGAATCAGGCAGCAATCAGGAGGTTATGA  2626

Qy   2102  AGTTTGTGGAGAAGGGGGGCCGTTGCCCCTGCCCTGCCCAGAGCTGTGTCCTCAGAGCTGTGTTCA  2161
                 ||                                  |||||
Db   2627  AGAGACATTGAGGATGGGTACCGGTTGCCCCTCCTGTGGACTGCCCGCCGCCGGCCACACTTC  2686

Qy   2162  GGCTCATGAGCGCAGTGCTGCGGCCCATGAGCCTGGGCAGCCGCCCAGCTTC  2211
                 |||||||||||||||
Db   2687  AGCTCATGAAGAACTGCTGGGCATATGACCCTGCCGCCCGGCCACACTTC  2736
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RESULT 10
US-09-949-016-628
; Sequence 628, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;   TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;   FILE REFERENCE: CL001307
;   CURRENT APPLICATION NUMBER: US/09/949,016
;   CURRENT FILING DATE: 2000-04-14
;   PRIOR APPLICATION NUMBER: 60/241,755
;   PRIOR FILING DATE: 2000-10-20
;   PRIOR APPLICATION NUMBER: 60/237,768
;   PRIOR FILING DATE: 2000-10-03
;   PRIOR APPLICATION NUMBER: 60/231,498
;   PRIOR FILING DATE: 2000-09-08
;   NUMBER OF SEQ ID NOS: 207012
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 628
;   LENGTH: 3921
;   TYPE: DNA
;   ORGANISM: Human
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; Sequence 15795, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;   TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;   FILE REFERENCE: CL001307
;   CURRENT APPLICATION NUMBER: US/09/949,016
;   CURRENT FILING DATE: 2000-04-14
;   PRIOR APPLICATION NUMBER: 60/241,755
;   PRIOR FILING DATE: 2000-10-20
;   PRIOR APPLICATION NUMBER: 60/237,768
;   PRIOR FILING DATE: 2000-10-03
;   PRIOR APPLICATION NUMBER: 60/231,498
;   PRIOR FILING DATE: 2000-09-08
;   NUMBER OF SEQ ID NOS: 207012
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15795
;   LENGTH: 19153
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-15795

Query Match             9.4%;  Score 213;  DB 4;  Length 19153;
Best Local Similarity   100.0%;  Pred. No. 4.4e-37;
Matches  213;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy      1  ATGGGCTTCTCTTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG   60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  18741  ATGGGCTTCTCTTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG  18800

Qy     61  GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGCCGGGTCAAGAGT  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  18801  GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGCCGGGTCAAGAGT  18860

Qy    121  GACAGGAGAGTATGCAGGACTGCTTCACCACATGTCCCTGAGACAGTGCCCAGAGC  180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  18861  GACAGGAGAGTATGCAGGACTGCTTCACCACATGTCCCTGAGACAGTGCCCAGAGC  18920

Qy    181  CGGGCCATCAGCCCTGACAGCCCCATCAGTCAG  213
           |||||||||||||||||||||||||||||||||
Db  18921  CGGGCCATCAGCCCTGACAGCCCCATCAGTCAG  18953
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RESULT 9
US-09-814-915A-82
; Sequence 82, Application US/09814915A
; Patent No. 6750015
; GENERAL INFORMATION:
;   APPLICANT: Horwitz, Kathryn
;   APPLICANT: Richer, Jennifer
;   TITLE OF INVENTION: Progesterone Receptor-Regulated Gene Expression and Methods Relat
;   TITLE OF INVENTION: Thereto
;   FILE REFERENCE: 2848-39
;   CURRENT APPLICATION NUMBER: US/09/814,915A
;   CURRENT FILING DATE: 2002-03-21
;   PRIOR APPLICATION NUMBER: 60/214,870
;   PRIOR FILING DATE: 2000-06-28
;   NUMBER OF SEQ ID NOS: 108
;   SOFTWARE: Patentin version 3.1
; SEQ ID NO 82
;   LENGTH: 3370
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-814-915A-82

Query Match             8.8%;  Score 198;  DB 4;  Length 3370;
Best Local Similarity   54.7%;  Pred. No. 5.2e-34;
Matches  421;  Conservative  0;  Mismatches  340;  Indels  9;  Gaps  1;

Qy   1451  GGGTGCTGAACCATGAGCTGAGGACCTGGTGTTGGGTGAGCAGATTGGACGGGGGAACTTTGGGCG  1510
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1967  GGGAGCTTGATCCAGCCGCTGGCTGATGGTGGACACTGTCATAGGAGGAAGAGGAGTTTGGGG  2026
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Left column

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US-09-949-016-628

Query Match      .8.2%;  Score 185.4;  DB 4;  Length 3921;
Best Local Similarity 55.1%;  Pred. No. 3.3e-31;
Matches 385;  Conservative  0;  Mismatches 311;  Indels  3;  Gaps  1;

Qy 1546 CTGGTGCGGTGAAGTCTTGTCGAGAGACGCTCCCACCTGACCTCAAGGCCAAGTTCTA 1605
            |||||| ||||  |||  ||  |||||||||   |||  |||| ||||
Db 2037 CCGGTGCCATCAAGACGCTGAAAGCCGGCTACACAGAGAAGCAGCGAGTGGACTTCCTC 2096

Qy 1606 CAGGAAGCAGGAGGATCCTGAAGCAGTTGTGCAGGGGGGGACTTCCTG 1665
            |||||||  ||||| ||| ||||
Db 2097 GGCGAGGCCGGCATCACGGAGGGGGCCCGGAATGGGGCCTGGAC 2156

Qy 1666 TGCACCCAGAAGCAGCAGCCATCTACATCGTCATGGAGTTGTGCAGGGGGGGACTTCCTG 1725
            |||
Db 2157 ATCTCCAAATACAAGCCCATGATGATCATCACTGAGTACATCACTGGAGAATGGGGCCCTGGAC 2216

Qy 1726 ACCTTCCTCCGCACGGAGGGGCCCGGAATGGGGCCTGGAC 1785
            |||
Db 2217 AAGTTCCTTCGGGAGAAGGATGGCGAGTTCAGCGTGCTGGTGGGCATGCTGCGCGG 2276

Qy 1786 GATGCAGCTGCTGGCATGGAGGCAAGTGCTCATCACCGGGACCTGGCT 1845
            |||
Db 2277 GGCATCGCAGCTGGCATGGAGTACCTGGCCAACATGTGCACCGTGACCTGGCT 2336

Qy 1846 GCTCGGAACTGCCTGGTGACAGAGAGAAATGTCCTGAAGATCAGTGACTTTGGGATGTCC 1905
            |||
Db 2337 GCCCGCAACATCCTCGTCAACAGCAACCTGGTCTCGAAGGTGTCTGACTTTGGCCTGTCC 2396

Qy 1906 CGAGAGGAAGCCGATGGGGTCTATGCAGCCT---CAGGGGGCCTCAGACAAGTCCCCGTG 1962
            |||
Db 2397 CGCGTGCTGGAGGACGACCCCGAGGCCACCTACACACCAGTGCGCGGACAGTGTGG 2456

Qy 1963 AAGTGGACCGACCACCTGAGGCCCTAACTACACGGCCGCTACTCCTCCGAAAAGCGACGTGTGG 2022
            |||
Db 2457 CGCTGGACCGCCCCGGAGGCCATTTCCTACCGGAAGTTCACCTCTGCCAGCGAGTGTGTGG 2516

Qy 2023 AGCTTTGGCATCTTGCTCTGGGAGACTTCAGCCTGGGGCCTATCCCAACCTC 2082
            |||
Db 2517 AGCTTTGGCATTGTCATGTGGGAGGTGATGACCTATGGGAGGCGCCCTACTGGGAGTTG 2576

Qy 2083 AGCAATCAGCAGACACGGAGTTTGTGGAGAAGGGGGCCGTCTGCCCGCCAGAGCGG 2142
            |||
Db 2577 TCCAACCACGAGGTGATGAAAGCCATCAATGATGGCTTCCGGCCTCCCACACCCATGCGGAC 2636

Qy 2143 TGTCCTGATGCCGTGTTCAGGCTCATGGAGCAGCGGCAGCGG 2202
            |||
Db 2637 TGCCCCTCCGCCATCTACCAGCTCATGATGCTCTGCTGGCAGCAGGACAAGCTC 2696

Qy 2203 CCCAGCTTCAGCAGCACCATCTACCAGGAGCTGCAGAGCATC 2241
            |||
Db 2697 CCCAAGTTCGGCTGACATCGTCAGCATCCTGACAAGCTC 2735
```

```
RESULT 11
US-09-949-016-2120
; Sequence 2120, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;    APPLICANT: VENTER, J. Craig et al.
;    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;    FILE REFERENCE: CL001307
;    CURRENT APPLICATION NUMBER: US/09/949,016
;    CURRENT FILING DATE: 2000-10-20
;    PRIOR APPLICATION NUMBER: 60/241,755
;    PRIOR FILING DATE: 2000-04-14
;    PRIOR APPLICATION NUMBER: 60/237,768
;    PRIOR FILING DATE: 2000-10-03
;    PRIOR APPLICATION NUMBER: 60/231,498
;    PRIOR FILING DATE: 2000-09-08
;    NUMBER OF SEQ ID NOS: 207012
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Right column

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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2120
; LENGTH: 3921
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2120

Query Match        8.2%;  Score 185.4;  DB 4;  Length 3921;
Best Local Similarity 55.1%;  Pred. No. 3.3e-31;
Matches 385;  Conservative  0;  Mismatches 311;  Indels  3;  Gaps  1;

Qy 1546 CTGGTGCGGTGAAGTCTTGTCGAGAGACGCTCCCACCTGACCTCAAGGCCAAGTTCTA 1605
            |||||| ||||  |||  ||  |||||||||   |||  |||| ||||
Db 2037 CCGGTGCCATCAAGACGCTGAAAGCCGGCTACACAGAGAAGCAGCGAGTGGACTTCCTC 2096

Qy 1606 CAGGAAGCAGGAGGATCCTGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTC 1665
            |||     |||||  |||  ||||
Db 2097 GGCGAGGCCGGCATCACGGAGGGGGGGACTTGTCAGGGGGGGGGGGTC 2156

Qy 1666 TGCACCCAGAAGCAGCAGCCATCTACATCGTCATGGAGTTGTGCAGGGGGGGACTTCCTG 1725
            |||
Db 2157 ATCTCCAAATACAAGCCCATGATGATCATCACTGAGTACATCACTGGAGAATGGGGCCCTGGAC 2216

Qy 1726 ACCTTCCTCCGCACGGAGGGGCCCGGAATGGGGCCTGGAC 1785
            |||
Db 2217 AAGTTCCTTCGGGAGAAGGATGGCGAGTTCAGCGTGCTGGTGGGCATGCTGCGCGG 2276

Qy 1786 GATGCAGCTGCTGGCATGGAGAGCAAGTGCTGCATCACCGGGACCTGGCT 1845
            |||
Db 2277 GGCATCGCAGCTGGCATGGAGTACCTGGCCAACATGTGCACCGTGACCTGGCT 2336

Qy 1846 GCTCGGAACTGCCTGGTGACAGAGAGAAATGTCCTGAAGATCAGTGACTTTGGGATGTCC 1905
            |||
Db 2337 GCCCGCAACATCCTCGTCAACAGCAACCTGGTCTCGAAGGTGTCTGACTTTGGCCTGTCC 2396

Qy 1906 CGAGAGGAAGCCGATGGGGTCTATGCAGCCT---CAGGGGGCCTCAGACAAGTCCCCGTG 1962
            ||                                          |||
Db 2397 CGCGTGCTGGACGACGACCCCGAGGCCCACCTACACACCAGTGCGCGGACGAGTGTGG 2456

Qy 1963 AAGTGGACCGACCACCTGAGGCCCTACTACACGGCCGCTACTCCTCCGAAAAGCGACGTGTGG 2022
            |||                                       |||||||
Db 2457 CGCTGGACCGCCCCGGAGGCCATTTCCTACCGGAAGTTCACCTCTGCCAGCGACGTGTGG 2516

Qy 2023 AGCTTTGGCATCTTGCTCTGGGAGACTTCAGCCTGGGGCCTATCCCAACCTC 2082
            ||||||||                                |||   |||
Db 2517 AGCTTTGGCATTGTCATGTGGGAGGTGATGACCTATGGGAGGCGCCCTACTGGGAGTTG 2576

Qy 2083 AGCAATCAGCAGACACGGAGTTTGTGGAGAAGGGGGCCGTCTGCCCGCCAGAGCTG 2142
            |||   |||
Db 2577 TCCAACCACGAGGTGATGAAAGCCATCAATGATGGCTTCCGGCCTCCCACACCCATGCGGAC 2636

Qy 2143 TGTCCTGATGCCGTGTTCAGGCTCATGGAGCAGCGGCAGCGG 2202
            |||
Db 2637 TGCCCCTCCGCCATCTACCAGCTCATGATGCTCTGCTGGCAGCAGGACAAGCTC 2696

Qy 2203 CCCAGCTTCAGCAGCACCATCTACCAGGAGCTGCAGAGCATC 2241
            |||   |||
Db 2697 CCCAAGTTCGGCTGACATCGTCAGCATCCTGACAAGCTC 2735
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RESULT 12
US-09-949-016-5662
; Sequence 5662, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;    APPLICANT: VENTER, J. Craig et al.
;    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;    FILE REFERENCE: CL001107
;    CURRENT APPLICATION NUMBER: US/09/949,016
;    CURRENT FILING DATE: 2000-04-14
;    PRIOR APPLICATION NUMBER: 60/241,755
;    PRIOR FILING DATE: 2000-10-20
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; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5662
; LENGTH: 3386
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5662

Query Match   7.7%;   Score 174.6; DB 4; Length 3386;
Best Local Similarity 54.7%;   Pred. No. 7.5e-29;
Matches 392; Conservative   0; Mismatches 319; Indels   6; Gaps   2;

Qy 1498 GGGAACTTTGGCGAAGTGTTCAGCGGACGCCTGCGAGCCGACAACACCCTGGTGCGGGTG 1557
         ||||| ||| ||||||||||| |||||| ||| ||||
Db 1386 GGGGAGGTCTATGAAGGTGTCTACACAAATCACAAGGGGAGAAAATCAATGTAGCTGTC 1445

Qy 1558 AAGTCTTGTCGAGAGACGCTCCCAACTGACCTCAAGGCCAAGTTCTACAGGAAGCGAGG 1617
         || || |||| ||||||
Db 1446 AAGACCTGCAAGAAAGACTGCACTCTGGACAACAAGGAGAAGTTCATGAGCGAGGCAGTG 1505

Qy 1618 ATCCTGAAGCAGTACAGCCACCCCAACATCTGCGTCTCATTGGTGTCTCGCACCCAGAAG 1677
         ||||| |||| |||| |||||| ||
Db 1506 ATCATGAAGAACCTCGACCACCCGCACATCGTGAAGCTGAAGCTGCAT---CATTGAAGAG 1562

Qy 1678 CAGCCCATCTACATCGTCATGGTTGTGCAGGGGGCCACTTCCTGACCTTCCTCCGC 1737
         ||| ||| ||| ||||||||| ||| |||
Db 1563 GAGCCCACCTGGATCATCATGGAATTGTATCCCTATGGGGAGCTGGGCCACTACCTGGAG 1622

Qy 1738 ACGGAGGGGGCCCGCTCGCGGGTGAAGACTTCGTCTGCAGATGGTGGTGCAGCTGCTGCT 1797
         |||||||| || ||
Db 1623 CGGAACAAGAACTCCCTGAAGGTGCTCACCCTGTCGTGCTGTACTCACTGCAGATATGCAAA 1682

Qy 1798 GGCATGGAGTACCTGGGAATCATCAACTACTGCTGCTGCTCGGAACTGC 1857
         ||| ||||||||||| |
Db 1683 GCCATGGCCTACCTGCTGGAGAGCAGCATCAACTACTGCTGCTCGTCCGGAACATC 1742

Qy 1858 CTGGTGACAGAGAAGAATGTCCTGAAGATCAGTCAGTGATGTCCCGAGAGGAAGCC 1917
         ||||| |||
Db 1743 CTGGTGGCCTCCCGAGTGTGTGAAGCTGGGGGACTTTGGTCTTTCCCGGTACATTGAG 1802

Qy 1918 GATGGGGTCTATGCAGCCCAGGGGGCCTCAGACAGACTCCCGTGAAGTGACCGCACCT 1977
         ||| ||||||| |||||
Db 1803 GACGAGGACTAT---TACAAAGCCTGTGACTGCGTCTCCCCATCAAATGATGTCCCCA 1859

Qy 1978 GAGGGCCCTTAACTACGGCCGCTACTCCTCCGAAAGCGACGTGTGGAGCTTTGGCATCTTG 2037
         ||| ||| ||||||
Db 1860 GAGTCCATTAACTTCCGACGCGTTCGACGCTCGCAGTGAGTTCATGAGCGAGGCAGCAGTG 1919

Qy 2038 CTCTGGAGACCTTCAGCTGGGGGCCTCGGGGGCCTCCCCATCCCAACCTCAACAATCAGCAGACA 2097
         ||||| |||
Db 1920 ATGTGGAGGATCCTGAGCTTTGGAAGCAGCCCTCTTCTGGCTGGAGAACAAGGATGTC 1979

Qy 2098 CGGGAGTTTGTGAGAGGGGGCCGTGTCTGCCCTGATGCGTG 2157
         ||| |||||||||| |
Db 1980 ATCGGGGGTGCTGGAGAAGAGGACCCGGCCTGCTCGGGACGCCGCCCAGCTTCAGC 2039

Qy 2158 TTCAGGCTCATGGAGCAGTGCTGGGCCTATGAGCCTGGGAACTGC 2214
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Db 2040 TATACCCTGCTCATGACCCTGCTGGGACTACGACCCGCCCGCGTTCACC 2096

RESULT 13
US-08-357-642A-2
; Sequence 2, Application US/08357642A
; Patent No. 5837524
; GENERAL INFORMATION:
; APPLICANT: Sima Lev
; APPLICANT: Joseph Schlessinger
; TITLE OF INVENTION: PYK2 RELATED PRODUCTS

; TITLE OF INVENTION: AND METHODS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/357,642A
; FILING DATE: December 15, 1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/070
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3416
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: nucleic
US-08-357-642A-2

Query Match   7.7%;   Score 174.6; DB 2; Length 3416;
Best Local Similarity 54.7%;   Pred. No. 7.5e-29;
Matches 392; Conservative   0; Mismatches 319; Indels   6; Gaps   2;

Qy 1498 GGGAACTTTGGCGAAGTGTTCAGCGGACGCCTGCGAGCCGACAACACCCTGGTGCGGGTG 1557
         ||||| ||| ||||||||||| |||||| ||| ||||
Db 1416 GGGGAGGTCTATGAAGGTGTCTACACAAATCACAAGGGGAGAAAATCAATGTAGCTGTC 1475

Qy 1558 AAGTCTTGTCGAGAGACGCTCCCAACTGACCTCAAGGCCAAGTTCTACAGGAAGCGAGG 1617
         || || |||| ||||||
Db 1476 AAGACCTGCAAGAAAGACTGCACTCTGGACAACAAGGAGAAGTTCATGAGCGAGGCAGTG 1535

Qy 1618 ATCCTGAAGCAGTACAGCCACCCCAACATCTGCGTCTCATTGGTGTCTCGCACCCAGAAG 1677
         ||||| |||| |||| |||||| ||
Db 1536 ATCATGAAGAACCTCGACCACCCGCACATCGTGAAGCTGAAGCTGCAT---CATTGAAGAG 1592

Qy 1678 CAGCCCATCTACATCGTCATGGTTGTGCAGGGGGCCACTTCCTGACCTTCCTCCGC 1737
         ||| ||| ||| ||||||||| ||| |||
Db 1593 GAGCCCACCTGGATCATCATGGAATTGTATCCCTATGGGGAGCTGGGCCACTACCTGGAG 1652

Qy 1738 ACGGAGGGGGCCCGCTCGCGGGTGAAGACTTCGTCTGCAGATGGTGGTGCAGCTGCTGCT 1797
         |||||||| || ||
Db 1653 CGGAACAAGAACTCCCTGAAGGTGCTCACCCTGTCGTGCTGTACTCACTGCAGATATGCAAA 1712

Qy 1798 GGCATGGAGTACCTGGGAATCATCAACTACTGCTGCTGCTCGGAACTGCT 1857
         ||| ||||||||||| |
Db 1713 GCCATGGCCTACCTGCTGGAGAGCAGCATCAACTGCTGTCGTCCGGAACATC 1772

Qy 1858 CTGGTGACAGAAGAATGTCGAGATCAGTGAGTGTGAAGCTGGGGGGCAGTG 1917
         ||||| |||
Db 1773 CTGGTGGCCTCCCCCGAGTGTGTGAAGCTGGGGGACTTTGGTCTTTCCCGGTACATTGAG 1832

Qy 1918 GATGGGGTCTATGCAGCCCAGGGGGCCTCAGACAAGTCCCCGTGAAGTGACCGCACCT 1977
         ||| ||||||| |||||

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Db  1416  GGGGAGGTCTATGAGGTGTCTACACAAATCACAAAGGGGAGAAAATCAATGTAGCTGTC  1475
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Qy  1558  AAGTCTTGTCGAGAGACGCTCCCACCTGACCTCAAGGCCAAGTTTCTACAGGAGGCAGAGG  1617
               || |   |    |||  || |||| |   | |   ||||
Db  1476  AAGACCTGCAAGAAAGACTGCACTCTGGACAACAAGGAGAAGTTCATGAGCGAGGCAGTG  1535

Qy  1618  ATCCTGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCCAGAAG  1677
          ||  |||||    ||| |||| ||| | |||||||  |  || |
Db  1536  ATCATGAAGAACCTGCACCACCCGCACATCGTGAAGCTGATCGGCAT---CATTGAAGAG  1592

Qy  1678  CAGCCCATCTACATCGTCATGAGCTTGTGCAGGGGCGGCGACTTCCTGACCTTCCTCCGC  1737
          | ||||| ||| | ||| ||| ||  |  |   |  |  ||   |
Db  1593  GAGCCCACCTGGATCATCATGGAATTGTATCCCTATGGGGAGCTGGGCACTACCTGGAG  1652

Qy  1738  ACGGAGGGGCGCCCTGCCGGGTGAAGACTCTGCTGCAGGACTGTGGGGATGGCAGCTGCT  1797
          | ||| |    | || ||| |||    | | |   |   |  ||
Db  1653  CGGAACAAGAACTCCCTGAAGGTGCTCACCCTGTCGTACTACTGCGATATGCAAA  1712

Qy  1798  GGCATGAGTAGTACCTGGAGGAGCAAGTGCTGCATCCACCGGGACCTGCTGCTCGGAACTGC  1857
          |||| |  |    ||  | |||  | |  | | | ||  |  ||| ||  |  |||||
Db  1713  GCCATGCCTACCTGGAGAGCATCAACTGCGCTGCACAGGGACATTGTGTCCGGAACATC  1772

Qy  1858  CTGGTGACAGAGAAGAAGAATGTCCTGAAGATCCAGTGACTTTGGGATGGTCCGAGAGGAAGCC  1917
          | ||| |  | ||||| |      | | |   ||   | || ||| |  |   || |||
Db  1773  CTGGTGGCCTCCCCTGAGTGTGTGAAGCTGGGGGACTTTGGTCTTTCCCGGTACATTGAG  1832

Qy  1918  GATGGGGTCATGCAGCCTCAGGGGGCCTCAGACAGTCCCGTGAGTGGACCGCACCT  1977
          ||  ||  ||| |||  ||  |  ||| |  | |   || |
Db  1833  GACGAGGACTAT---TACAAAGCCTGTCGTGTCCCCATCAAATGGATGTCCCCA  1889

Qy  1978  GAGGCCCTTAACTACGGCCGCTACTCCTCCGAAAGCGACGTGTGGAGCTTTGGAGCATCTTG  2037
          ||  | ||| || |   |||  | || |   |||  || ||| |  |  || |||  ||
Db  1890  GAGTCCATTAACTTCCGACGTTCACGACAGCAGCAGTGACGTGTGGAGCTTCGGCGTGTGC  1949

Qy  2038  CTCTGGGAGACCTTCAGCCTGGGGGCCCGCTGCCCAGAGCTGTGTCCTGATGCCGTG  2097
          ||| |||||| || |||||| ||| | |  |  |   |  |  ||| || | | |
Db  1950  ATGTGGGAGATCCTGAGCTTTGGGAAGCAGCCCTTCTTCTTCGGCTGGAACAAGGATGTC  2009

Qy  2098  CGGGAGTTTGTGGAGGAGGGGGCCCGTGCCCTGCGCCCTGCGTGTCCTGATGCCGTG  2157
          |  ||||| ||| || || | | |  |   | ||  | |  |  | |||  | ||
Db  2010  ATCGGGGTGCTGGAGAAGGAGACCGGCGGTGCCCAAGCCTGATCTGTGCCACCGGTCCTT  2069

Qy  2158  TTCAGGCTCATGGAGCAGTGCTGGGCCTATGAGCGTGGCAGCGGCCCCAGCTTCAGC  2214
          || |||||||||||| || |||||||| |||  | |  | | || ||||| ||||||
Db  2070  TATACCCTCATGAGCAGGTGCTGGGACTACGACCCCAGTGACCGGCCCCGCTTCACC  2126
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RESULT 14
US-08-460-626-2
; Sequence 2, Application US/08460626
; Patent No. 5837815
; GENERAL INFORMATION:
; APPLICANT: SIMA LEV
; APPLICANT: JOSEPH SCHLESSINGER
; TITLE OF INVENTION: PYK-2 RELATED PRODUCTS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,626
; FILING DATE: June 2, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/357,642
; FILING DATE: December 15, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 211/121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3416
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-460-626-2

Query Match 7.7%; Score 174.6; DB 2; Length 3416;
Best Local Similarity 54.7%; Pred. No. 7.5e-29;
Matches 392; Conservative 0; Mismatches 319; Indels 6; Gaps 2;

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Qy  1498  GGGAACTTTGGCGAAGTGTTCAGCGAGCCTGCCGAGCCGCCGACCACACCCGGTCGCGGTG  1557
          ||  ||  |     | |  |     |   || ||   || ||   |    |  ||||||||
Db  1833  GACGAGGACTAT---TACAAAGCCTGTCGTGTCCCCATCAAATGGATGTCCCCA  1889

Qy  1978  GAGGCCCTTAACTACGGCCGCTACTCCTCCGAAAGCGACGTGTGGAGCTTTGGAGCATCTTG  2037
Db  1890  GAGTCCATTAACTTCCGACGTTCACGACAGCAGCAGTGACGTGTGGAGCTTCGGCGTGTGC  1949

Qy  2038  CTCTGGGAGACCTTCAGCCTGGGGGCCCGCTGCCCAGAGCTGTGTCCTGATGCCGTGACA  2097
Db  1950  ATGTGGGAGATCCTGAGCTTTGGGAAGCAGCCCTTCTTCTTCGGCTGGAACAAGGATGTC  2009

Qy  2098  CGGGAGTTTGTGGAGGAGGGGGCCCGTGCCCTGCGCCCTGCGTGTCCTGATGCCGTG  2157
Db  2010  ATCGGGGTGCTGGAGAAGGAGACCGGCGGTGCCCAAGCCTGATCTGTGCCACCGGTCCTT  2069

Qy  2158  TTCAGGCTCATGGAGCAGTGCTGGGCCTATGAGCGTGGCAGCGGCCCCAGCTTCAGC  2214
Db  2070  TATACCCTCATGAGCAGGTGCTGGGACTACGACCCCAGTGACCGGCCCCGCTTCACC  2126
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RESULT 15
US-09-016-434-1483
; Sequence 1483, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1483:
SEQUENCE CHARACTERISTICS:
LENGTH: 3416 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g988304
US-09-016-434-1483

Query Match   7.7%;   Score 174.6; DB 4; Length 3416;
Best Local Similarity 54.7%; Pred. No. 7.5e-29;
Matches 392; Conservative 0; Mismatches 319; Indels 6; Gaps 2;

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Qy  1498 GGGAACTTTGCGGAAGTGTTCAGCGGACGCTGCGAGCCGACCAACACCCTGGTGGCGGTG 1557
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Db  1416 GGGGAGGTCTCATGAGAGGTGTCTACACAAATCACAAGGGGAGAAAATCAATGTAGCTGTC 1475

Qy  1558 AAGTCTTGTCGAGAGACGCTCCCACCTGACCTCAAGGCCAAGTTCTACAGGAAGCGAGG 1617
         ||  ||||| |||| | |   || || | |  |||||| ||||| || |||||| |||
Db  1476 AAGACCTGCAAGAAAGACTGCACTCTGGACAACAAGGAGAAGTTCATGAGCGAGGCAGTG 1535

Qy  1618 ATCCTGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGTGTCTGCACCCAGAAG 1677
         ||||| |||  | || || || || |||| | |  |  || |||   ||   |||||||
Db  1536 ATCATGAAGAACCTGCACCACCCCGACATCGTGAAGCTGATCGGCAT---CATTGAAGAG 1592

Qy  1678 CAGCCCATCTACACATCGTCATGGAGCTTGTGCAGGGGGCCACTTCCTGACCTTCCTCCGC 1737
         |||||| || |||    | | ||||    ||| || ||| ||  ||   |||| || ||
Db  1593 GAGCCCACCTGGATCATCATGGAATTGTATCCCTATGGGAGCTGGCCACTACCTGGAG 1652

Qy  1738 ACGGAGGGGGCCCGCCTGCGGGTGAAGACTTCGTCTGCAGATGGTGGGGGATGCAGCTGCT 1797
         | ||||| ||| | || ||||| |||||  ||  || |  || || |  |||| || ||
Db  1653 CGGAACAAGAACTCCCTGAAGGTGCTCACCCCTGCGTGCTGTACTCACTGCAGATATGCAAA 1712

Qy  1798 GGCATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGACCTGCTCGGAACTGC 1857
         ||||| ||| || ||| || || ||   | |||  || ||  ||||||| || |
Db  1713 GCCATGGCCTACCTGGAGAGCATCAACTGCCTGCACAGGGACCATTGCTGTCCGGAACATC 1772

Qy  1858 CTGGTGACAGAGAAGAATGTCCTGAAGATCAGTGACTTTGGGATGTCCCGAGAGGAAGCC 1917
         ||| || ||| ||     || | |  |  | ||||   |||||| |   || || ||||
Db  1773 CTGGTGGCCTCCCCCTGAGTGTGTGAAGCTGGGGGACTTTGTCTTTCCCGGTACATTGAG 1832

Qy  1918 GATGGGGTCTATGCAGCCTCAGGGGGCCTCAGGACAACGTCCCGTGAAGTGGACCGCACCT 1977
         |  ||||| || ||      ||     || |  |  ||   || || ||  |||| | ||
Db  1833 GACGAGGACTAT---TACAAAGCCTCTGGTGACTGGTCTCCCCATCAAAATGGATGTCCCCA 1889

Qy  1978 GAGGGCCCTTAACTACGGGCCGCTACTCCTCCGAAAGCGACGTTTGGCATCTTG 2037
         ||   ||| || |||   |  |  || |  |  ||| | || ||| |||| | |
Db  1890 GAGTCCATTAACTTCCGACGCTTCACGACAGCCAGTCTCGGATGTTCGCCGTGC 1949

Qy  2038 CTCTGGGAGACCTTCAGCCTTCGGGGGCCTCCCCCATCCCAACCTCAGCAATCAGCAGACA 2097
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Db  1950 ATGTGGGAGATCCTGAGCTTTGGGAAGCAGCCCTTCTTCTGGCTGGAGAACAAGGATGTC 2009

Qy  2098 CGGGAGTTTGTGGAGAAGGGGGGCCCGCTCGCCCTGCCCCAGAGCTGTGTCCTGATGCCGTG 2157
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Db  2010 ATCGGGGTGCTGGAGAAAAGGAGACCGGCTGCCCAAGCCGTCGATCTCTGTCCACCGGTCCTT 2069

Qy  2158 TTCAGCTCATGGAGCAGTGCTGGCCTATGAGCCTGGGCAGCCCCAGCTTCAGC 2214
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Db  2070 TATACCCTCATGACCCGCTGCTGGGACTACGACCCCCAGTGACCCGCCCGCTTCACC 2126
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                GenCore version 5.1.6
          Copyright (c) 1993 - 2005  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:     August  9, 2005, 20:15:00 ; Search time 2382.73 Seconds
                                        (without alignments)
                                        7274.725 Million cell updates/sec

Title:      US-10-660-763-1
Perfect score: 2674
Sequence:   1 tccggggtccgcaccgggcc.........aaaaaaaaaaaaaaaaa 2674

Scoring table: IDENTITY NUC
            Gapop 10.0, Gapext 1.0

Searched:   7297361 seqs, 324162794 residues

Total number of hits satisfying chosen parameters:      14594722

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications NA:*
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         2:  /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
         3:  /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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         5:  /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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        11:  /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
        12:  /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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        14:  /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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        26:  /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

                            SUMMARIES
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2674	100.0	2674	13	US-10-003-295-1	Sequence 1, Appli
2	2674	100.0	2674	18	US-10-660-763-1	Sequence 1, Appli
3	2326.4	87.0	2889	16	US-10-240-965-256	Sequence 256, App
4	362.4	13.6	15297	13	US-10-003-295-3	Sequence 3, Appli
5	328.8	13.6	15297	18	US-10-660-763-3	Sequence 3, Appli
6	328.8	12.3	2950	21	US-10-887-553A-240	Sequence 240, App
7	326.8	12.2	449	10	US-09-918-995-1503	Sequence 1503, Ap

	Score	%				Description
8	296.2	11.1	361	9	US-09-948-802-5	Sequence 5, Appli
9	296.2	11.1	361	15	US-10-121-925-5	Sequence 5, Appli
10	271.6	10.2	1779	18	US-10-280-576-19	Sequence 19, Appl
11	201.2	7.5	3875	15	US-10-101-510-525	Sequence 525, App
12	198	7.4	2955	9	US-10-384-339C-1	Sequence 1, Appl
13	198	7.4	3370	9	US-09-967-768A-144	Sequence 144, App
14	198	7.4	3370	16	US-10-354-358-101	Sequence 101, App
15	198	7.4	3370	16	US-10-210-120-19	Sequence 19, Appl
16	198	7.4	3370	19	US-10-776-827-82	Sequence 82, Appl
17	198	7.4	3370	20	US-10-473-974-219	Sequence 219, App
18	198	7.4	3370	21	US-10-843-641A-6289	Sequence 6289, Ap
19	198	7.4	3370	22	US-10-909-035-19	Sequence 19, Appl
20	185.4	6.9	3042	19	US-10-384-339C-2	Sequence 2, Appli
21	185.4	6.9	3921	15	US-09-921-406C-29	Sequence 29, Appl
22	185.4	6.9	3921	10	US-10-007-926A-222	Sequence 222, App
23	185.4	6.9	3921.	16	US-10-269-909-19	Sequence 19, Appl
24	185.4	6.9	3921	17	US-10-366-288-1	Sequence 1, Appli
25	185.4	6.9	3921	17	US-10-172-118-1036	Sequence 1036, Ap
26	185.4	6.9	3921	18	US-10-342-887-1036	Sequence 1036, Ap
27	185.4	6.9	3921	18	US-10-287-226-319	Sequence 319, App
28	185.4	6.9	3921	19	US-10-648-593-1	Sequence 1, Appli
29	185.4	6.9	3921	20	US-10-473-974-223	Sequence 223, App
30	185.4	6.9	3921	21	US-10-616-403-5	Sequence 5, Appli
31	185.4	6.9	3935	21	US-10-897-711-1	Sequence 1, Appli
32	176.2	6.6	1518	18	US-10-280-576-24	Sequence 24, Appl
33	174.6	6.5	816	19	US-10-377-268-3	Sequence 3, Appli
34	174.6	6.5	1050	19	US-10-377-268-4	Sequence 4, Appli
35	174.6	6.5	3030	16	US-10-325-430-8	Sequence 8, Appli
36	174.6	6.5	3416	8	US-08-987-689A-1	Sequence 1, Appli
37	174.6	6.5	3416	15	US-10-292-524-1	Sequence 1, Appli
38	174.6	6.5	3416	17	US-10-464-805-2	Sequence 2, Appli
39	174.6	6.5	3416	17	US-10-305-720-1483	Sequence 1483, Ap
40	174.6	6.5	3416	21	US-10-860-066-1	Sequence 1, Appli
41	174.6	6.5	3544	14	US-10-161-803-51	Sequence 51, Appl
42	174.6	6.5	4089	17	US-10-291-808-13	Sequence 13, Appl
43	174.6	6.5	4089	19	US-10-620-052A-7	Sequence 7, Appli
44	174.6	6.5	4151	14	US-10-161-803-52	Sequence 52, Appl
45	174.6	6.5	4151	16	US-10-325-430-7	Sequence 7, Appli

ALIGNMENTS

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RESULT 1
US-10-003-295-1
; Sequence 1, Application US/10003295
; Publication NO. US20020168741A1
; GENERAL INFORMATION:
;  APPLICANT: GAN, Weiniu et al.
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION: THEREOF
;  FILE REFERENCE: CL001183DIV
;  CURRENT APPLICATION NUMBER: US/10/003,295
;  CURRENT FILING DATE: 2001-12-06
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;  LENGTH: 2674
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-003-295-1

Query Match             100.0%;  Score 2674;  DB 13;  Length 2674;
Best Local Similarity   100.0%;  
Matches 2674;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         1 TCCGGGGTCCGCACCGGGCCTGAGTCGGTCCGAGGCGTCCCAGGAGCAGCTGCCCGTGC 60
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Db         1 TCCGGGGTCCGCACCGGGCCTGAGTCGGTCCGAGGCGTCCCAGGAGCAGCTGCCCGTGC 60

Qy        61 GGAACAGCACTATGGGCTTCTTCTTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGC 120
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Qy   1201  TGCAGGCCCAGCAGCAGGAGTTGCTGCAGACCAAGCTGAGCACCTGGGCCCCGCGGCCCC  1260
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Db   1201  TGCAGGCCCAGCAGCAGGAGTTGCTGCAGACCAAGCTGAGCACCTGGGCCCCGCGGCCCC  1260

Qy   1261  CGCCTGTGTCGTGCTCCTGCAGGATGACCGCGCACTCCACGTCGTCCTCCGGAGCAGGCGAG  1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1321  AGGGGGAAGGACACCCACGCTGGAGATCCTTAAGACCACATCTCAGGAATCTTCCGCC  1380
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Qy   1381  CCAAGTTCTCGAACCTGTACCGACTGGAAGGGGAAGGCTTTCCTAGCATTCCTTTGCTCA  1440
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Db   1381  CCAAGTTCTCGAACCTGTACCGACTGGAAGGGGAAGGCTTTCCTAGCATTCCTTTGCTCA  1440

Qy   1441  TCGACCACCTACTGAGACACCCAGCAGCAGCTTCGCAAGACCTACA  1500
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Qy   1501  GGGCTGTGCCCAAGACAAGTGGGTGCTGAACCATGAGACCTGGTGTTGGGTGTGAGCAGA  1560
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Qy   1561  TTGGACGGGGAACTTTGGCGAAGTGTTCAGCGAAGTGTTCAGCGAGCCGCACACACCCCTGG  1620
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Qy   1621  TGGCGGTGAAGTCTTGTGTCGAGACGCTCCACCTGACCTGACCTTCTACAGG  1680
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Qy   1681  AAGGGAGGATCCTGAAGAGTACAGCCACCACCCAACATCGTGCGTCTCATTGGTGTCTGCA  1740
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Qy   1801  TCCTCCGCACCGAGGGGCCCGCCCTGCTGCGGGTGAAGACTCTGCTGAGATGGGGATG  1860
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Qy   1861  CAGCTGCTGGCATGGAGGTACCTGGAGAGCAAGTGCTCATCCACCGGGACCTGGCTGCTC  1920
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Qy   1921  GGAACTGCCTGGACAGAGAGAATGTCCTGAAGATCAGTCAGTGTCCCGAG  1980
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Qy   1981  AGGAAGCCGATGGGGTCTATGCCAGCCTACTCCTCCGAAAGCGACGTGGGAGCTTTG  2040
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Qy   2041  CCGCACCTGAGCCTTAACTACGGCGCCTTCGGGGGCCTTCCCCCTATCCCAACCTCAGCAATC  2100
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Db   2221  ATGCCGTGTTCAGGCTCATGGAGCTGTGGCCTATGAGCCTGGGCGCGCCCAGCT  2280
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Qy   121  AGCAAATGCAGGAGGCCGAGACTTCGCTTCTACTGAGTGAGGGCCATGAGGAAAGTGGATGGCCCAGC  180
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Db   121  AGCAAATGCAGGAGGCCGAGACTTCGCTTCTACTGAGTGAGGGCCATGAGGAAAGTGGATGGCCCAGC  180

Qy   181  GGGTCAAGAGTGACAGGAGTATGCAGAACTGCTTCACCACATGTCCCTGCGCAGACACGTG  240
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Qy   241  GGGGCCAGAGCCGGGCCATCAGCAGCCCCATCAGTCAGTGCTGGGCTGAGATCA  300
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Qy   301  CCAGCCAAACTGAGGGCCTTGAGCCGTCTGCGCAGCACGCAGAGATCTGAACTCAG  360
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Db   301  CCAGCCAAACTGAGGGCCTTGAGCCGTCTGCGCAGCACGCAGAGATCTGAACTCAG  360

Qy   361  GGCCCCTGAGCAAGCTGAGCGTTCATCCGGGAACGGCCAGCTTCGCAAGACCTACA  420
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Db   361  GGCCCCTGAGCAAGCTGAGCGTTCATCCGGGAACGGCCAGCTTCGCAAGACCTACA  420

Qy   421  GCGAGCAGTGCGAGCAGTGCGAGCAGTCACCAAGACCCCACAGCCCAGCACATTGAGA  480
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Db   421  GCGAGCAGTGCGAGCAGTGCGAGCAGTCACCAAGACCCCACAGCCCAGCACATTGAGA  480

Qy   481  AGCTGAAGAGCCAGTACCGACCTCGCACGGACTGCGCCCAAGCCAAGCGCAAGTACC  540
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   481  AGCTGAAGAGCCAGTACCGACCTCGCACGGACTGCGCCCAAGCCAAGCGCAAGTACC  540

Qy   541  AGGAGAGGCCAGCAAAGACAAGGACCGTGACAAGGCCAAGGCCGTGACCAAGAAGACAAGCCACAGCCCAGCACATTGCGCAGCCAGTGT  600
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   541  AGGAGAGGCCAGCAAAGACAAGGACCGTGACAAGGCCAAGGCCGTGACCAAGAAGACAAGCCACAGCCCAGCACATTGCGCAGCCAGTGT  600

Qy   601  GGAAGCTCTTTGCTCACCACAACCGCTATGTGCTGGGGCGTGCGGGGCGTGCGGCGCAGCTACACC  660
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Db   601  GGAAGCTCTTTGCTCACCACAACCGCTATGTGCTGGGGCGTGCGGGGCGTGCGGCGCAGCTACACC  660

Qy   661  ACCAGCACCACCACCAGCTTCCTGCTGCGGGCGTCTGCGGTCACTGCAGGACCCTGCACG  720
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Db   661  ACCAGCACCACCACCAGCTTCCTGCTGCGGGCGTCTGCGGTCACTGCAGGACCCTGCACG  720

Qy   721  AGGAGATGGCTTGCATCCTGCGAAGGAGATCCTGCAGGAATACCTGGAGATTAGCAGCCTGG  780
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Db   721  AGGAGATGGCTTGCATCCTGCGAAGGAGATCCTGCAGGAATACCTGGAGATTAGCAGCCTGG  780

Qy   781  TGCAGGATGAGGTGGTGGCCATTCACCGGAGATGGCTGCAGCTGCTGCCCCCGCCATCCAGC  840
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   781  TGCAGGATGAGGTGGTGGCCATTCACCGGAGATGGCTGCAGCTGCTGCCCCCGCCATCCAGC  840

Qy   841  CTGAGGCTTGACAAGGCTTCCTGCGACAGCGTGCAGGAGGTGAACCGGCTGGCAGCCTGAGGAGCTCC  900
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   841  CTGAGGCTTGACAAGGCTTCCTGCGACAGCGTGCAGGAGGTGAACCGGCTGGCAGCCTGAGGAGCTCC  900

Qy   901  GTGTCACGTTCGATGAGTCGTTCGACAGCGTGTGAGAGATGTTACGGACCTGCAGCTGACAGATGAGC  960
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Db   901  GTGTCACGTTCGATGAGTCGTTCGACAGCGTGTGAGAGATGTTACGGACCTGCAGCTGACAGATGAGC  960

Qy   961  AGCTCCGGAATGAAGAGAGAGGAGAACACGCTGCAGCACACGCTGCTCGCTGTCTGGGCAGGCCAAGAGA  1020
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Db   961  AGCTCCGGAATGAAGAGAGAGGAGAACACGCTGCAGCACACGCTGCTCGCTGTCTGGGCAGGCCAAGAGA  1020

Qy  1021  TGGCTGTGGCCACCGAGATGGTGTTCAGGCGGGATGGTTACGGCACTGCTGCAACAGG  1080
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Db  1021  TGGCTGTGGCCACCGAGATGGTGTTCAGGCGGGATGGTTACGGCACTGCTGCAACAGG  1080

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Db  1081  AGCTCCGGAATGAAGAGCACTGCAGTGTCTGAGCTGTCGCAGCTGTCTGGGCAAGA  1140

Qy  1141  GGCAAGTGCTGCAAGAGCACTGCGCAGCGGGGCTGCAGCCCAGGTAGCTGTGGCGCTGCAGCCCAGCT  1200
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Qy   301 CCAGCAAACTGAGGGCCTGAGCCGCTTGCTGCGCAGCACGCACGCAGAGAGGATCTGAACTCAG 360
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Db   361 GGCCCCTGAGCAAGCTGAGCTGCTGCTCGCAGCGGAACACGGCAGCAGCAGCTTCGCAAGACCTACA 420

Qy   421 GCGAGCAGTGGCAGCAGCTGCGAGCTGCGAGCAGCCCACAGCAGCAGCCCAAGCATTGAGA 480
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Qy   541 AGGAGGCCAGCAAAGACAAGACCGTGACAAGGCCAAGGACAAGTATGTGCCAGCCTGT 600
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Qy   661 ACCAGCACCACCAGCTCCTGCTCCGGCGTCTGCTGCGCGTCTGCTGGGTCACTGCGACCTGCACG 720
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Db   661 ACCAGCACCACCAGCTCCTGCTCCGGCGTCTGCTGCGCGTCTGCTGGGTCACTGCGACCTGCACG 720

Qy   721 AGGAGATGGCTTGCATCCTGAAGGAGATCTCTCAGGAATACCTGGAGAATACCTGGAGATTAGCAGCCTGG 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 AGGAGATGGCTTGCATCCTGAAGGAGATCTCTCAGGAATACCTGGAGAATACCTGGAGATTAGCAGCCTGG 780

Qy   781 TGCAGGATGAGGTGGTGGCCATTCACCGGGAGATGGCTGCAGCTGCTGCCCCATCCAGC 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   841 CTGAGCTGAGTACCAAGGCTTCCTGCGACAGTATGGGTCCGACACCTGAGCGTCCCACCCT 900
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Db   841 CTGAGCTGAGTACCAAGGCTTCCTGCGACAGTATGGGTCCGACACCTGAGCGTCCCACCCT 900

Qy   901 GTGTCACGTTCGATGAGTCACTGCTTGAGGAGGTGAACCGTCGAGCCGTCGATGACACACATGAGAC 960
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Qy   961 AGCTGAACGAGCTGACTGTGGAGAGCGTGCGAGCACACGCTGACCTCAGTGACACAGATGAGC 1020
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Db  1321 AGGGGGGAAGGACACACCCACCCGTGGAGATCTTAAGGACCACATCTCAGGAATCTTCCGCC 1380

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Db  2281 TCAGCACCATCTACCAGGAGCTGCAGAGCATCGGAAAGCGGCATCCGGTGAGGCTGGGACC 2340

Qy  2341 CCCTTCTCAAGCTGGTGGTGGCCTCCTCGACTCCTGACTCCTGCCACCAGCGGCGTCCCAGCTCA 2400
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 CCCTTCTCAAGCTGGTGGTGGCCTCCTCGACTCCTGACTCCTGCCACCAGCGGCGTCCCAGCTCA 2400

Qy  2401 TATGCTGACAGCTCTTCACAGTCTGACTCCTGACTCCTGCCACCACTGCCGGCGAGG 2460
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 TATGCTGACAGCTCTTCACAGTCTGACTCCTGACTCCTGCCACCACTGCCGGCGAGG 2460

Qy  2461 ATGCACGCGCCGTGTCCTCTCTGTCCCTGCGCTGCCAGGGCTTCCTCTTCCGGGCAGA 2520
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 ATGCACGCGCCGTGTCCTCTCTGTCCCTGCGCTGCCAGGGCTTCCTCTTCCGGGCAGA 2520

Qy  2521 AACAATAAAACCCACTTGTGCCCACTGACTGAAAAAAAAAAAAAAAAAAAAAAA 2580
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521 AACAATAAAACCCACTTGTGCCCACTGACTGAAAAAAAAAAAAAAAAAAAAAAA 2580

Qy  2581 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2640
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2640

Qy  2641 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2674
         ||||||||||||||||||||||||||||||||||
Db  2641 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2674
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RESULT 2
US-10-660-763-1

; Sequence 1, Application US/10660763
; Publication No. US20040063130A1
; GENERAL INFORMATION:
;   APPLICANT: GAN, Weiniu et al.
;   TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;   TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;   TITLE OF INVENTION: THEREOF
;   FILE REFERENCE: CL001183DIVI
;   CURRENT APPLICATION NUMBER: US/10/660,763
;   CURRENT FILING DATE: 2003-09-12
;   NUMBER OF SEQ ID NOS: 4
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 2674
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-660-763-1

Query Match   100.0%; Score 2674; DB 18; Length 2674;
Best Local Similarity   100.0%;
Matches 2674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy     1 TCCGGGGTCCGACACCGGCCTGAGTCGTCGGTCGAGCTGGCCGTGCCCGTGC 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 TCCGGGGTCCGACACCGGCCTGAGTCGTCGGTCGAGCTGGCCGTGCCCGTGC 60

Qy    61 GGAACAGCACTATGGGGCTTCCTTCTTCTGAGCTGTGAGCTGCGAGGGGTCCTGC 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GGAACAGCACTATGGGGCTTCCTTCTTCTGAGCTGTGAGCTGCGAGGGGTCCTGC 120

Qy   121 AGCAAATGCAGGAGGCCGAGCTTCGTCGTACTGGAGGGCATGAGAGAAAGTGATGGCCCAGC 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGCAAATGCAGGAGGCCGAGCTTCGTCGTACTGGAGGGCATGAGAGAAAGTGATGGCCCAGC 180

Qy   181 GGGTCAAGAGTGACAGGGAGTATGCAGGACCCTGACTGCTTCACCACAGCCTGCGAGCAGTC 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GGGTCAAGAGTGACAGGGAGTATGCAGGACCCTGACTGCTTCACCACAGCCTGCGAGCAGTC 240

Qy   241 GGGGCCAGAGCCGGCCGGCCCATCAGCCCCATCAGTCAGTCAGTCAGTCTGGGCTGAGATCA 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GGGGCCAGAGCCGGCCGGCCCATCAGCCCCATCAGTCAGTCAGTCAGTCTGGGCTGAGATCA 300
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RESULT 3
US-10-240-965-256
; Sequence 256, Application US/10240965
; Publication No. US20030165924A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: SHIFFMAN, Dov
; APPLICANT: SOMOGYI, Roland
; APPLICANT: LAWN, Richard M.
; APPLICANT: SEILHAMER, Jeffrey J.
; APPLICANT: PORTER, Gordon J.
; APPLICANT: MIKITA, Thomas
; APPLICANT: TAI, Julie
; TITLE OF INVENTION: GENES EXPRESSED IN FOAM CELL DIFFERENTIATION
; FILE REFERENCE: PA-0025 PCT
; CURRENT APPLICATION NUMBER: US/10/240,965
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: 60/195,106
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: PERL Program
; SEQ ID NO 256
; LENGTH: 2889
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US2003016592A1 997347.6
US-10-240-965-256

Query Match   87.0%; Score 2326.4; DB 16; Length 2889;
Best Local Similarity 92.3%; Pred. No. 0;
Matches 2558; Conservative 0; Mismatches 1; Indels 211; Gaps 2;

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Qy    361 GGCCCCTGAGCAAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCTTCGCAAGACCTACA 420
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db    478 GGCCCCTGAGCAAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCTTCGCAAGACCTACA 537

Qy    421 GCGAGCAGTGGCAGCAGCTGCAGCGCAGCTCCAGCAGGACCACCAAGAGCCAGACCACAC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    538 GCGAGCAGTGGCAGCAGCTGCAGCGCAGCTCCAGCAGGACCACCAAGAGCCAGACCACAC 597

Qy    481 AGTGAAGAGCCAGTACCGAGCTCTGCACGGACAGTGCCCAAGCCAAGCGCAAGTACC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    598 AGTGAAGAGCCAGTACCGAGCTCTGCACGGACAGTGCCCAAGCCAAGCGCAAGTACC 657

Qy    541 AGGAGGCCAGCAAAGACAAGGACCGGTGACAAGGCCAAGGACAAGTATGTGCGCAGCCTGT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    658 AGGAGGCCAGCAAAGACAAGGACCGGTGACAAGGCCAAGGACAAGTATGTGCGCAGCCTGT 717

Qy    601 GGAAGCTCTTGCTCCACCAACCGCTATGTGCGGGCGTGCCGGCGTCAGCTACACC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    718 GGAAGCTCTTTGCTCCACCAACCGCTATGTGCGGGCGTGCCGGCGTCAGCTACACC 777

Qy    661 ACCAGCACCACCAGCTCCTGCTCCGGCCTGCTGCGGTCACTGCAGGACCTGCACG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    778 ACCAGCACCACCAGCTCCTGCTCCGGCCTGCTGCGGTCACTGCAGGACCTGCACG 837

Qy    721 AGGAGATGGCTTGCATCCTGAAGGAGATCCTGCAGGAATACCTGAGGATTAGCAGCCTGG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    838 AGGAGATGGCTTGCATCCTGAAGGAGATCCTGCAGGAATACCTGAGGATTAGCAGCCTGG 897

Qy    781 TGCAGGATGAGGTGGTGGCCATTCACCGAGGAGATGCTGCAGCTGCCCGGCATCCAGC 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    898 TGCAGGATGAGGTGGTGGCCATTCACCGAGGAGATGCTGCAGCTGCCCGGCATCCAGC 957

Qy    841 CTGAGGCTGAGTACCAAGGCTTCCTGCGACAGTATGGTCGCACCTGAGCTCCCACCCT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    958 CTGAGGCTGAGTACCAAGGCTTCCTGCGACAGTATGGTCGCACCTGAGCTCCCACCCT 1017

Qy    901 GTGTCACGTTCGATGAGTCACTGCTTGAGGAGGGTGAACCGCTGGGAGCCTCC 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1018 GTGTCACGTTCGATGAGTCACTGCTTGAGGAGGGTGAACCGCTGGGAGCCTCC 1077

Qy    961 AGCTGAACGAAGCTGACTGGTGGCAAGAAGCTGTGCAGCACGCGTGCAGCACAGATGAGC 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1078 AGCTGAACGAAGCTGACTGGTGGCAAGAAGCTGTGCAGCACGCGTGCAGCACAGATGAGC 1137

Qy   1021 TGGCTGTGGGCCACCGAGATGTGTTCAGGCGCAGGAGATGTTACGCAGCTGCAACAGG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1138 TGGCTGTGGGCCACCGAGATGTGTTCAGGCGCAGGAGATGTTACGCAGCTGCAACAGG 1197

Qy   1081 AGCTCCGGAATGAACGAGGAGAACACCACCCCGGGAGCCGGTGCAGCTGCTCGGGCAAGA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1198 AGCTCCGGAATGAACGAGGAGAACACCACCCCGGGAGCCGGTGCAGCTGCTCGGGCAAGA 1257

Qy   1141 CGGCAACTGCTGCAAGAAGCACTGCAGGAGGGCTGCAGTGGCTGTCGCAGCAGGCCAAGC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1258 GGCAAGTGCTGCAAGAAGCACTGCAGGAGGGCTGCAGTGGCTGTCGCAGCAGGCCAAGC 1317

Qy   1201 TGGCTGTGGGCCCAGCAGGAGTTGCTCGAGACCAAGCTGAGCACCTCACGTCGTCTGGGCCCCGAGCCCC 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1318 TGGCTGTGGGCCCAGCAGGAGTTGCTCGAGACCAAGCTGAGCACCTCACGTCGTCTGGGCCCCGAGCCCC 1377

Qy   1261 CGGCTGTGCTGCTCTGCAGGATGACCGCCACTCCACGTCGTCCACGTGGGCTCCTCGGAGGAGGGCGAG 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1378 CGGCTGTGCTGCTCTGCAGGATGACCGCCACTCCACGTCGTCCACGTGGGCTCCTCGGAGGAGGGCGAG 1437

Qy   1321 AGGGGGGAAGGAACACCCACCACCCGGAGATCCTTAAGAGCCACATCTCAGGAATCTTCGCC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1438 AGGGGGGAAGGAACACCCACCACCCGGAGATCCTTAAGAGCCACATCTCAGGAATCTTCGCC 1497

Qy   1381 CCAAGTTCTCG------------------------------------- 1391
          ||||||||||||
Db   1498 CCAAGTTCTCGCCTCCGCTCCCCACCCGCTGCAGTCATTCCGGAGGTGCGAGAAGCCCCTGCATG 1557

Qy   1392 ------------------------------------------------- 1391
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Db   1558 AGCAGCTGTGTGTACCACGGGGCCCATCCCGAGGGCAGAGAGGCGCAGAGGTGCTGCTGAGCTGCTGGTGCACT 1617
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1391 ------------------------------------------------- 1391

Db   1618 CTGGGGACTTCCTCGGTGCGGGAGGAGAGCCAGGGCAAGCAGCAGGGAGTACGTGCTGTCGGTGCTGTGT 1677
          |||||||||||||||||||||||||||||||||||||||||||
Qy   1392 ------------------------AACCTGTACCGACTGGAAG 1410

Db   1678 GGGATGGTCTGCCCCGGCACTTCATCATCCAGTCCTTGGATAACCTGTACCGACTGGAAG 1737
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Qy   1411 GGGAAGGCTTTCCTAGCATTCCTTTGCTCATCGAGTTCATCGAGCACTGAGCACCACCAGCCCC 1470
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1738 GGGAAGGCTTTCCTAGCATTCCTTTGCTCATCGAGTTCATCGAGCACTGAGCACCACCAGCAGCCCC 1797

Qy   1471 TCACCAAGAGAGTGGTGTTGTTGTCCTGCACAGGGCTGTGCCCAAGGACAAGTGGGTGCTGA 1530
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1798 TCACCAAGAGAGTGGTGTTGTTGTCCTGCACAGGGCTGTGCCCCAAGGACAAGTGGGTGCTGA 1857

Qy   1531 ACCATGAGGAGACCTGGTTGTTGGGGTGAGCAGATTGGACGGGGGGAACTTTGGGAAGTGTTCA 1590
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1858 ACCATGAGGAGACCTGGTTGTTGGGGTGAGCAGATTGGACGGGGGAACTTTGGGAAGTGTTCA 1917

Qy   1591 GCGGACGCCTGCGAGCCGACAACACCCTGGTGCGGGTGAAGTCTTGTGAGAGACGCGTCC 1650
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1918 GCGGACGCCTGCGAGCCGACAACACCCTGGTGCGGGTGAAGTCTTGTGAGAGACGCGTCC 1977

Qy   1651 CACCTGACCTCAAGGCCAAGTTCTACAGAGAAGCGAGGATCTGAAGCAGTACAGCACCACC 1710
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1978 CACCTGACCTCAAGGCCAAGTTCTACAGAGAAGCGAGGATCTGAAGCAGTACAGCACCACC 2037

Qy   1711 CCAACATCGTGCGTCTCATTGGTGTCGTCACCGAGAAGCAGCCATCGTACATCGTCATGG 1770
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2038 CCAACATCGTGCGTCTCATTGGTGTCGTCACCGAGAAGCAGCCCATCGTACATCGTCATGG 2097

Qy   1771 AGCTTGTGCAGGGGGGCGACTTCCTGACCTTCCTCCCGCACGGAGGGGGCCCGGAGGGGG 1830
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2098 AGCTTGTGCAGGGGGGCGACTTCCTGACCTTCCTCCCGCACGGAGGGGGCCCGGAGGGGG 2157

Qy   1831 TGAAGACTCTGCTGCAGATGGTGGGGGATCAGCTGCTGGGATGGAGTGAGACTTGGAGAGCA 1890
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2158 TGAAGACTCTGCTGCAGATGGTGGGGGATGGCAGTGCAGCTGCTGGGATGGAGTGAGACTTGGAGAGCA 2217

Qy   1891 AGTGCTGCATCCACCGGACCTGGCTGCCTGCGTGCTGTGACAACTGCCTGGTGCACAGAATGTCC 1950
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2218 AGTGCTGCATCCACCGGACCTGGCTGCCTGCGTGCTGTGACAACTGCCTGGTGCACAGAATGTCC 2277

Qy   1951 TGAAGATCAGTGACTTTGGGATGTCCCGGAGAGAGAGCCGATGGGGTCTATGCAGCCTCAG 2010
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2278 TGAAGATCAGTGACTTTGGGATGTCCCGGAGAGAGAGCCGATGGGGTCTATGCAGCCTCAG 2337

Qy   2011 GGGGCCTCAGACAAGTCCCGTGAGTGGACCGACCTGAGCGCCCTGAACTACGGACCGCT 2070
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2338 GGGGCCTCAGACAAGTCCCGTGAGTGGACCGACCTGAGCGCCCTGAACTACGGACCGCT 2397

Qy   2071 ACTCCTCCGGAAAGCGACGACTTGTGCTCTTGCTCTCTGGGGAGACCTTCAGCCTGG 2130
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2398 ACTCCTCCGGAAAGCGACGACTTGTGCTCTTGCTCTCTGGGGAGACCTTCAGCCTGG 2457

Qy   2131 GGGGCCTCCCCTATCCCAACGTGAATCAGACACGCAGGAGGCGGAG 2190
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2458 GGGGCCTCCCCTATCCCAACGTGAATCAGACACGCAGGAGGCGGAG 2517

Qy   2191 GCCGTCTGCCCTGCCCTGCGGGAGCTGTGTCATGGAGCTTCAGCCTCATGGAGAAGGCGCT 2250
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2518 GCCGTCTGCCCTGCCCTGCGGGAGCTGTGTCATGGAGCTTCAGCCTCATGGAGAAGGCGCT 2577

Qy   2251 GGGCCTATGAGCCTGGGCAGCGGCCCAGCTTCAGCAGGGCCACCATCTACCAGGAGCTGCAGAGCA 2310
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2578 GGGCCTATGAGCCTGGGCAGCGGCCCAGCTTCAGCACCATCTACCAGGAGCTGCAGAGCA 2637

Qy   2311 TCCGAAAGCCGGCATCGGTGAGGCTGGGACCCCCTTCAAGCTGCTGGCCTCTGCAGGCC 2370
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US-10-660-763-3
; Sequence 3, Application US/10660763
; Publication No. US20040063130A1
; GENERAL INFORMATION:
;   APPLICANT: GAN, Weiniu et al.
;   TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;   TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;   TITLE OF INVENTION:  THEREOF
;   FILE REFERENCE: CL001183DIVII
;   CURRENT APPLICATION NUMBER: US/10/660,763
;   CURRENT FILING DATE: 2003-09-12
;   NUMBER OF SEQ ID NOS: 4
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 15297
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-660-763-3

  Query Match             13.6%;  Score 362.4; DB 18;  Length 15297;
  Best Local Similarity   99.7%;  Pred. No. 1.3e-46;
  Matches   363;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2187 GGGGGCCGTCTGCCCTGCCCAGAGCTGTGTCCTGATGCCGTGTTCAGGCTCATGGAGCAG 2246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12938 GGGGGCCGTCTGCCCTGCCCAGAGCTGTGTCCTGATGCCGTGTTCAGGCTCATGGAGCAG 12997

Qy       2247 TGCTGGGCCTATGAGCCGGCAGCGGCCCAGCTTCAGCACCATCTACCAGGAGCTGCAG 2306
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12998 TGCTGGGCCTATGAGCCGGCAGCGGCCCAGCTTCAGCACCATCTACCAGGAGCTGCAG 13057

Qy       2307 AGCATCCGAAAGCCGGCATCCGTGAGGCTGGGACCCCCTTCAAGCTGGTGGCCTCTGCA 2366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      13058 AGCATCCGAAAGCCGGCATCCGTGAGGCTGGGACCCCCTTCAAGCTGGTGGCCTCTGCA 13117

Qy       2367 GGCCTAGGTGCAGCTCCTCAGCGGCTCCAGCTCCTCAGCGGCTCTGACAGTCTTCACAGTCCTG 2426
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      13118 GGCCTAGGTGCAGCTCCTCAGCGGCTCCAGCTCCTCAGCGGCTCTGACAGTCTTCACAGTCCTG 13177

Qy       2427 GACTCCTGCCACCAGCATCCACACTGCCGCAGGATGCAGCGCCGTGTCCTCTCTGTGTC 2486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      13178 GACTCCTGCCACCAGCATCCACACTGCCGCAGGATGCAGCGCCGTGTCCTCTCTGTGTC 13237

Qy       2487 CCTGCTTGCTGCCCAGGGCTTCCTCTTCCGGGGCAGAAACAATAAAACCACTTGTGCCCACTG 2546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      13238 CCTGCTTGCTGCCCAGGGCTTCCTCTTCCGGGGCAGAAACAATAAAACCACTTGTGCCCACTG 13297

Qy       2547 AAAA 2550
              ||||
Db      13298 AACA 13301


RESULT 6
US-10-887-553A-240
; Sequence 240, Application US/10887553A
; Publication No. US20050008436A1
; GENERAL INFORMATION:
;   APPLICANT: Garza, Dan
;   APPLICANT: Li, Hao
;   TITLE OF INVENTION: Method to treat conditions associated
;   TITLE OF INVENTION:  with insulin signalling dysregulation
;   FILE REFERENCE: 4-33262
;   CURRENT APPLICATION NUMBER: US/10/887,553A
;   CURRENT FILING DATE: 2004-07-08
;   PRIOR APPLICATION NUMBER: 60/485,883
;   PRIOR FILING DATE: 2003-08-07
;   NUMBER OF SEQ ID NOS: 1208
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 240
;   LENGTH: 2950
;   TYPE: DNA
;   ORGANISM: human
US-10-887-553A-240
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Db       2638 TCCGAAAGCCGGCATCGGTGAGGCTGGGACCCCCTTCTCAAGCTGGTGGCCTCTGCAGGCC 2697

Qy       2371 TAGGTGCAGCTCCTCAGCGGCTCCAGCTCGATATGCTGACAGCTCTTCACAGTCCTGGACT 2430
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2698 TAGGTGCAGCTCCTCAGCGGCTCCAGCTCGATATGCTGACAGCTCTTCACAGTCCTGGACT 2757

Qy       2431 CCTGCCACCAGCATCCACACTGCCGCGGCAGATGCAGCGCGCCGTGTCCTCTGTGTCCCTG 2490
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2758 CCTGCCACCAGCATCCACACTGCCGCGGCAGATGCAGCGCGCCGTGTCCTCTGTGTCCCTG 2817

Qy       2491 CTGCTGCCAGGGGCTTCCTCTTCCGGGCAGAAACAATAAAACCACTTGTGCCCACTGAAAA 2550
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2818 CTGCTGCCAGGGGCTTCCTCTTCCGGGCAGAAACAATAAAACCACTTGTGCCCACTGAAAA 2877

Qy       2551 AAAAAAAAAA 2560
              ||||||||||
Db       2878 AAAAAAAAAA 2887


RESULT 4
US-10-003-295-3
; Sequence 3, Application US/10003295
; Publication No. US2002016B741A1
; GENERAL INFORMATION:
;   APPLICANT: GAN, Weiniu et al.
;   TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;   TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;   TITLE OF INVENTION:  THEREOF
;   FILE REFERENCE: CL001183DIV
;   CURRENT APPLICATION NUMBER: US/10/003,295
;   CURRENT FILING DATE: 2001-12-06
;   NUMBER OF SEQ ID NOS: 4
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 15297
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-003-295-3

  Query Match             13.6%;  Score 362.4; DB 13;  Length 15297;
  Best Local Similarity   99.7%;  Pred. No. 1.3e-46;
  Matches   363;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    0;

Qy       2187 GGGGGCCGTCTGCCCTGCCCAGAGCTGTGTCCTGATGCCGTGTTCAGGCTCATGGAGCAG 2246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12938 GGGGGCCGTCTGCCCTGCCCAGAGCTGTGTCCTGATGCCGTGTTCAGGCTCATGGAGCAG 12997

Qy       2247 TGCTGGGCCTATGAGCCGGCAGCGGCCCAGCTTCAGCACCATCTACCAGGAGCTGCAG 2306
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12998 TGCTGGGCCTATGAGCCGGCAGCGGCCCAGCTTCAGCACCATCTACCAGGAGCTGCAG 13057

Qy       2307 AGCATCCGAAAGCCGGCATCGGTGAGGCTGGGACCCCCTTCTCAAGCTGGTGGCCTCTGCA 2366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      13058 AGCATCCGAAAGCCGGCATCGGTGAGGCTGGGACCCCCTTCTCAAGCTGGTGGCCTCTGCA 13117

Qy       2367 GGCCTAGGTGCAGCTCCTCAGCGGCTCATATGCTGACAGTCTTCACAGTCCTG 2426
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      13118 GGCCTAGGTGCAGCTCCTCAGCGGCTCATATGCTGACAGTCTTCACAGTCCTG 13177

Qy       2427 GACTCCTGCCACCAGCATCCACACTGCCGGCAGGGGCTTCCTCTTCCTCTGTGTCCTGTGTC 2486
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      13178 GACTCCTGCCACCAGCATCCACACTGCCGGCAGGGGCTTCCTCTTCCTCTGTGTCCTGTGTC 13237

Qy       2487 CCTGCTGCTGCCAGGGGCTTCCTCTTCCGGGGCAGAAACAATAAAACCACTTGTGCCCACTG 2546
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      13238 CCTGCTGCTGCCAGGGGCTTCCTCTTCCGGGGCAGAAACAATAAAACCACTTGTGCCCACTG 13297

Qy       2547 AAAA 2550
              ||||
Db      13298 AACA 13301


RESULT 5
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Query Match　　　　12.3%;　　Score 328.8;　DB 21;　Length 2950;
Best Local Similarity　62.0%;　Pred. No. 1.5e-41;
Matches　573;　Conservative　0;　Mismatches 342;　Indels　9;　Gaps　3;

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Qy  1392 AACCTGTACCGACTGGAAGGGAAGGCTTTCCTAGCATTCCTTGCTCATCGACCACCTA 1451
              ||| | ||| |||||| |||||||| | |||| | |||||| | | | |||||
Db  1918 AACATGTATCGATTCGAGGGCACTGGGTTTCAAACATTCCTCAACTTATAGATCATCAC 1977

Qy  1452 CTGAGACACCCAGCAGCCCCTCACCCAAGAAGAGTGGTGTTGTCCTGCACAGGGCTGTGCCC 1511
              |||||                                              ||||
Db  1978 TATACAACAAAACAGGTCATCACTAAGAAATCAGGTTCGCTGAATCCTATTCCT 2037

Qy  1512 AAGGACAAG---TGGGTGCTGAACACCTGGTGTTGGGTGGCAGATTGGACGG 1568
              ||||||||      |||| | || | |||| ||| | | ||| ||||
Db  2038 AAGGACAAGAAATGGATTCTCAGTCATGAAGATGTCATATTGGGAGAATTACTGGGCAAG 2097

Qy  1569 GGGAACTTTGGCGAAGTTGTTCAGCGGACGCCTGCGAGCCGACAACACCCTGTGTGGCGGTG 1628
              |  |||| || ||||||   ||||  | |||| |
Db  2098 GGAAATTTTGGTGAAGTATATAAGG---GCACATTAAAGGATAAAACTTCTGTTGCTGTT 2154

Qy  1629 AAGTCTTGTCTGGAGAGACGCTCCCACCTGACCTCAAGGCCAAGTTTCTACAGGAAGGCGAGG 1688
              || || | | ||||||| | |     ||||  |||||  || |||| |||||| |||
Db  2155 AAAACATGTAAAAGAAGATCTTCCTCAGGAATTGAAAAATAAAATTTTTACAGAAGGCCAAA 2214

Qy  1689 ATCCTGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCCAGAAG 1748
              ||||||| |||||| | ||| || ||||||| | |  | ||  || |||||  ||||||
Db  2215 ATTCTCAAGCAATATGATCATCCCAATATTGTCAAACTTATAGGAGTTTGCACACAAAGA 2274

Qy  1749 CAGCCCATCTACACATCGTCATGAGCCGACTTCGTGTGCGAGGGTGACCTTCCTCCGC 1808
              ||| |||  | | || | | ||||| |||| || |||||||  | |  | |||| |
Db  2275 CAGCCCTGTCTACATGATGGTTTCAGGAGGTGATTCCTCACCTTTCTGAGA 2334

Qy  1809 ACGGAGGGGCCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGATGCAGCTGCT 1868
              | |  ||| | ||   | | ||  | | || | |||   |  |   || | | || || |
Db  2335 AGGAAGAGGATGAACTAAAACTCAAACAGTTAGTGAAAACTCAAACAGTTAGACGCTGCTGCT 2394

Qy  1869 GGCATGGAGTACCTGGAGAGCAAGTGCTCGATCATCCACCGGAACCTGCTCGGAACTGC 1928
              |||||||||| ||||||||| |||| |  | ||| |   |  |  |||| | ||| ||
Db  2395 GGTATGTTGTATCTCGAGAGTAAAAACTGTATACACAGGAACCTTGCTCAAGAAAACTGC 2454

Qy  1929 CTGGTGACAGAGAAGAATGTCTGAAGATCAGTAGCTTTGGATGTGTCCCGAGAGGAAGCC 1988
              ||| |   |  ||| ||| | |||  | || |  ||| ||| |||  | |||| | ||
Db  2455 CTGGTAGGTGAAAATAATGTTCTGAAAATCAGTGACTTTGGAATGTCTCGTCGTCAAGAGGAT 2514

Qy  1989 GATGGGGGTCTATGCAGCCTCAGACAAGTCCCCGTGAAGTGGACCGCCACCT 2048
              ||| ||||| || | ||||| | | ||||| || | || ||||| |||||||
Db  2515 GGTGGAGTGTATTCATCTTC---TGGCTTAAAGCAGATTCCCATTAAATGGACAGCACCG 2571

Qy  2049 GAGGCCCTTAACTACACGGCCGCTACTCCTCCGAAAGCGACGTGTGGACGTTTGGCATCTTG 2108
              ||| ||||| ||| | |||| || |||| ||||||||| || || ||| | |||||||||
Db  2572 GAAGCTCTTAATTATGGGAGTACAGTTCAGAGAGTGACGTGTGGAGCTTTGGCATCTT 2631

Qy  2109 CTCTGGGAGACCTTCAGCCTGGGCCTCCCCCATCCCAACCTCAGCAATCAGCAGACA 2168
              |||||||| | |||| ||||||| || ||   |||  ||| |  ||||||| || ||
Db  2632 CTCTGGGAGACCTTCAGCTTCAGGGTTTTGTCTCGTACCCTGGAATGCAAATCAGCAAGCA 2691

Qy  2169 CGGGAGTTTGTGGGAGAAGGGGGCCGTGCTCCGCCCAGAGCTGTGTCCTGATGCCGTG 2228
              | ||||||| | |  ||| | || |  | | | |    ||||| || || | | |||||
Db  2692 AGAGACAAGTAGAAAGAGGATACCGGATGTCAGCTCCCAGCACTGTCCAGCAGGATATT 2751

Qy  2229 TTCAGGCTCATGGAGCAGTGCTGGGCCTATGAGCCTGGCAGCGGCCCAGCTTCAGCACC 2288
              ||||||| | ||| |||| ||| |||||| ||||| |||| | || || |||  || |||
Db  2752 TCCAAAATCATGATGAAGTGTTGGATTAAAAACCTGAAAAATCGCCCTAAGTTCAGTGAA 2811

Qy  2289 ATCTACCAGGAGCTGCGAGCATC 2312
              |||||||  | |  | | ||||||
Db  2812 CTTCAGAAAGAGCTCACTATCATC 2835
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; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1503
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(449)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-1503

Query Match　　　　12.2%;　　Score 326.8;　DB 10;　Length 449;
Best Local Similarity　99.4%;　Pred. No. 2.4e-41;
Matches　328;　Conservative　0;　Mismatches　2;　Indels　0;　Gaps　0;

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Qy  1778 GCAGGGGGGGGACTTCCTGACCTTCCTCCGCACGGAGGGGCCCGCTGCGGGTGAAGAC 1837
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   120 GGGAGGGGGGCGACTTCCTGACCTTCCTCCGCACGGAGGGGCCCGCTGCGGGTGAAGAC 179

Qy  1838 TCTGCTGCAGATGGTGGGGGATGCAGCTGCTGGCATGGAGTACCTGGAGAGCAAGTGCTG 1897
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   180 TCTGCTGCAGATGGTGGGGGATGCAGCTGCTGGCATGGAGTACCTGGAGAGCAAGTGCTG 239

Qy  1898 CATCCACCGGAACCTGCTCGGAACTGCCTCGGTGACAGAGAAGAATGTCCTGAAGAT 1957
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   240 CATCCACCGGAACCTGCTCGGAACTGCCTCGGTGACAGAGAAGAATGTCCTGAAGAT 299

Qy  1958 CAGTGACTTTGGGATGTCCCGAGAGGAAGCCGATGGGGTCTATGCAGCCTCAGGGGCCT 2017
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   300 CAGTGACTTTGGGATGTCCCGAGAGGAAGCCGATGGGGTCTATGCAGCCTCAGGGGCCT 359

Qy  2018 CAGACAAGTCCCCGTGAAGTGGACCGCCACCTGAGGCCCTTAACTACACGGCCGCTACTCCTC 2077
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   360 CAGACAAGTCCCCGTGAAGTGGACCGCCACCTGAGGCCCTTAACTACACGGCCGCTACTCCTC 419

Qy  2078 CGAAAGCGACGTGTGGAGCTTTGGCATCTT 2107
              ||||||||||||||||||||||||||||||
Db   420 CGAAAGCGACGTGTGGAGCTTTGGCATCTT 449
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Qy   200  CTGCTGGCATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACCTGGCTGCTCGGA  259
Db

Qy  1924  ACTGCCTGGTGACAGAGAAGAATGTCCTGAAG-ATCAGTGACTTT-GGGATGTCCCGAGA  1981
          ||||||| ||||||||| ||||||||||||||  ||||||||||   ||||||||||||||
Db   260  ACTGCCTGGTGACAGAGAAGAATGTCCTGAAGAATCAGTCAGTGACTTTGGGGATGTCCCGAGA  319

Qy  1982  GGAAGCC---GATGGGGTCATGCAGCCTCAGGGGGCCTCAG  2020
          ||||||    ||||||
Db   320  GGAAGCCCGATTGGGGTCTATGCAGCCTCAGCGGGGCCTCAG  361
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RESULT 10

US-10-280-576-19
; Sequence 19, Application US/10280576
; Publication No. US20040044405A1
; GENERAL INFORMATION:
;   APPLICANT: Wolff, Matthew R.
;   TITLE OF INVENTION: VASCULAR STENT OR GRAFT COATED OR IMPREGNATED WITH PROTEIN
;   FILE REFERENCE: 09820.189
;   CURRENT APPLICATION NUMBER: US/10/280,576
;   CURRENT FILING DATE: 2002-10-22
;   PRIOR APPLICATION NUMBER: 60/343,732
;   PRIOR FILING DATE: 2001-10-25
;   NUMBER OF SEQ ID NOS: 25
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 1779
;   TYPE: DNA
;   ORGANISM: Drosophila melanogaster
US-10-280-576-19

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Query Match             10.2%;  Score 271.6; DB 18;  Length 1779;
Best Local Similarity   57.0%;  Pred. No. 9.3e-33;
Matches  518;  Conservative   0;  Mismatches  384;  Indels   6;  Gaps   1;

Qy  1398  TACCGACTGGAAGGGGAAGGCTTCTCATCGACCACTACTGAGC  1457
          |||||  |||| |||  |||  |||| |||||  ||||||||||
Db   844  TTCCGGTTCGAGGGACCACCATTTGCAGCATCCAGGAGCTGATCAGTCAGTATCAC  903

Qy  1458  ACCCAGCAGCCCCTCACCCAAGAAGAGTGGTGTTGTTCCTGCACAGGGAC  1517
          |||||||||||  |||  |||||||  |||| |||  |||||||||||||
Db   904  TCGGAATTGCCAGTGACCGTGAAATCGGAGACCATACTCCGACGACACCCGTTGCCGGGGAG  963

Qy  1518  AAGTGGTGCTGAAACCATGACGACCTGGTGTGTTGGGTGAGCGATTGGACGGGGGAACTTT  1577
          ||||| |||| | |||||||| |||  || ||  |||  |||||||  ||||||||||
Db   964  CGCTGGGAGCTGAGCAACGATGATGTGTACTTCTGGAGACGATTGGTCGGGGAAACTTT  1023

Qy  1578  GGCGAAGTGTTCAGCGACGCCTGCGAGCCGACGCCGCCACACACCCGGTGCGGCGGTGAAGTCTTGT  1637
          |||||| ||| ||| ||  |||  |||||||||||  |||
Db  1024  GGGGATGTCTACAAGGCCAAACTGACCTCAAGGTTCTACAGGAAGCGGAGGATCCTGAAG  1083

Qy  1638  CGAGACGCGTCCACCTGACCTCAAGGCGAACAGAAGCGTAAATTCCTACAGGAAGAGGCGCATCCTCAAG  1697
          ||| ||  ||| |||  || |||||| ||||| ||  |||| |  |||||| |||||
Db  1084  CGAATGACCCTGCCCGACGAACAGAAGCGTAAATTCCTACAGGAAGAGGCGCATCCTCAAG  1143

Qy  1698  CAGTACAGCCACCCCAACATCGTCGCTCTCATTGGTGTCTCGCACCCAGAAGCAGCCCATC  1757
          ||  ||||||| |||  ||||| |||  |||  ||| ||  ||||  |||||||||||||||
Db  1144  CAATACCGATCATCCAAATATCGTAAAATTGATTGGCATTTGTGTGCAGAAGCAGCCCATC  1203

Qy  1758  TACATCGTCATGGAGCTTGTGCAGGGGGCGACTTCCTGACCTTCCTCCCGACGCACGAGGGGG  1817
          ||||| |||| ||||| |||  |||||| ||| ||   ||  ||  ||| ||||| |||
Db  1204  ATGATTGTCATGGAATTGGTCGGTGGTTGCCTTTTAACTTATTTACGCAAGAACTCC  1263

Qy  1818  GCCCGCCTTGCGGGTGAAGACTCGTCCAGGGGGGATGGTGCAGCTGCAGCTGGCCATGGAG  1877
          |||  ||| | ||||| |||||  || |||||||  || ||||| | | | |  ||||
Db  1264  AATGGCCTCACCACTCGCCACACTGGCATGGCATGTGCGGCGGCATGCGGACTCCGA  1323

Qy  1878  TACCTGGAGACAAGTGCTGCATCCACCGGGGATGCAG  1937
          |||  ||||| |||  | |||||  ||||  || ||||
Db  1324  TATCTGCAGTCCAAAAACTGCATTCATCGCATGGCCGCGCCTAATTGTCTCGTTGAC  1383

Qy  1938  GAGAGAATGTCCTGAAGATCAGTGACTTTGGGGATGGGGTC  1997
          |||||||  || ||| || ||||||  ||  ||||
Db
```

Db 1384 TTGGAGCACAGTGTGAAGATCTCCGATTTCGGAATGTCTCGCGAGAA------GAGGAA 1437
         ||| || |||| ||| ||||| || ||| || ||||| ||||||| ||||||
Qy 1998 TATGCAGCCTCAGGGGGCCTCAGACAAGTCCCGTGAAGTGGACCGCACCTGAGGCCCTT 2057
         || || |||| ||| ||| ||| || ||||| ||| |||| |||| |||||| |||| |
Db 1438 TATATAGTTTCCGATGGCATGAGAAACAAATACCTGTGAAGTGGACAGCTCCCGAGGCCTTG 1497

Qy 2058 AACTACCGGCCGTACTCCTCCGAAAGGCACGTGTGAGCTTGGCATCTTGCTCTGGGAG 2117
         ||| ||| || ||| ||| |||| |||| | ||||| ||||| || || || |||||
Db 1498 AATTTCCGGCAAGTACACTTCGTTGTGCGATGTGTCCTATGCATACTGATGTGGGAG 1557

Qy 2118 ACCTTTCAGCCTGGGGGCCTCCCCTATCCAACTCAGCAATCAGCACGCACACGGAGTTT 2177
         |||||||| || |||||| || || |||||| || || |||| || ||||| ||| |
Db 1558 ATCTTTCTCCAAGGGCGACACACCCTACTCCGGCATGACCAACTCCAGACCAGAGAGCGC 1617

Qy 2178 GTGGAGAAGGGGGGCCCGTCTGCCCTGCGTGTGCCGTGTTCAGGCTC 2237
         ||| ||| ||| ||||| || |||| ||| |||| ||| |||||| |
Db 1618 ATCGATACGGGATATCGTATGCCGCAACGCCGAGAGCACGCCCGAGGATGTACCGACTG 1677

Qy 2238 ATGGAGCAGTGCTGGGGCCTATGAGCCTCAGCAGCTTCAGCACCATCTACCAG 2297
         |||| || ||||| ||||| ||| || || || ||| || || || || ||||
Db 1678 ATGCTCCAGTGCTGGGCAGCCGACGCGCCGAATCCCGACCGCATTTCGATGAGATCTACAAT 1737

Qy 2298 GAGCTGCA 2305
         | ||| ||
Db 1738 GTGGTGGA 1745

RESULT 11
US-10-101-510-525
; Sequence 525, Application US/10101510
; Publication No. US2003014B295A1
; GENERAL INFORMATION:
; — APPLICANT: WAN, JACKSON
; — APPLICANT: WANG, YIXIN
; — TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; — FILE REFERENCE: 15117.0012
; — CURRENT APPLICATION NUMBER: US/10/101,510
; — CURRENT FILING DATE: 2002-03-20
; — PRIOR APPLICATION NUMBER: 60/276,947
; — PRIOR FILING DATE: 2001-03-20
; — NUMBER OF SEQ ID NOS: 805
; — SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 525
; LENGTH: 3875
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-525

Query Match   7.5%;   Score 201.2; DB 15;   Length 3875;
Best Local Similarity 54.9%;   Pred. No. 7.2e-22;
Matches   423;   Conservative   0; Mismatches 338;   Indels   9;   Gaps   1;

Qy 1522 GGGTGCTGAACCATGAGGACTTGGTGTTGGGTGAGCAGATTGGACGGGGGAACTTTGGCG 1581
         |||||| |||||| ||||| ||||||||||||||| ||||| || ||||| |||||||||
Db 1969 GGGAGCTTGATCCAGCGTGGCTGGGATGGTGCACTGTCATAGGAGAAGGAGAGTTTGGGG 2028

Qy 1582 AAGTGTTCAGCGACGCGCTGCGAGCC-------GACAACACCCTGGTGCGGGTGAAGT 1632
         ||||| ||| ||| ||||| || | |||
Db 2029 AAGTGTATCGAGGGACCCTGGCTCCCAGCCAGGACTGTGCGCCATTAAGA 2088

Qy 1633 CTTGCTGCGAGAGACGCTCCACCTGACCTCAAGGCCAGTGTTCTACAGGAAGCGAGGATCC 1692
         |||| || || || |||||| || ||| || |||| ||| || |||||| ||||||
Db 2089 CCTTAAAGACACACATCCCCAGGTGGCCAGTGGCAGTCTTCCTTCGAGAGGCAACTATCA 2148

Qy 1693 TGAAGCAGTACAGCACCCACCCAACATCGTGCGTCTCATTGGTGTCTGCACCCAGAAGCAGC 1752
         || |||| || | ||| | | || || |||||| || |||| |||||| |||||||
Db 2149 TGGGCCAGTTTAGCCACCAGGTGGCATATTCTGCATCTGGAAGCGGTCGTCACAAAGCGAAAGC 2208

Qy 1753 CCATCTACATCGTCATGGAGCTTGTGCAGGGGGCGACTTCCTCCCGCACGG 1812
         ||||| | ||| || ||||| || || || ||||| |||| |||||||
Db 2209 CGATCATGATCATCACAGAATTTATGGAGAATGGAGCCTTCCTGAGGGAGC 2268

Qy 1813 AGGGGCCCGCCCGGGGTGAAGACTCTGCTCGCGAATGGTGGGGATGGGGAGTTGGGGA 1872

RESULT 12
US-10-384-339C-1
; Sequence 1, Application US/10384339C
; Publication No. US2004017570JA1
; GENERAL INFORMATION:
; — APPLICANT: Kreutzer, Roland
; — TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF A TARGET GE:
; — FILE REFERENCE: 20200/2002
; — CURRENT APPLICATION NUMBER: US/10/384,339C
; — CURRENT FILING DATE: 2003-03-07
; — PRIOR APPLICATION NUMBER: PCT/EP02/00152
; — PRIOR FILING DATE: 2002-01-09
; — PRIOR APPLICATION NUMBER: DE 10100586.5
; — PRIOR FILING DATE: 2001-01-09
; — PRIOR APPLICATION NUMBER: DE 10155280.7
; — PRIOR FILING DATE: 2001-10-26
; — PRIOR APPLICATION NUMBER: DE 10158411.3
; — PRIOR FILING DATE: 2001-11-29
; — PRIOR APPLICATION NUMBER: DE 10160151.4
; — PRIOR FILING DATE: 2001-12-07
; — NUMBER OF SEQ ID NOS: 173
; — SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2955
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; — TITLE: Eph A1
; — PATENT DOCUMENT NUMBER: NM00532
US-10-384-339C-1

Query Match   7.4%;   Score 198; DB 19;   Length 2955;
Best Local Similarity 54.7%;   Pred. No. 2.2e-21;
Matches   421;   Conservative   0; Mismatches 340;   Indels   9;   Gaps   1;

Qy 1522 GGGTGCTGAACCATGAGGACTTGGTGTTGGGTGAGCAGATTGGACGGGGGAACTTTGGCG 1581
         |||||| |||||| ||||| ||||||||||||||| ||||| || ||||| |||||||||
Db 1874 GGGAGCTTGATCCAGCGTGGCTGGGATGGTGCACTGTCATAGGAGAAGGAGAGTTTGGGG 1933

Qy 1582 AAGTGTTCAGCGACGCGCTGCGAGCC-------GACAACACCCTGGTGCGGGTGAAGT 1632
         ||||| ||| ||| ||||| || | |||

Db 2269 GGGAGGACCAGCTGGTCCCTGGGCATGCTCCATGGCCATGGGTCGTGCAGGGCATAGCATCTGCA 2328
         ||| || |||||| | || |||| || || |||| ||||| || || ||||| ||| |||||
Qy 1873 TGGAGTACCTGGAGAGACAAGTGCTGATCCACCGGACGGGGAACCTGCTGCCGGACACTGCCTGG 1932

Db 2329 TGAACTACCTCAGTAATCACAATTATGTCCACCGGACGGGGAACCTGGCGCCAGAAACATCTTGG 2388
         |||| |||| || ||| ||| || |||| || ||||| ||||||| | ||||||| || ||||
Qy 1933 TGACAGAGAAGAATGTCCTGAAGATCAGTCAGTGAGGTGTCTGCAAGGTGTCGACTTTCTGGGAG 1992

Db 2389 TGAATCAAAACCTGTCGTCAAGGTGTCTGACTTTGGCCTGACTCGCTCCTCCTGGATGACT 2448
         |||| || |||| || || ||||||||| || |||||| ||| || || | |||||| ||
Qy 1993 GGTCTATGCAGCCTCAGGGGGCCTCAGACAAGTCCCGTGAAGTGGACCGCACCTGAGG 2052

Db 2449 TTGATGGCACATACGAAACCAAGGGACGGAGAAAGATCCCTATCCTGGACAGCCCTGAAG 2508
         || ||||| || |||| |||||| | ||||||| ||| ||||| ||||||||||
Qy 2053 CCCTTAACTACGGCCGCTACTCCTCCGAAAGGCACGTGTGAGCTTTGGCATCTTGCTCT 2112

Db 2509 CCATTGCCCATCGGGATCTTCACCACAGCCGATGTGTGGGCTTTGGGATTGTGATGT 2568
         || || || |||||||| |||| | |||| |||| |||| |||||||| || |||
Qy 2113 GGGAGACCTTCAGCCTGGGGGCCTCCCCTATCCAACTCAGCAATCAGCACACGGG 2172

Db 2569 GGGAGGTGCTGAGCTTTGGGGACAAGCCTTATGGGAGATGAGCAATCAGGAGGTTATGA 2628
         ||||| | ||| || |||| || ||||| |||| |||||| ||| ||| | ||||
Qy 2173 AGTTTGTGGAGAAGGGGGGCCCGTCTGCCCTGCGTGTGCCGTGTTCA 2232

Db 2629 AGAGCATTGAGGATGGGTACCGGTTGCCCGTTGGGCATATGACCGTGCCCGGCCCACACTTC 2688
         ||||| |||| || |||| ||| || || |||| || | |||| | |||||| ||| ||
Qy 2233 GGCTCATGGAGCAGTGCTGGGCCGATGCTGGCCTATGAGCCTGGGCAGGCCCCAGCTTC 2282

Db 2689 AGCTCATGAAGAACTGCTGGGCCATATGACCGTGCCCGGCCCACACTTC 2738

Best Local Similarity 54.7%;   Pred. No. 2.2e-21;
Matches 421;   Conservative   0;   Mismatches 340;   Indels   9;   Gaps   1;

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Qy  1522 GGGTGCTGAACCATGAGGACCTGGTGTTGGTGGTGAGCAGATTGGACGGGGAACTTGGCG 1581
              |||| |||| |     |||  ||    ||     | |||       || ||||||
Db  1967 GGGGAGCTTGATCCAGCGTGGCTGGCTGATGGTGGACACTGTCATAGGAGAAGGAGAGTTGGGG 2026

Qy  1582 AAGTGTTCAGCGGACGCGCTGCGAGCC--------GACAACACCCTGGTGCGGTGAAGT 1632
              |||||| |    || ||  |  |        | |   |   |  ||      ||||
Db  2027 AAGTGTATCGAGGGACCCTCAGGGTCCCCAGCCACAGGCTCAAGACTGTGGCCATTAAGA 2086

Qy  1633 CTTGTCGAGAGACGCTCCACCTGACCTCAAGGCCAAGTTCTACAGGAGCGAGGATCC 1692
              |||  |||||   ||| ||||  |   ||||| |||||||| |||| || ||
Db  2087 CCTAAAAGACACATCCCCAGGTGGCCAGTGGTGGAACTTCCTTCGAGAGGCAACTATCA 2146

Qy  1693 TGAAGCAGTACAGCCACCCCAACATCGTGGTCTCATTGTGTCTGCACCCAGAAGCAGC 1752
              |||   ||| ||||| |  |  || || |  |||   ||| | |||| |||| ||
Db  2147 TGGGCCAGTTTAGCCACCCGCATATTCTGCATCTGGAAGGCGTCGTCACAAAGCGAAAGC 2206

Qy  1753 CCATCTACATCGTCATGAGAGCTTGTGCAGGGGGCGACTTCCTGACCTTCCTCCGCACGG 1812
              | || ||| |   |||| |  |  |  ||||| || | |  |   || ||
Db  2207 CGATCATGATCATCACAGAATTTATGGAGAATGCAGCCCTGGAGATGCGCTGCTGGAGC 2266

Qy  1813 AGGGGCCCGCTCGGGGTGAAGACTCGCTGCAGAGTGGGGATGCGCAGCTGCTGCGCA 1872
              ||||  |  |||| | |  ||| | |  ||| ||    ||| |  ||| | ||||
Db  2267 GGGAGGACCAGCTGGTCCTGGCAGTAGTGGCCATGGCTGCAGGGCATAGCATCTGGCA 2326

Qy  1873 TGGAGTACCTGGAGAGCAAGTGCTGTCATCCACCGGGACCTGGCTGTCTCGGAACTGCCTGG 1932
              |||| ||||| | | ||  |  || || |||||||||||||||||| | ||| || ||||
Db  2327 TGAACTACCTCAGTAATCACAATTATGTCCACCGGGACCTGGCTGCCAGAAACATCTTGG 2386

Qy  1933 TGACAGAGAAGAATGTCCTGAAGATCAGTGACTTTGGGATGTCCCGAGAGGAAGCCGATG 1992
              || | || ||  ||  || ||| | ||| ||||||||| |    ||||| | |   || |
Db  2387 TGAATCAAAACCTGTGTCGCAAGGTGTCTGACTTTGGGAGCTTTGGGATTGTGTGATGACT 2446

Qy  1993 GGGTCTATGCAGCCTCAGGGGCGCCTCAGACAAGTCCCGTGAAGTGGACCGCACCGAGG 2052
              |||||||| ||||  || || | ||||| | |||| || ||||   |||| |  | |||
Db  2447 TTGATGGCACATACGAAACCAGGAGGAGAAAGATCCTATCCGTTGGACAGACCCCTGAAG 2506

Qy  2053 CCCTTAACTACGGCCCGCTACTCCTCCGCAAGAGGCTTTGGCATCTTGCTCT 2112
              ||  | ||| | || |  | | || || ||  ||||||||| ||||| | |
Db  2507 CCAATTGCCCATCGGATCTTCACCAGCCAGCGATGTGTGGAGCTTTGGGATTGTGATGT 2566

Qy  2113 GGGAGACCTTCAGCCTGGGGGCCTCCCCCATCCCAACCTCAGCATCAGCAATCAGCGGGG 2172
              |||||  | |||| ||||||| | ||||||| || |||| ||||||||| ||||  | |
Db  2567 GGGAGGTGCTGAGCTTTGGGGACAAGCCTTATGGGGAGGATGAGCAATCAGGAGGTTATGA 2626

Qy  2173 AGTTTGTGGGAGAAGGGGGGCCGTCTTGCCCTGCCCCAGAGCTGTGTCCTGATGCCGTGTTCA 2232
              || | | ||| | || ||  ||| | ||||| | ||| || |  |  | |    ||||  |||
Db  2627 AGAGCATTGAGGATGGGTACCGGGTTGCCCCTCGTGGACTGGCAGCGGCCCAGCTTC 2686

Qy  2233 GGCTCATGGAGCAGTGCTGGCTGGCCCATGAGCCTGGGCAGCGGGCCAGCTTC 2282
              ||||||||||| | | ||| |  ||| ||||  | || |  |  ||||||||||
Db  2687 AGCTCATGAAGAACTGCTGGGCATATGACCGTGCCCGGCCGCCCACACTTC 2736
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Db  1934 AAGTGTATCGAGGGACCCTCAGGGACTGCTCCCCAGCCAGGACTGCAAGACTGTGGCCATTAAGA 1993
Qy  1633 CTTGTCGAGAGACGCTCCACCTGACCTCAAGGCCAAGTTCTACAGGAGCGAGGATCC 1692
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; TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,
; TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
; TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES
; FILE REFERENCE: MPIO2-020P1RNOMNIM
; CURRENT APPLICATION NUMBER: US/10/354,358
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/353,600
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 60/364,517
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/371,075
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/371,507
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US 60/372,984
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/374,194
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/382,995
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/385,023
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/388,853
; PRIOR FILING DATE: 2002-05-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 101
; LENGTH: 3370
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (94)...(3048)
US-10-354-358-101

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; Publication No. US20030175736A1
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;   APPLICANT: Chinnaiyan, Arul M.
;   APPLICANT: Rubin, Mark A.
;   APPLICANT: Sreekumar, Arun
;   TITLE OF INVENTION: Expression Profile of Prostate Cancer
;   FILE REFERENCE: UM-07221
;   CURRENT APPLICATION NUMBER: US/10/210,120
;   CURRENT FILING DATE: 2002-08-01
;   PRIOR APPLICATION NUMBER: US 60/309,581
;   PRIOR FILING DATE: 2001-08-02
;   PRIOR APPLICATION NUMBER: US 60/334,468
;   PRIOR FILING DATE: 2001-11-15
;   NUMBER OF SEQ ID NOS: 123
;   SOFTWARE: PatentIn version 3.2
;   SEQ ID NO 19
;   LENGTH: 3370
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-210-120-19

Query Match        7.4%;      Score 198; DB 16;  Length 3370;
Best Local Similarity   54.7%;   Pred. No. 2.2e-21;
Matches  421;  Conservative   0;  Mismatches 340;  Indels   9;  Gaps   1;
US-10-210-120-19

Qy  1522 GGGTGCTGAACCATGAGGAGGACCTGGTGTTGGGTGAGCAGATTGGACGGGGGAACTTTGGGCG 1581
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Wed Aug 10 16:17:22 2005

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Job time : 2389.73 secs

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          Copyright (c) 1993 - 2005  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:    August  9, 2005, 16:42:25 ; Search time 591.209 Seconds
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Searched:       1202784 seqs, 818138359 residues

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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	362.4	13.6	15297	3	US-09-817-180-3	Sequence 3, Appli
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5	296.2	11.1	361	3	US-09-387-212-5	Sequence 3, Appli
6	296.2	11.1	361	3	US-09-948-802-5	Sequence 5, Appli
7	223.4	8.4	19152	4	US-09-949-016-12110	Sequence 12110, A
8	223.4	8.4	19153	4	US-09-949-016-15795	Sequence 15795, A
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ALIGNMENTS

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; Patent No. 6340584
; GENERAL INFORMATION:
;  APPLICANT: GAN, Weiniu et al.
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION: THEREOF
;  FILE REFERENCE: CL001183
;  CURRENT APPLICATION NUMBER: US/09/817,180
;  CURRENT FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 4
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; SEQ ID NO 1
;  LENGTH: 2674
;  TYPE: DNA
;  ORGANISM: Human
US-09-817-180-1

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Qy  1081 AGCTCCCGGAATGAAAGAGGAGAGACACCACCCCCCGGGAGGGAGCTGCTGCGGCAAGA 1140
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Db  1081 AGCTCCCGGAATGAAAGAGGAGAGACACCACCCCCCGGGAGGGAGCTGCTGCGGCAAGA 1140

Qy  1141 GGCAAGTGCTGCAAGAAGCACTGCAGGGGCTGCAGTAGCCGTGTCAGCGCCAGGCCAAGC 1200
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 GGCAAGTGCTGCAAGAAGCACTGCAGGGGCTGCAGTAGCCGTGTCAGCGCCAGGCCAAGC 1200

Qy  1201 TGCAGGGCCCAGCGAGTTGCTGCAGACCAAGTGGACCACTCTGGCGCCCGCGAGCCC 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 TGCAGGGCCCAGCGAGTTGCTGCAGACCAAGTGGACCACTCTGGCGCCCGCGAGCCC 1260

Qy  1261 CGGCCTGTGCTGCTTCCTGCAGGATGACGCCGGTCTCCTCGGAGGAGGAGGCGAG 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 CGGCCTGTGCTGCTTCCTGCAGGATGACGCCGGTCTCCTCGGAGGAGGAGGCGAG 1320

Qy  1321 AGGGGGGAAGGACACCCACCCACGCTGAGATCCTTAAGAGCCACATCTTCCGCC 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 AGGGGGGAAGGACACCCACCCACGCTGAGATCCTTAAGAGCCACATCTTCCGCC 1380

Qy  1381 CCAAGTTCTGCGAACCTGTACCGACTGGAAGGGGAAGGCTTTCCTTGGTGTCCTTGCTCA 1440
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Db  1381 CCAAGTTCTGCGAACCTGTACCGACTGGAAGGGGAAGGCTTTCCTTGGTGTCCTTGCTCA 1440

Qy  1441 TCGACCACTACTGAGACCCCAGCAGCCCCAGCGCCCCACCAAGAAGAGTGGTGTTGTCCTGCACA 1500
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Db  1441 TCGACCACTACTGAGACCCCAGCAGCCCCAGCGCCCCACCAAGAAGAGTGGTGTTGTCCTGCACA 1500
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Right column (positions 1501–2580):

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Qy  1501 GGGCTGTGCCCAAGGACACAAGTGGGTGCTGAACCATGAGACCTGGTGTGTTGGGTGGTGAGCAGA 1560
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Db  1501 GGGCTGTGCCCAAGGACACAAGTGGGTGCTGAACCATGAGACCTGGTGTGTTGGGTGGTGAGCAGA 1560

Qy  1561 TTGGACGGGGGAACTTGCTGAACGTGTTCAGCGGAGTGTTCAGCGGACGTGCGGAGCCGACAACACCCTGG 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 TTGGACGGGGGAACTTGCTGAACGTGTTCAGCGGAGTGTTCAGCGGACGTGCGGAGCCGACAACACCCTGG 1620

Qy  1621 TGGGCGGTGAAGTCTTGTCTCGAGAGACGCTCCACCTGACCTGACCTGACCTCAAGGCCAAGTTTCTACAGG 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621 TGGGCGGTGAAGTCTTGTCTCGAGAGACGCTCCACCTGACCTGACCTGACCTCAAGGCCAAGTTTCTACAGG 1680

Qy  1681 AAGGCAGGATCCTGAAGCAGTACAGCAGTGCTCACCAAACATCGTGCGTCTCATTGGTGTCTGCA 1740
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Db  1681 AAGGCAGGATCCTGAAGCAGTACAGCAGTGCTCACCAAACATCGTGCGTCTCATTGGTGTCTGCA 1740

Qy  1741 CCCAGAAGCAGCCCATCTACATCGTGCTCATGGAGCTTGTGCGACTTCCTGACCT 1800
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Db  1741 CCCAGAAGCAGCCCATCTACATCGTGCTCATGGAGCTTGTGCAGGGGCGACTTCCTGACCT 1800

Qy  1801 TCCTCCGCACGGAGGGGCCCGCTGCGGGGTCTGAAGACTCTGCTGCAGATGGTGTGGGGGATG 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801 TCCTCCGCACGGAGGGGCCCGCTGCGGGGTCTGAAGACTCTGCTGCAGATGGTGTGGGGGATG 1860

Qy  1861 CAGCTGCTGCTGGCATGGAGTCACTGCATGGAGCAAGTGCTCGGACGACCTGGCTCTC 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 CAGCTGCTGCTGGCATGGAGTCACTGCATGGAGCAAGTGCTCGGACGACCTGGCTCTC 1920

Qy  1921 GGAACTGCCTGGTGACAGAGAAGAATGTCTGAGAGATCAGTGACTTTGGGATGTCCCGAG 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 GGAACTGCCTGGTGACAGAGAAGAATGTCTGAGAGATCAGTGACTTTGGGATGTCCCGAG 1980

Qy  1981 AGGAAGCCGATGGGGTCTATGCAGCCTCAGGGGCTCAGGGGGCTCAGACAAGTCCCCGTGAAGTGGA 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 AGGAAGCCGATGGGGTCTATGCAGCCTCAGGGGCTCAGGGGGCTCAGACAAGTCCCCGTGAAGTGGA 2040

Qy  2041 CCGCACCTGAGGCCCTTAACTACGGCCGCTACTCCTCCGAAAGCGACGTGTGGAGCTTTG 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041 CCGCACCTGAGGCCCTTAACTACGGCCGCTACTCCTCCGAAAGCGACGTGTGGAGCTTTG 2100

Qy  2101 GCATCTTGCTCTGGGAGACCTTCAGCCTGGGGGCCTCCCCATCCCCAACCTCAGCAATC 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 GCATCTTGCTCTGGGAGACCTTCAGCCTGGGGGCCTCCCCATCCCCAACCTCAGCAATC 2160

Qy  2161 AGCAGACACGGAGTTGTGGACAAGGGGGCCGTCTGCCCGTGCTGTGTCCTG 2220
             |||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 AGCAGACACGGAGTTGTGGACAAGGGGGCCGTCTGCCCGTGCTGTGTCCTG 2220

Qy  2221 ATGCCGTGTTCAGGCTCATGGAGCTCATGGAGCAGTGCTGGGCCTATGAGCCTGGGCAGGCCCAGCT 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 ATGCCGTGTTCAGGCTCATGGAGCTCATGGAGCAGTGCTGGGCCTATGAGCCTGGGCAGGCCCAGCT 2280

Qy  2281 TCAGCACCATCTACCAGGAGCTGCAGACTGCAGAGCATCCGAAAGCCGGCATCGGTGGAGGCTGGGACC 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 TCAGCACCATCTACCAGGAGCTGCAGACTGCAGAGCATCCGAAAGCCGGCATCGGTGGAGGCTGGGACC 2340

Qy  2341 CCCTTCTCAAGCTGGTGGCCTCTGCAGGCTGCAGTTGCAGCTCTGCAGCTCCAGCTCA 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 CCCTTCTCAAGCTGGTGGCCTCTGCAGGCTGCAGTTGCAGCTCTGCAGCTCCAGCTCA 2400

Qy  2401 TATGCTGACAGCTCTTCACAGTGTCCTGCACTCCTGACTCCTGCTGCTGCACCACCTGCCGGCAGG 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 TATGCTGACAGCTCTTCACAGTGTCCTGCACTCCTGACTCCTGCTGCTGCACCACCTGCCGGCAGG 2460

Qy  2461 ATGCAGCGGCCGTGTCCTCGTGTCCTGCTGCTGCTCCTGCTGCTTCTCTTCCGGGGCAGA 2520
             |||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 ATGCAGCGGCCGTGTCCTCGTGTCCTGCTGCTGCTCCTGCTGCTTCTCTTCCGGGGCAGA 2520

Qy  2521 AACAATAAAACCACTTGTGCCCACTCGAAAGAGTGGTTGTCTCGGCACA 2580
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Db  2521 AACAATAAAACCACTTGTGCCCACTCGAAAGAGTGGTTGTCTCGGCACA 2580
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Qy    2581  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  2640
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Db    2581  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  2640

Qy    2641  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  2674
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Db    2641  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  2674
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RESULT 2
US-10-003-295-1
; Sequence 1, Application US/10003295
; Patent No. 6686187
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001183DIV
; CURRENT APPLICATION NUMBER: US/10/003,295
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2674
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-003-295-1

Query Match   100.0%; Score 2674; DB 4; Length 2674;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1  TCCGGGGTCCGCACCGGGCCTGAGTCGGTCCGAGGAGCAGCTGCCCGTGC    60
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Db       1  TCCGGGGTCCGCACCGGGCCTGAGTCGGTCCGAGGAGCAGCTGCCCGTGC    60

Qy      61  GGAACAGCACTATGGGCTTCTTCTTCTGAGCTGTGCAGCCCACGGGGTCCTGC   120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61  GGAACAGCACTATGGGCTTCTTCTTCTGAGCTGTGCAGCCCACGGGGTCCTGC   120

Qy     121  AGCAAATGCAGAGAGGCCGAGCTTCGTCTACTGGAGGGCATGAGGACCCAGC   180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121  AGCAAATGCAGAGAGGCCGAGCTTCGTCTACTGGAGGGCATGAGGACCCAGC   180

Qy     181  GGGTCAAGAGTGACAGGGAGTATGCAGGGACTGCTTCACCACATGTCCCTGC   240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181  GGGTCAAGAGTGACAGGGAGTATGCAGGGACTGCTTCACCACATGTCCCTGC   240

Qy     241  GGGGCCAGAGCCGGGCCATCAGCCCTGACAGCCCGCTTGCTGCGGCAGTCGG   300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241  GGGGCCAGAGCCGGGCCATCAGCCCTGACAGCCCGCTTGCTGCGGCAGTCGG   300

Qy     301  CCAGCCAAACTGAGGGCCTGAGCCTGCTGCCGCTGCTCATCCGGGAACGGC   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301  CCAGCCAAACTGAGGGCCTGAGCCTGCTGCCGCTGCTCATCCGGGAACGGC   360

Qy     361  GGCCCCTGAGCAAGCTGAGCCTGCTCATCCGGGGAACGGCAGCCAGCTTCGC   420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361  GGCCCCTGAGCAAGCTGAGCCTGCTCATCCGGGGAACGGCAGCCAGCTTCGC   420

Qy     421  GCGAGCAGTGGCAGCAGCTGCAGCAGAGACCTCACGAGCTCAGCAGGACATTGAGA   480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421  GCGAGCAGTGGCAGCAGCTGCAGCAGAGACCTCACGAGCTCAGCAGGACATTGAGA   480

Qy     481  AGCTGAAGAGCCAGTACCGAGCTCTGCACGGGACAGTGCCCAAGGCCAAGTACC   540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481  AGCTGAAGAGCCAGTACCGAGCTCTGCACGGGACAGTGCCCAAGGCCAAGTACC   540

Qy     541  AGGAGGCCAGCAAAGACAAGGACAAGGACCGTGACAAGGCCAAGGCCAAGTATGTGCGGCAGCCTGT   600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541  AGGAGGCCAGCAAAGACAAGGACAAGGACCGTGACAAGGCCAAGGCCAAGTATGTGCGGCAGCCTGT   600
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Qy     601  GGAAGCTCTTGCTCACCACCACCGCTATGTGCTGGGCGTGCGCAGCTACACC   660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601  GGAAGCTCTTTGCTCACCACCACCAACCGCTATGTGCTGGGGGTGCGCAGCTACACC   660

Qy     661  ACCAGCACCACCAGCTCCTGCTGCTGGTCTGCGGTCCGGTCGCGCTGCACTGCACG   720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661  ACCAGCACCACCAGCTCCTGCTGCTGGTCTGCGGTCCGGTCGCGCTGCACTGCACG   720

Qy     721  AGGAGATGGCTTGCATCCTGAGGAGAATACCTGGAGATTAGAGCCTGG   780
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db     721  AGGAGATGGCTTGCATCCTGAGGAGAATACCTGGAGATTAGAGCCTGG   780

Qy     781  TGCAGGATGAGGTGGTGGCCATTCACCGGGAGATGGCTGCAGCTGCTGCCCGGATCCAGC   840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781  TGCAGGATGAGGTGGTGGCCATTCACCGGGAGATGGCTGCAGCTGCTGCCCGGATCCAGC   840

Qy     841  CTGAGGCTGAGTACCAAGGCTTCCTGCGACACAGTGGGTCCGACACCTTGACGTCCCACCCT   900
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841  CTGAGGCTGAGTACCAAGGCTTCCTGCGACACAGTGGGTCCGACACCTTGACGTCCCACCCT   900

Qy     901  GTGTCAGTTCGATGAGTCACTGCTTGAGGAGGTGAACCGCTGGAGCGTCGGGGAGCTCC   960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901  GTGTCAGTTCGATGAGTCACTGCTTGAGGAGGTGAACCGCTGGAGCGTCGGGGAGCTCC   960

Qy     961  AGCTGAACGAGCTGACTGTGGAGAGGTGCAGCACACGCTGACCTCAGTGACAGATGAGC   1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961  AGCTGAACGAGCTGACTGTGGAGAGGTGCAGCACACGCTGACCTCAGTGACAGATGAGC   1020

Qy    1021  TGGCTGTGGCCACCGAGATGGTGTTCAGGCGGCGGCCACCCCCCGGGAGCTGCTGGGCAAGA   1080
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021  TGGCTGTGGCCACCGAGATGGTGTTCAGGCGGCGGCCACCCCCCGGGAGGTGCTGGGCAAGA   1080

Qy    1081  AGCTCCGGAATGAAGAGGAGAACACCCACCCCCCGGGAGCGGGTGCAGCGTGCTGCGGCCAGC   1140
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081  AGCTCCGGAATGAAGAGGAGAACACCCACCCCCCGGGAGCGGGTGCAGCGTGCTGCGGCCAGC   1140

Qy    1141  GGCAAGTGCTGCAAGAAGCACTGCAGGGCTGTGCAGCCCCCGCGGGCCGAGCCCC   1200
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141  GGCAAGTGCTGCAAGAAGCACTGCAGGGGTGCAGCGTGCTGGAGACCAAGAGCCCC   1200

Qy    1201  TGCAGGGCCCAGCAGGAGTGCTGCAGGATGACCGCCACTCCAGTCGTCCCAGCAGGAGGCGAG   1260
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201  TGCAGGGCCCAGCAGGAGTGCTGCAGGATGACCGCCACTCCAGTCGTCCCAGCAGGAGGCGAG   1260

Qy    1261  CGCCCTGTGCTGCTCCTGCAGGACTGCTTCACCACGTGTCCAGGACAGTG   1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261  CGCCCTGTGCTGCTCCTGCAGGATGCTTCACCACGTGTCCAGGACAGTG   1320

Qy    1321  AGGGGGAAGGACACCCCACGCTGGAGATCCTTAAGGACCACATCTTCCGCC   1380
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321  AGGGGGAAGGACACCCCACGCTGGAGATCCTTAAGGACCACATCTTCCGCC   1380

Qy    1381  CCAAGTTCTGAACCTGTACCGACTCGGAGGGAAGGGCTTTCCTAGCATTCTTTGTCTCA   1440
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381  CCAAGTTCTGAACCTGTACCGACTCGGAGGGAAGGGCTTTCCTAGCATTCTTTGTCTCA   1440

Qy    1441  TCGACACCTACTGGAGCACCTGAGCAGCCCTCACCGAGAGTGGTTGTTCCTGCACA   1500
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441  TCGACACCTACTGGAGCACCTGAGCAGCCCTCACCGAGAGTGGTTGTTCCTGCACA   1500

Qy    1501  GGGCTGTGCCAAGGACAAGTGGGTGCTGGTTGGTGGTGAGCAGAGA   1560
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Db    1501  GGGCTGTGCCAAGGACAAGTGGGTGCTGGTTGGTGTGGGTGAGCAGAGA   1560

Qy    1561  TTGGACGGGGGAACTTTGGCGAAGTGTTCAGCGGCAAGTACC   1620
            ||||||||||||||||||||||||||||||||||||||||||
Db    1561  TTGGACGGGGGAACTTTGGCGAAGTTTGGCAAGTACC   1620

Qy    1621  TGGCGGTGAAGTCTTGTCGTGAGAGACGTCCCACCTGACCTCAAGGCCAGCCTGT   1680
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621  TGGCGGTGAAGTCTTGTCGTGAGAGACGTCCCACCTGACCTCAAGGCCAGCCTGT   1680

Qy    1681  AAGCGAGGATCCTGAAGCAGTACAGCAGTACACCCAACATCGTGCGTCTCATTGGTGTCTGCA   1740
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Db  1681  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
           AAGCGAGGATCCTGAGCAGTACAGCCACCCAAACATGTGCGTCTCATTGGTGTCTGCGA  1740
Qy  1741  CCCAGAAGCAGCCATCTACATCGTCATGGAGCTTGTGCAGGGGGGCGACTTCCTGACCT  1800
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741  CCCAGAAGCAGCCATCTACATCGTCATGGAGCTTGTGCAGGGGGGCGACTTCCTGACCT  1800
Qy  1801  TCCTCCGCACGGAGGGGGCCCCTGCCGGGTGAAGACTCTGCTGCAGATGTGGGGGATG  1860
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801  TCCTCCGCACGGAGGGGGCCCCTGCCGGGTGAAGACTCTGCTGCAGATGTGGGGGATG  1860
Qy  1861  CAGCTTGCTGGCATGGAGTACCTGGAGCAAGTGCTGCATCCACCGGGACCTGGCTGCTC  1920
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861  CAGCTTGCTGGCATGGAGTACCTGGAGCAAGTGCTGCATCCACCGGGACCTGGCTGCTC  1920
Qy  1921  GGAACTGCCTCGGTGACAGAGAAGAATGTCCTGAAGATCAGTGACTTGGATGTCCCGAG  1980
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921  GGAACTGCCTCGGTGACAGAGAAGAATGTCCTGAAGATCAGTGACTTGGATGTCCCGAG  1980
Qy  1981  AGGAAGCCGATGGGGTCTATGCAGCAAGTCCCCGTGAAGTGGA  2040
           |||||||||||||||||||||||||||||||||||||||||||
Db  1981  AGGAAGCCGATGGGGTCTATGCAGCAAGTCCCCGTGAAGTGGA  2040
Qy  2041  CCGCACCTGAGCGCCTTAACTACGGCCGCTACTCCTCCGAAAGCGACGTGTGGAGCTTTG  2100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041  CCGCACCTGAGCGCCTTAACTACGGCCGCTACTCCTCCGAAAGCGACGTGTGGAGCTTTG  2100
Qy  2101  GCATCTTGCTCTGGGAGACCTTCAGCCTGGGGGCCTCCCCCTATCCCAACCTCAGCAATC  2160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101  GCATCTTGCTCTGGGAGACCTTCAGCCTGGGGGCCTCCCCCTATCCCAACCTCAGCAATC  2160
Qy  2161  AGCAGACACGGGAGTTTGTGGAGAACGAGGGCCGTGCCCTGCCCAGAGCTGTGTCCTG  2220
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161  AGCAGACACGGGAGTTTGTGGAGAACGAGGGCCGTGCCCTGCCCAGAGCTGTGTCCTG  2220
Qy  2221  ATGCCCGTGTTCAGGCTCATGGAGCAGTGCTGGGCCTATGAGCCTCGGCCCAGCT  2280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221  ATGCCCGTGTTCAGGCTCATGGAGCAGTGCTGGGCCTATGAGCCTCGGCCCAGCT  2280
Qy  2281  TCAGGACCATCTACCAGGAGCTGCAGAGCATCCGAAAGGCGCATCGGTGAGGCTGGGACC  2340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281  TCAGGACCATCTACCAGGAGCTGCAGAGCATCCGAAAGGCGCATCGGTGAGGCTGGGACC  2340
Qy  2341  CCCTTCTCAAGCTGTGGCCTCTCGAGGCCTAGGTGCAGCTCCTCAGCGGCTCCAGCTCA  2400
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341  CCCTTCTCAAGCTGTGGCCTCTCGAGGCCTAGGTGCAGCTCCTCAGCGGCTCCAGCTCA  2400
Qy  2401  TATGCTGACAGTCTTCACAGTCCTGGACTCCTGCCACCAGCATCCACACTGCCGGCAGG  2460
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401  TATGCTGACAGTCTTCACAGTCCTGGACTCCTGCCACCAGCATCCACACTGCCGGCAGG  2460
Qy  2461  ATGCAGCGCGCCGTGTCCTCTCGTGTCCCTGCTGCGCTGCCAGGGGCTTCCCTTCCCGGGCAGA  2520
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Db  2461  ATGCAGCGCGCCGTGTCCTCTCGTGTCCCTGCTGCGCTGCCAGGGGCTTCCCTTCCCGGGCAGA  2520
Qy  2521  AACAATAAACCACTTGTGCCCACTGAAAAAAAAAAAAAAAAA  2580
           ||||||||||||||||||||||||||||||||||||||||||
Db  2521  AACAATAAACCACTTGTGCCCACTGAAAAAAAAAAAAAAAAA  2580
Qy  2581  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  2640
           ||||||||||||||||||||||||||||||||||||||||||
Db  2581  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  2640
Qy  2641  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  2674
           ||||||||||||||||||||||||||||||||
Db  2641  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  2674
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RESULT 3
US-09-817-180-3
; Sequence 3, Application US/09817180
; Patent No. 6340584
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001183
; CURRENT APPLICATION NUMBER: US/09/817,180
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15297
; TYPE: DNA
; ORGANISM: Human
US-09-817-180-3

Query Match   13.6%;   Score 362.4; DB 3; Length 15297;
Best Local Similarity   99.7%;   Pred. No. 5.1e-55;
Matches 363; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

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Qy   2187  GGGGGCCGTCTGCCCTGCCCAGAGCTGTGTCCTGATGCCCGTGTTCAGGCTCATGGAGCAG  2246
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Db  12938  GGGGGCCGTCTGCCCTGCCCAGAGCTGTGTCCTGATGCCCGTGTTCAGGCTCATGGAGCAG  12997
Qy   2247  TGCTGGGCCTATGAGCCTCGGCCCAGCTTCAGCACCATCTCAGCACTTCACCAGGAGCTGCAG  2306
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  12998  TGCTGGGCCTATGAGCCTCGGCCCAGCTTCAGCACCATCTCAGCACTTCACCAGGAGCTGCAG  13057
Qy   2307  AGCATCCGAAAGCGGCATCGGTGAGGCTGGGACCCCCTTCTCAAGCTGGTGGCCTCTGCA  2366
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Db  13058  AGCATCCGAAAGCGGCATCGGTGAGGCTGGGACCCCCTTCTCAAGCTGGTGGCCTCTGCA  13117
Qy   2367  GGCCTAGGTGCAGCTCCTCAGCACTCCAGCTCCAGCTCATATGCTGACAGTCTTCACAGTCCTG  2426
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  13118  GGCCTAGGTGCAGCTCCTCAGCACTCCAGCTCCAGCTCATATGCTGACAGTCTTCACAGTCCTG  13177
Qy   2427  GACTCCTGCCACCAGCATCCACACTGCCGCAGGATGCAGAGATGCAGAGCGCCGTGTCCTCTGTC  2486
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  13178  GACTCCTGCCACCAGCATCCACACTGCCGCAGGATGCAGAGATGCAGAGCGCCGTGTCCTCTGTC  13237
Qy   2487  CCTGCTGCTGCCAGGGCTTCCTCCTGCTGCCAGGGGCTGCAGAAACAATAAAACCACTTGTGCCCACTG  2546
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  13238  CCTGCTGCTGCCAGGGCTTCCTCCTGCTGCCAGGGGCTGCAGAAACAATAAAACCACTTGTGCCCACTG  13297
Qy   2547  AAAA  2550
           ||||
Db  13298  AACA  13301
```

RESULT 4
US-10-003-295-3
; Sequence 3, Application US/10003295
; Patent No. 6686187
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001183DIV
; CURRENT APPLICATION NUMBER: US/10/003,295
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15297
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-003-295-3

Query Match   13.6%;   Score 362.4; DB 4; Length 15297;
Best Local Similarity   99.7%;   Pred. No. 5.1e-55;
Matches 363; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

```
Qy   2187  GGGGGCCGTCTGCCCTGCCCAGAGCTGTGTCCTGATGCCCGTGTTCAGGCTCATGGAGCAG  2246
```

```
Db  12938  |||||||||||||||||||||||||||||||||||
           GGGGGCCGTCTGCCCTGCCCAGAGCTGTGTCCTGATGCCGTGTTCAGGCTCACCAGGAGCAG  12997
Qy  2247   TGCTGGGCCTATGAGCCTGGGCAGCGGCCCAGCTTCAGCACCATCTACCAGGAGCTGCAG  2306
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  12998  TGCTGGGCCTATGAGCCTGGGCAGCTGGGCAGCGGCCCCAGCTTCAGCACCATCTACCAGGAGCTGCA  13057
Qy  2307   AGCATCCGAAAGCGGCATCGGTCGGTGAGGCTGGGACCCCCTTCTCAAGCTGGTGGCCTCTGCA  2366
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  13058  AGCATCCGAAAGCGGCATCGGTCGGTGAGGCTGGGACCCCCTTCTCAAGCTGGTGGCCTCTGCA  13117
Qy  2367   GGCCTAGGTGCGAGCTCCTCAGCGGCTCCAGCTCATATGCTGACAGTCTTCACAGTCCTG  2426
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  13118  GGCCTAGGTGCAGCTCCTCCAGCGCGTCCAGCTCATATGCTGACAGTCTTCACAGTCCTG  13177
Qy  2427   GACTCCTGCGCCACCAGCATCCACACTGCCGCGGATGCAGCGCGCCGTGCTCCTCCTGTGTC  2486
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  13178  GACTCCTGCGCCACCAGCATCCACACTGCCGCGGATGCAGCGCGCCGTGCTCCTCTGTGTC  13237
Qy  2487   CCTGCTGCTGCCCAGGCTTCCTCTTCCGGGCAGAAACAATAAAACCACTTGTGCCCACTG  2546
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  13238  CCTGCTGCTGCCCAGGCTTCCTCTTCCGGGCAGAAACAATAAAACCACTTGTGCCCACTG  13297
Qy  2547   AAAA  2550
           ||
Db  13298  AACA  13301
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RESULT 5
US-09-387-212-5
; Sequence 5, Application US/09387212A
; Patent No. 6309849
; GENERAL INFORMATION:
;   APPLICANT: ROBISON, KEITH E.
;   TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
;   TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR
;   FILE REFERENCE: MNI-090
;   CURRENT APPLICATION NUMBER: US/09/387,212A
;   CURRENT FILING DATE: 1999-08-31
;   NUMBER OF SEQ ID NOS: 18
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 361
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: All occurences of n indicate any nucleotide
US-09-387-212-5

Query Match   11.1%; Score 296.2; DB 3; Length 361;
Best Local Similarity   97.4%; Pred. No. 1.1e-43;
Matches 333; Conservative 0; Mismatches 4; Indels 5; Gaps 3;

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Qy  1684  CGAGGATCCTGAAGCAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTGTCTGCACCC  1743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    20  CNAGGATCCTGAAGCAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTGTCTGCACCC  79
Qy  1744  AGAAGCAGCCCATCTACATCGTCATGGAGCTTGTGCAGGGGGGGCGACTTCCTGACCTTCC  1803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    80  AGAAGCAGCCCATCTACATCGTCATGGAGCTTGTGCAGGGGGGGCGACTTCCTGACCTTCC  139
Qy  1804  TCCGCACGGAGGGGGCCCGCCTGCGGGTGAAGACTTCGCTGCAGATGGTGGGGGATGCAG  1863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   140  TCCGCACGGAGGGGGCCCGCCTGCGGGTGAAGACTTCGCTGCAGATGGTGGGGGATGCAG  199
Qy  1864  CTGCTGGCATGGAGTACCTGGAGAGCAAGTGCTCATCCACCGGGACCTGCTGCTCGGA  1923
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   200  CTGCTGGCATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACCTGCTGCTCGGA  259
Qy  1924  ACTGCCTGGTGACAGAGAAGAATGTCCTGAAG-ATCAGTGACTTT-GGGATGTCCCGAGA  1981
          |||||||||||||||||||||||||||||| |||||||||||||| ||||||||||||||
Db   260  ACTGCCTGGTGACAGAGAAGAATGTCCTGAAGAATCAGTGACTTTGGGGATGTCCCGAGA  319
```

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Qy  1982  GGAAGCC---GATGGGTCTATGCAGCCTCAGGGGGCCTCAG  2020
          |||||||        |||||||||||||||||||||||||
Db   320  GGAAGCCCGATTGGGGGTCTATGCAGCCTCAGGGGGCCTCAG  361
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RESULT 6
US-09-948-802-5
; Sequence 5, Application US/09948802
; Patent No. 6465232
; GENERAL INFORMATION:
;   APPLICANT: ROBISON, KEITH E.
;   TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
;   TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR
;   FILE REFERENCE: MNI-090
;   CURRENT APPLICATION NUMBER: US/09/948,802
;   CURRENT FILING DATE: 2001-09-07
;   PRIOR APPLICATION NUMBER: 09/387,212
;   PRIOR FILING DATE: 1999-08-31
;   NUMBER OF SEQ ID NOS: 18
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 361
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: All occurences of n indicate any nucleotide
US-09-948-802-5

Query Match   11.1%; Score 296.2; DB 3; Length 361;
Best Local Similarity   97.4%; Pred. No. 1.1e-43;
Matches 333; Conservative 0; Mismatches 4; Indels 5; Gaps 3;

```
Qy  1684  CGAGGATCCTGAAGCAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCC  1743
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    20  CNAGGATCCTGAAGCAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCC  79
Qy  1744  AGAAGCAGCCCATCTACATCGTCATGGAGCTTGTGCAGGGGGGCGACTTCCTGACCTTCC  1803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    80  AGAAGCAGCCCATCTACATCGTCATGGAGCTTGTGCAGGGGGGCGACTTCCTGACCTTCC  139
Qy  1804  TCCGCACGGAGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGATGGCAG  1863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   140  TCCGCACGGAGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGATGGCAG  199
Qy  1864  CTGCTGGCATGGAGTACCTGGAGAGCAAGTGCTCGTCATCCACCGGGACCTGCTGCTCGGA  1923
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   200  CTGCTGGCATGGAGTACCTGGAGAGCAAGTGCTCGTCATCCACCGGGACCTGCTGCTCGGA  259
Qy  1924  ACTGCCTGGTGACAGAGAAGAATGTCCTGAAG-ATCAGTGACTTT-GGGATGTCCCGAGA  1981
          |||||||||||||||||||||||||||||| |||||||||||||| ||||||||||||||
Db   260  ACTGCCTGGTGACAGAGAAGAATGTCCTGAAGAATCAGTGACTTTGGGGATGTCCCGAGA  319
Qy  1982  GGAAGCC---GATGGGTCTATGCAGCCTCAGGGGGCCTCAG  2020
          |||||||        |||||||||||||||||||||||||
Db   320  GGAAGCCCGATTGGGGGTCTATGCAGCCTCAGGGGGCCTCAG  361
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RESULT 7
US-09-949-016-12110
; Sequence 12110, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;   TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;   FILE REFERENCE: CL001307
;   CURRENT APPLICATION NUMBER: US/09/949,016
;   CURRENT FILING DATE: 2000-04-14
;   PRIOR APPLICATION NUMBER: 60/241,755
;   PRIOR FILING DATE: 2000-10-20
;   PRIOR APPLICATION NUMBER: 60/237,768
;   PRIOR FILING DATE: 2000-10-03
;   PRIOR APPLICATION NUMBER: 60/231,498

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Db    18909 GGGGGCCAGAGCCGGGGCCATCAGCCCTGACAGCCCCATCAGTCAG 18953
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RESULT 9
US-09-814-915A-82
; Sequence 82, Application US/09814915A
; Patent No. 6750015
; GENERAL INFORMATION:
;   APPLICANT: Horwitz, Kathryn
;   APPLICANT: Richer, Jennifer
;   TITLE OF INVENTION: Progesterone Receptor-Regulated Gene Expression and Methods
;   TITLE OF INVENTION: Thereto
;   FILE REFERENCE: 2848-39
;   CURRENT APPLICATION NUMBER: US/09/814,915A
;   CURRENT FILING DATE: 2002-03-21
;   PRIOR APPLICATION NUMBER: 60/214,870
;   PRIOR FILING DATE: 2000-06-28
;   NUMBER OF SEQ ID NOS: 108
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
;   LENGTH: 3370
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-814-915A-82
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Query Match             7.4%;  Score 198; DB 4;  Length 3370;
Best Local Similarity   54.7%;  Pred. No. 5e-26;
Matches  421;  Conservative   0;  Mismatches  340;  Indels    9;  Gaps    1;

Qy   1522 GGTGCTGAACCATGAGGACCTGGTGTTGGGTGAGCAGATTGACGGGGGAACTTTGGCG 1581
               |||||  || |||||||| ||| |||  ||| |  ||| |||  ||  ||||| |||
Db   1967 GGGAGCTTGATCCAGCGTGGCTGGCTGATGGTGGACACTGTCATAGGAGAAGGAGAGTTTGGGG 2026

Qy   1582 AAGTGTTCAGCGGACGCCCTGCGAGCC--------GACAACACCCTGCGGCGGTGAGT 1632
               |||||                                    |||  ||| |||||
Db   2027 AAGTGTATCGAGGGACCTTCAGGCTCCCCAGCCAGGACTGCAAGACTGGCCATTAAGA 2086

Qy   1633 CTTGTCGAGAGACGCTCGACCTGACTCAAGGCCAAGTTTCTACAGGAAGCGAGGATCC 1692
               || ||| |||| | || | |  ||| ||||||  ||| ||| || |||||| |||
Db   2087 CCTTAAAAGACACATCCCCAGGTGGCCAGTGGTGGAACTTCCTTCGACAGGGCAACTATCA 2146

Qy   1693 TGAAGCAGTACAGCACCACCCAACATCGTGCTTCATTGGTGTCTGACCCAGAAGCAGC 1752
               ||||| ||| |||| |||||||| || || ||||| |  |||  |||||| ||||
Db   2147 TGGGCCAGTTTAGCCACCCGCATATTCTGCATCTGGAAGGGCGTCGTCACAAAGCGAAAGC 2206

Qy   1753 CCATCTACATCGTCATGGGAGCTTGTGCAGGGGGGGACTTCCTGCAGGGGATGCAGCTGCTGGCA 1812
               ||||| |||| ||| || ||  || |||||||| ||| ||||||| || || | ||||
Db   2207 CGATCATGCATCATCACAGAATTTATGAGAATGCAGCCCTGGATGTGGGGGATGGCAGCTGCTGGCA 2266

Qy   1813 AGGGGGCCCGCCTGGAAGACTCTGCTGCTGCTGCTGCGTGGGGAACTGCCTCGG 1872
               |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2267 GGGAGGACCAGCTGGTCCTGCAGCTGGTGCCCATGCTGGGGATGGCAGCTGCCTGGGAACTGCTGGCA 2326

Qy   1873 TGGAGTACCTGGAGAGCAAGTGCTCGCATCCACCGGGACCTGCTCGGGAACTGCCTGG 1932
               ||||| ||||||||| |||||||| || ||||||||||||||||||||||| |||||
Db   2327 TGAACTACCTCAGTAATCACAATTATGTCCACCGGGACCTGCTGCCAGAAACATCTTGG 2386

Qy   1933 TGACAGAGAAGAAATGTCCTGAAGATCAGTGACTTTGGGATGTCCCGAGAGGAAGCCGATG 1992
               |||||| |||||||||||||||||||||||| |||||||||||||||||||| |||||
Db   2387 TGAATCAAAACCTGTCTGCAAGGTGTCTGACTTTGGCCTGACTTTGGCGTGAAGTCGGATGACT 2446

Qy   1993 GGGTCTATGCAGCCTCAGACAGTCCCGTGAAGTGGACCACCTGAGG 2052
               |||| |||||| |||| |||||| |||| ||||| |||  |||| |
Db   2447 TTGATGGCACATACGAAACCCAGGAGAAGATCCTATCCGTTGGACAGCCCCCTGAAG 2506

Qy   2053 CCCTTAACTACGGCCGCTACTCCTCCGAAAGCGACGTGTGGACATCTTGCTCT 2112
               ||||| |||| || ||  || || || || |||  ||| ||  |||| | | |
Db   2507 CCATTGCCCATCCGGATCTTCACCAGCACGATGTGTGGAGTTTGGGATTGTGATGT 2566

Qy   2113 GGGAGACCTTCAGCCTGGGGGGCCTCGGGGGGCTCCCCCTATCCAACCTCAGCAATCAGTCAG 2172
               ||||| || ||| |   |||| |  ||||  || || || | | |||  | |||||| |||
Db   2567 GGGAGGTGCTGAGCTTTGGGGCAGCAAGCCTTGGGGAGATGAGCAATCAGGAGGTTATGA 2626
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; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12110
;   LENGTH: 19152
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-12110
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Query Match             8.4%;  Score 223.4; DB 4;  Length 19152;
Best Local Similarity  99.6%;  Pred. No. 2.4e-30;
Matches  224;  Conservative   0;  Mismatches  1;  Indels    0;  Gaps    0;

Qy     60 CGGAACAGCACTATGGGCTTCTTCTTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTG 119
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   18729 CAGAACAGCACTATGGGCTTCTTCTTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTG 18788

Qy    120 CAGCAAATGCAGAGAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGATGGCCCAG 179
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   18789 CAGCAAATGCAGAGAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGATGGCCCAG 18848

Qy    180 CGGGTCAAGAGTGACAGGGAGTATGCAGGAGACTGCTTCACCACAATGTCCCTGCAGGACAGT 239
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   18849 CGGGTCAAGAGTGACAGGGAGTATGCAGGAGACTGCTTCACCACAATGTCCCTGCAGGACAGT 18908

Qy    240 GGGGGCCAGAGCCGGGGCCATCAGCCCTGACAGCCCCATCAGTCAG 284
               |||||||||||||||||||||||||||||||||||||||||||||
Db   18909 GGGGGCCAGAGCCGGGGCCATCAGCCCTGACAGCCCCATCAGTCAG 18953
```

```
RESULT 8
US-09-949-016-15795
; Sequence 15795, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;   TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;   FILE REFERENCE: CL001307
;   CURRENT APPLICATION NUMBER: US/09/949,016
;   CURRENT FILING DATE: 2000-04-14
;   PRIOR APPLICATION NUMBER: 60/241,755
;   PRIOR FILING DATE: 2000-10-20
;   PRIOR APPLICATION NUMBER: 60/237,768
;   PRIOR FILING DATE: 2000-10-03
;   PRIOR APPLICATION NUMBER: 60/231,498
;   PRIOR FILING DATE: 2000-09-08
;   NUMBER OF SEQ ID NOS: 207012
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15795
;   LENGTH: 19153
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-15795
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Query Match             8.4%;  Score 223.4; DB 4;  Length 19153;
Best Local Similarity  99.6%;  Pred. No. 2.4e-30;
Matches  224;  Conservative   0;  Mismatches  1;  Indels    0;  Gaps    0;

Qy     60 CGGAACAGCACTATGGGCTTCTTCTTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTG 119
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   18729 CAGAACAGCACTATGGGCTTCTTCTTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTG 18788

Qy    120 CAGCAAATGCAGAGAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGATGGCCCAG 179
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   18789 CAGCAAATGCAGAGAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGATGGCCCAG 18848

Qy    180 CGGGTCAAGAGTGACAGGGAGTATGCAGGAGACTGCTTCACCACAATGTCCCTGCAGGACAGT 239
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   18849 CGGGTCAAGAGTGACAGGGAGTATGCAGGAGACTGCTTCACCACAATGTCCCTGCAGGACAGT 18908

Qy    240 GGGGGCCAGAGCCGGGGCCATCAGCCCTGACAGCCCCATCAGTCAG 284
               |||||||||||||||||||||||||||||||||||||||||||||
Db   18909 GGGGGCCAGAGCCGGGGCCATCAGCCCTGACAGCCCCATCAGTCAG 18953
```

Left column

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Qy  2173 AGTTTGTGGAGAAGGGGGGCCGTCTGCCCTGCCCAGAGCTGTGTCTGATGCCGTGTTCA 2232
         |||||||| |  |||          |   ||  || |||   |  |  |||
Db  2627 AGAGCATTGAGGATGGTACCGGTTGCCCCCTCTGTGGACTGCCCCTCTGTATG 2686

Qy  2233 GGCCTCATGGCAGTGCTGGGCCTATGAGCCTGGGCAGCCGGCCCAGCTTC 2282
         |||||||| || ||  |     ||| ||  ||||| |||||||||||
Db  2687 AGCTCATGAGAAGAACTGCTGGGCATGACCGTGCCCGCCGGCCCACACTTC 2736
```

RESULT 10
US-09-949-016-628
; Sequence 628, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 628
; LENGTH: 3921
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-628

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Query Match           6.9%;    Score 185.4;  DB 4;   Length 3921;
Best Local Similarity 55.1%;   Pred. No. 8.9e-24;
Matches 385;  Conservative  0;  Mismatches 311;  Indels  3;  Gaps  1;

Qy  1617 CTGGTGGCGGTGAAGTCTTGTGCGAGACGCTCCCACCTGACCTCAAGGCCAAGTTTCTA 1676
Db  2037 CCGGTGGCCATCAAGACGCTGAAAGCGCCGGCTACACAGAGAAGCAGCGAGTGGACTTCCTC 2096

Qy  1677 CAGGAAGCAGGAGGATCCTGAAGCAGTACAGCCACCCAAACTCGTGCGTCCATTGGTGTC 1736
Db  2097 GGGCGAGGCCCGCATCATGGCGCCAGTTGCAGCCACCAACATCATCCGCCTAGAGGGCGTC 2156

Qy  1737 TGCACCCAGAAGCAGCCCATCTACATCGTTGCTGCGGGTGAAGACTCTGCTGCAGATGGTGGG 1796
Db  2157 ATCTCCAAATACAAGGCCCATGATGATCATCACTGAGTACATGGCAGCTGCTGCGG 2216

Qy  1797 ACCTTCCTCCGACCACGGAGGGGGCCCGCT 1856
Db  2217 AAGTTCCTTCGGGAGAAGGATGGGCCAGTTCAGCGTGCTGGGCATGCTGCGG 2276

Qy  1857 GATGCAGCTGCTGGCATGGAGTACCTGGAGAGCAAGTGTCGCATCCACCGGGACCTGGCT 1916
Db  2277 GGCATCGCAGCTGGCATGGAGTACCTGGGCCCAACATATGTGACTTTGGCCCTGTCC 2336

Qy  1917 GCTCCGGAACTGCCTGGTGCAGAGGAAGAATGTCTGAGATCAGTGACTTTGGGATGTCC 1976
Db  2337 GCCCGCAACATCCTCGTCAACAGCAACCTGGTCTGCAAGGTGTCGACTTTGGCCCTGTCC 2396

Qy  1977 CGAGAGAAGCCGATGGGGTCTATGCAGCCT---CAGGGGGCCTCAGACAAGTCCCCGTG 2033
Db  2397 CGCGTGCTGGAGGAGGACGACCCCGAGGCCCATTTCCTGCCGGGAAGTTCACCTTCTGG 2456

Qy  2034 AAGTGGACCGCCACCTGAGGCCCTTAACTACGGCCGCTACCTCCTCCCCAACCTC 2093
Db  2457 CGCTGACCGCCCCCGCGAGGGCCCATTTCCTACCGGAAGTTCACCTTCCTGG 2516

Qy  2094 AGTTTGGCATCTTGCTCTCGGGAGACTTCAGCCTGGGGGCCCTCCCCTATCCCAACCTC 2153
Db  2517 AGCTTGGGCATTGTCATGTGTGGGAGGTGATGACCTATGGGCGAGCGGCCCTACTGGAGTTG 2576
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Right column

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Qy  2154 AGCAATCAGCAGACACCGGAGTTGTGTGGAGAAGGGGGGCCGTCTGCCCTGCCCAGAGCTG 2213
Db  2577 TCCAACCACGAGGTGATGAAAGCCATCAATGATGGCTTCCGGCCTCCCCACACCCATGGAC 2636

Qy  2214 TGTCCTGATGCCGTGTTCAGGCCTCATGAGCAGTCATGGCAGTGCTGGGCAGCGG 2273
Db  2637 TGCCCCTCCGCCATCCACCAGCTCACCAGTCATGATGCAGTGCTGGCAGCAGGCGTGCCCGCCGC 2696

Qy  2274 CCCAGCTTCAGCACCACCATCTACCAGGAGCTGCGAGAGCATC 2312
Db  2697 CCCAAGTTCGCTGACATCGTCAGCATCCTGGACATCCTGGGACAAGCTC 2735
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RESULT 11
US-09-949-016-2120
; Sequence 2120, Application US/0994901 6
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2120
; LENGTH: 3921
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2120

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Query Match           6.9%;    Score 185.4;  DB 4;   Length 3921;
Best Local Similarity 55.1%;   Pred. No. 8.9e-24;
Matches 385;  Conservative  0;  Mismatches 311;  Indels  3;  Gaps  1;

Qy  1617 CTGGTGGCGGTGAAGTCTTGTGCGAGACGCTCCCACCTGACCTCAAGGCCAAGTTTCTA 1676
Db  2037 CCGGTGGCCATCAAGACGCTGAAAGCCGGCTACACAGAGAAGCAGCGAGTGGACTTCCTC 2096

Qy  1677 CAGGAAGCGAGGATCCTGAAGCAGTACAGCCACCACCCAACATCGTGCGTCATTGGTGTC 1736
Db  2097 GGCGAGGCCCGGCCGCATCATGGGCGCCAGTTCAGCCACCAACATCATCCGCCTAGAGGGCTC 2156

Qy  1737 TGCACCCAGAAGCAGCCCATCTACACTCGTCATGGGGTGAAGACTCTGCTGCAGATGGTGGG 1796
Db  2157 ATCTCCAAATACAAGGCCCATGATGATCATCACTGAGTACATGGCAGCTGCTGGGCCTG 2216

Qy  1797 ACCTTCCTCCGCCACCGGAGGGGGCCCCGCT 1856
Db  2217 AAGTTCCTTCGGGAGAGGATGGGCCAGTTCAGCGTGCTGGGCATGCTGCGG 2276

Qy  1857 GATGCAGCTGCCTGGTGCATGGAGTACCTGGAGAGCAAGTGTCGCATCCACCGGGACCTGGCT 1916
Db  2277 GGCATCGCAGCTGGCATGGAGTACCTGGGCCCAACATATGTGACTTTGGCCCTGTCC 2336

Qy  1917 GCTCCGGAACTGCCTGGTGCAGAGGAAGAATGTCTGAGATCAGTGACTTTGGGATGTCC 1976
Db  2337 GCCCGCAACATCCTCGTCAACAGCAACCTGGTCTGCAAGGTGTCGACTTTGGCCCTGTCC 2396

Qy  1977 CGAGAGAAGCCGATGGGGTCTATGCAGCCT---CAGGGGGCCTCAGACAAGTCCCCGTG 2033
Db  2397 GCCCGCAACATCCTCGTCAACAGCAACCTGGTCTGCAAGGTGTCGACTTTGGCCCTGTCC 2456

Qy  1977 CGAGGGAAGCCGATGGGGTCTATGCAGCCT---CAGGGGGCCTCAGACAAGTCCCCGTG 2033
Db  2397 GCCGCAACATCCTCGTCAACAGCAACCTGGTCTGCAAGGTGTCGACTTTGGCCCTGTCC 2456

Qy  1977 CGAGAGGAAGCCGACCTGATGGGGTCTATGCAGCCT---CAGGGGGCCTCAGACAAGTGTGG 2033
Db  2397 CGCGGTGCTGGAGGAGGACGACCCCGAGGCCCTTAACTACGGCCGCTACCTCCTCCCCATC 2456

Qy  1977 CGAGAGAGGAAGCCGACCTGATGGGGTCTATGCAGCCT---CAGGGGGCCTCAGACGTGTGG 2033
Db  2397 GCCCGCAACATCCTCGTCAACAGCAACCTGGTCTGCAAGGTGTCGACTTTGGCCCTGTCC 2396

Qy  1977 CGAGAGGAAGCCGACGATGGGGTCTATGCAGCCT---CAGGGGGCCTCAGACAAGTCCCCGTG 2033
Db  2397 GCCCGCAACATCCTCGTCAACAGCAACCTGGTCTGCAAGGTGTCGACATCCCCATC 2456

Qy  1977 CGAGAGGAAGCCGATGGGGTCTATGCAGCCT---CAGGGGGCCTCAGACAAGTCCCCGTG 2033
Db  2397 GCCGTGCTGGAGGAGGACGACCCCGAGGCCCTTAACTACGGCCGCTACCTCCTCCCCATC 2456

Qy  1977 AAGTGGACCGCCACCTGAGGCCCTTAACTACGGCCGCTACCTCCTCCCCATC 2033
Db  2397 CGGGTGCTGGAGGAGGACGACCCCGAGGCCCTTAACTACGGCCGCTACCTCCTCCCCATC 2456

Qy  2034 AAGTGGACCGCCACCTGAGGCCCTTAACTACGGCCGCTACCTCCTCCCCGTG 2093
Db  2397 CGGGTGCTGGAGGAGGACGACCCCGAGGCCCTTAACTACGGCCGCTACCTCCTCCCCATC 2456
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Db  2457 CGCTGGACGCGCCCGGAGGCCATTCCTACCGGAAGTTCACCTCTGCCAGCGACGTGTGG 2516
Qy  2094 AGCTTTGGCATCTTGCTCTGGGAGACCTTCAGCCTGGGGGCCTCCCCTATCCCAACCTC 2153
Db  2517 AGCTTTGGCATTGTCATGTGGGAGGTGATGACCTATGGCAGCGGCCCTACTGGGAGTTG 2576
Qy  2154 AGCAATCAGACAGCACGGGAGTTTGTGGAGAAGGGGCCGTCTGCCCCAGAGCTG 2213
Db  2577 TCCAACCACGAGGTGATGAAAGCCATCAATGATGGCTTCCGGCTTCCCACCACCATGGAC 2636
Qy  2214 TGTCTGATGCCGTGTTCAGGCTCATGGAGCAGTGCTGGGCCTATGAGCCTGGGCAGCGG 2273
Db  2637 TGCCCCTCCCGCCATCTACCAGCTCATGATGCAGTCGTGCTGGCAGCAGGAGCGTGCCCGCCGC 2696
Qy  2274 CCCAGCTTCAGCAGGACTGACCATCTACCAGGAGCTGCAGAGCATC 2312
Db  2697 CCCAAGTTCGCTGACATCGTGACATCCTGCAGCAAGCTC 2735
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RESULT 12
US-09-949-016-5662
; Sequence 5662, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SEQ ID NO 5662
; LENGTH: 3386
; TYPE: DNA
; ORGANISM: Human
; SOFTWARE: FastSEQ for Windows Version 4.0
US-09-949-016-5662

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Query Match            6.5%;  Score 174.6;  DB 4;  Length 3386;
Best Local Similarity  54.7%;  Pred. No. 7.1e-22;
Matches  392;  Conservative  0;  Mismatches 319;  Indels 6;  Gaps 2;

Qy  1569 GGGAACTTTGGCGAAGTGTTCAGCGGACGGCCTGCGACGCCGACACACCCTGGTTGGCGTG 1628
Db  1386 GGGGGAGGTCTATGAAGGTGCTACACAACAAATCACAAAGGGGAGAAAATCAATGTAGTCTGTC 1445
Qy  1629 AAGTCTTGTCGAGAGAGACGCGCTCCCACCTGACCTCAAGGCCAAGTTTCTACAGGAAGCGAGG 1688
Db  1446 AAGAACCTGCAAGAAAGACTGCACTCTGGACAACAAGAGAAGTTCATGAGCCAGCAGCAGTG 1505
Qy  1689 ATCCTGAAGCAGTACAGCCACCCCAACATCGTGCGGTCTCATTGGTGTCTGCACCCAGAAG 1748
Db  1506 ATCATGAAGAACCTCGACCACCCCGCACATCGTGAAGCTGATCGGCAT---CATTGAAGAG 1562
Qy  1749 CAGCCCATCTACATCGTCATGGAGCTTCATGGAGGGGGCGACTTCCTCCGC 1808
Db  1563 GAGCCCACCTACCTGGATCATCATGAATTGTATCCCTATGGGAGCTGGGCCCACTACCTGGAG 1622
Qy  1809 ACGGAGGGGGCCCCGCTCGCCGGGGGTGAAGACTCTGCTGCAGATGTGGGGGATGCAGCTGCT 1868
Db  1623 CGGAACAAGAACTCCCTGAAGGTGCTCACCCTCGTGTCACTGCAGATATGCAAA 1682
Qy  1869 GGCATGGAGTACCTGGAAGCAGAAGTGCTGCATCCACCGGACCTGGCTGCTCGGAACTGC 1928
Db  1683 GCCATGGCCTACCTGGAGCAGAGAGCATCAACTGCCGTGACCAGGGACACATTGCTGTCGTCCCGGAACAATC 1742
Qy  1929 CTGGTGACAGAGAAGAATGTCCTGAAGATCAGTGACTTTGGGATGTCCCGAGAGGAAGCC 1988
```

RESULT 13
US-08-357-642A-2
; Sequence 2, Application US/08357642A
; Patent No. 5837524
; GENERAL INFORMATION:
; APPLICANT: Sima Lev
; APPLICANT: Joseph Schlessinger
; TITLE OF INVENTION: PYK2 RELATED PRODUCTS
; TITLE OF INVENTION: AND METHODS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/357,642A
; FILING DATE: December 15, 1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/070
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3416
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: nucleic
US-08-357-642A-2

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Query Match            6.5%;  Score 174.6;  DB 2;  Length 3416;

Db  1743 CTGGTGGCCTCCCTGAGTGTGTGAAGCTGGGGGACTTTGGTCTTTCCGGTACATTGAG 1802
Qy  1989 GATGGGGTCTATGCAGCCTCAGGGGAGGCCTCAGACAAGTCCCGTGAAGTGACCGCACCT 2048
Db  1803 GACGAGGACTAT---TACAAAGCCTCTGTGACTCGTCTCCCATCAAATGGATGTCCCCA 1859
Qy  2049 GAGGCCCTTAACTACGGCCGCTACTCCTCCGAAAGCGACGTGTGGAGCTTTGGCATCTTG 2108
Db  1860 GAGTCCATTAACTTCCGACGCTTCACGACAGCCAGTGAGCGTCGGATGTTCGCCGTGTGC 1919
Qy  2109 CTCTGGGAGACCTTCAGCCTGGGGGCCTCCCCTATCCCAAGCCCTGCCCAGAGCTGTGTG 2168
Db  1920 ATGTGGGAGATCTGAGCTTTGGGAAGCAGCCTGAGCTTTGGGAAGCAGCAACAAGGAGATGTC 1979
Qy  2169 CGGGAGTTTGTGGAGAAGGGGGCCGTCTGCCCGTCCCAAGCCTGCTCGGAGCTGTGTCCTGCCAGTGCCGTG 2228
Db  1980 ATCGGGGTGCTGGAGAAAGGAGACCGGCTGCTGGGGACTACGACCCCAGTGACCCGCCCGCTTCACC 2039
Qy  2229 TTCAGGCTCATGGACGAGTCGGCCTATGAGCCTGGAGGCCAGGCCGCCCAGCTTCAGC 2285
Db  2040 TATACCCTCATGGACCCGCTCTGGGACTACGACCCCAGTGACCCCAGTGACCCGCCGCTTCACC 2096
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Best Local Similarity 54.7%;   Pred. No. 7.1e-22;
Matches 392; Conservative 0; Mismatches 319; Indels 6; Gaps 2;

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Qy   1569 GGGAACTTTGGCGAAGTGTTCAGCGGACGCCTGCGAGCCGACAACACCCTGGTGGCGGTG 1628
               ||  |||| ||||  ||||||||||||||||||| ||||||| ||| |||| || |||
Db   1416 GGGGAGGTCTATGAAGGTGTCTACACAAATCACAAAGGGGAGAAAATCAATGTAGCTGTC 1475

Qy   1629 AAGTCTTGTCGAGAGACGCTCCCACCTGACCTCAAGGCCAAGTTCTACAGGAAGCGGAGG 1688
               ||||  |||  |||| |||||||  || |||||||||| ||| |||||||||||| |
Db   1476 AAGACCTGCAAGAAAGACTGCACTCTGGACAACAAGGAGAGTTCATGAGCGAGGCAGTG 1535

Qy   1689 ATCCTGAAGCAGTACAGCCACCCAACATGTGCGTCTCATTGGTGTCTGCACCCAGAAG 1748
               |||||||||||||   |||   |||| || |||  |||||  |   | |||||||
Db   1536 ATCATGAAGAACCTGCACCACCCGCACATCGTGAAGCTGATCGGCAT--CATTGAAGAG 1592

Qy   1749 CAGCCCATCTACATCGTCATGGAGCTTGTGCAGGGGGCGACTTCCTGACCTTCCTCCGC 1808
               |  || ||| || || |||||  ||  || |||||| |||| |||||| ||  |
Db   1593 GAGCCCACCTGCATCATCATGAATTGTATCCCTGCTGGGGAGCTGGGCACTACCTGGAG 1652

Qy   1809 ACGGAGGGGGCCCGCCTGCTCGCTCGCAGATCGTTGGGGGGATGCAGCTGCT 1868
               |||| || ||||||| || ||  ||||||| |||  |||||||| |||||||
Db   1653 CGGAACAAGAACTCCCTGAAGGTGCTCACCCTGTCTGTCGAGAACAAGGATGTC 1712

Qy   1869 GGCATGAGTACCTGGAGAGCAAGTGCTCATCCACCGGACCTGGCTGTCCGGAACTGC 1928
               || ||| ||| |||||||| || ||| ||||  ||  |||||||||||  ||| |||
Db   1713 GCCATGGCCTACCTGGAGAGCAGCATCAACTGCGTGCACAGGGACATTGGGACAACATC 1772

Qy   1929 CTGGTGACAGAGAAGAATGTCCTGAAGATCAGTGACTTTGGAGTGCTCCCGAGAGGAGCC 1988
               ||||||| ||||||||||||  |||||||||| ||| || ||||| ||||||| |||
Db   1773 CTGGTGCCTCCCCCTGAGTGTGAAGCTGGGGACTTGGCTCTTTCCCGGTACATTGAG 1832

Qy   1989 GATGGGGTCTATGCAGCCTCAGCGGCGCCTCAGACAAGTCCCCGTGAAGTGACCGCACCT 2048
               |||||||||||||| |||||||   |||||| ||||||| |||||||||||| ||||||
Db   1833 GACGAGGACTAT--TACAAAGCCTCTGACTCGTCTCCCATCAAATGATGTCCCCA 1889

Qy   2049 GAGGGCCCTTAACTACACGGCCGCTACTCCTCCGAAAGCCACGTGTGGAGCTTTGCATCTTG 2108
               ||||| | ||||  ||| ||| |||| |||||||||||| |||| ||| || |||||
Db   1890 GAGTCCATTAACTTCCGACGCTTCAGACAGCCAGTGACGTCGGATGTTCGCCGTGTGC 1949

Qy   2109 CTCTGGGAGACCTTCAGCCTTGGGGGGCCTCGGGGGGCCTCCCCTATCCCAACCTCAGCAACTGCAGCAGACA 2168
               |||||| |||||||| |||  || |||| |||||||||| | ||||||| |||
Db   1950 ATGTGGGAGATCCTGAGCTTTGGAGAAGCCTGGCTGGCTGGAGAACAAGGATGTC 2009

Qy   2169 CGGGAGTTTGTGGAGAAGGGGGTCCTGCCCGGGGTGTCTGATGCCGTG 2228
               ||||| |||||||||||| ||| ||| |||  |||| |||||||||
Db   2010 ATCGGGGGTGCTGGAGAAAGAGACCGGCGCTGCCAAGCCTGATCTCTGTCTGCACCGGTGCTCCTT 2069

Qy   2229 TTCAGGCTCATGAGGCAGTGCTGGGCCTATGAGCCTGGGCAGCCGGCCCAGCTTCAGC 2285
               || |||||||||||||||| || ||||||| ||||  ||||||||||||
Db   2070 TATACCCTCATGACCCGCTGCTGGGACTACGACCCCAGTGACCACTGGGCTTCACC 2126
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RESULT 14
US-08-460-626-2
; Sequence 2, Application US/08460626
; Patent No. 5837815
; GENERAL INFORMATION:
; APPLICANT: SIMA LEV
; TITLE OF INVENTION: PYK-2 RELATED PRODUCTS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Lyon & Lyon
;   STREET: 633 West Fifth Street
;   STREET: Suite 4700
;   CITY: Los Angeles
;   STATE: California
;   COUNTRY: U.S.A.
;   ZIP: 90071-2066
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;   MEDIUM TYPE: storage

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/460,626
 FILING DATE: June 2, 1995
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/357,642
 FILING DATE: December 15, 1994
ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 211/121
TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
  LENGTH: 3416
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
US-08-460-626-2

Query Match 6.5%; Score 174.6; DB 2; Length 3416;
Best Local Similarity 54.7%; Pred. No. 7.1e-22;
Matches 392; Conservative 0; Mismatches 319; Indels 6; Gaps 2;

Qy   1809 ACGGAGGGGGCCCGCTCGCGGTGAAGACTCTGCTCGCAGATGTGGGGGATCGCAGCGTGCT 1868
            ||||| |||| ||||| ||||||| |||| |||||||| ||| | |||||||
Db   1653 CGGACAAGAACTCCCTGAAGGTGCTCACCCTCGTCGTGACTCACTGCAGATATGCAAA   1712

Qy   1869 GGCATGGAGTACCTGGAGACGAAGTGCTGCATCCACCGGGACCTGGCTGCTCGGAACTGC 1928
            |||||| ||||||||||| ||| |||| ||||||||||||||||| |||||||
Db   1713 GCCATGGCCTACCTGGAGAGCATCAACTGCGTGCACAGGGACATTGCTGTCGTCCGGAACATC 1772

Qy   1929 CTGGTGCACAGAGAAGAAGAATGTCCTGAAGATCAGTCAGTCCCGAGAGGAAGCC 1988
            |||||| ||||| |||| | || |
Db   1773 CTGGTGGCCTCCCCTGAGTGTGTGAAGCTGGGGGACTTTGGTCTTTCCCGGTACATTGAG 1832

Qy   1989 GATGGGGTCTATGCAGCCCGCTACTCCTCCGAAAGCGACGTGTGGAGCTTTGGCATCTTG 2048
            || | || ||| || ||| ||| || ||||| | | |
Db   1833 GACGAGGACTAT---TACAAAGCCTCTGTGACTCGTCTCCCCATCAAATGATGTCCCCA 1889

Qy   2049 GAGGCCCTTAACTACGGCCCGCTACTCCTCCGAAACGACCGTGTGGAGCTTTGGCATCTTG 2108
            |||||| | || || | || | | ||
Db   1890 GAGTCCATTAACTTCCGACGCTTCACGACAGCCAGTGACGTCTGGAGTTCGCCGTGTGC 1949

Qy   2109 CTCTGGGAGACCTTCAGCCTGGGGGTC 2168
            ||||||| | |||||
Db   1950 ATGTCGGGAGATCCTGAGCTTTGGGAAGCAGCCCTTCTTCTTCTGGCTGGAGAACAAGGATGTC 2009

Qy   2169 CGGGAGTTTGTGGAGAAGGGGGCCGTCTTGCCCTGCCTGTCGTCTCGATGCCGTG 2228
            |||||| ||| || |||||||||||||
Db   2010 ATCGGGGTGCTGCAAGAAAGGAGACCGGCTTGCCCAAGCCTGATCTTCGTCTGTCACCGGTCCTT 2069

Qy   2229 TTCAGGCTCATGGAGCAGTCGTGGGCCTATGAGCCTGGGCAGCGGGCCCAGCTTCAGC 2285
            ||| |||| ||||||| | |||||||||||||||| ||||||||||||||
Db   2070 TATACCCTCATGCACCGCTGCTGGGACTACGACCCCAGTGACCGGCCCCGCTTCACC 2126

Search completed: August   9, 2005, 21:35:02
Job time : 595.209 secs

Qy   2229 TTCAGGCTCATGGAGCAGTCGTGGGCCTATGAGCCTGGGCAGCGGGCCCAGCTTCAGC 2285
            ||| |||| ||||||| | |||||||||||||||| ||||||||||||||
Db   2070 TATACCCTCATGCACCGCTGCTGGGACTACGACCCCAGTGACCGGCCCCGCTTCACC 2126

RESULT 15
US-09-016-434-1483
; Sequence 1483, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1483:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3416 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g988304
US-09-016-434-1483

Query Match   6.5%; Score 174.6; DB 4; Length 3416;
Best Local Similarity 54.7%; Pred. No. 7.1e-22;
Matches 392; Conservative   0; Mismatches 319; Indels   6; Gaps   2;

Qy   1569 GGGAACTTTGGCGAAGTGTTCAGCGAGCCGCCTGCGAGCCGACAACACCCTGGTGGCGGTG 1628
            |||| ||||| | || | ||| |||| ||||||| |||
Db   1416 GGGGAGGTCTATGAAGGTGTCTACACAGAAGTCACAAAGGGAGAAAATCAATGTAGCTGTC 1475

Qy   1629 AAGTCTTGTCGAGAGACGCTCCCACCTGACCTCAAGGCCAAGTTCTACAGGAGCGAGG 1688
            ||||| | || || |||| ||||
Db   1476 AAGACCTGCAAGAAGACTGCACTCTGGACAACAAGGAGAAGTTCATGCGAGCCAGCAGTG 1535

Qy   1689 ATCCTGAAGCAGTACAGCCACCCCAAACATCGTGCGTCTCATTGGTGTCTGCACCCAGAAG 1748
            ||| ||||| ||| | || | | || || | | | |||| ||||
Db   1536 ATCATGAAGAAACCTCGACCACCCCACACATCGTGAAGCTGAAGCTGGCAT---CATTGAAGAG 1592

Qy   1749 CAGCCCATCTACACTCGTCGTCATGGAGCTGTGTCGCAGGGGGGCGACTTCCTCCCTCCGC 1808
            |||||| | || | ||| || || || || |||
Db   1593 GAGCCCACCTGGATCATCATGGAATTGTATCCCTATGGGGAGCTGGGAGCTGGGCCACTACCTGGAG 1652